## Juan D RamÃ-rez

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3039263/publications.pdf

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191 papers 5,880 citations

76196 40 h-index 65 g-index

212 all docs

212 docs citations

times ranked

212

5235 citing authors

#	Article	IF	CITATIONS
1	Amplicon-based next-generation sequencing reveals the co-existence of multiple Leishmania species in patients with visceral leishmaniasis. International Journal of Infectious Diseases, 2022, 115, 35-38.	1.5	8
2	Striking lineage diversity of severe acute respiratory syndrome coronavirus 2 from non-human sources. One Health, 2022, 14, 100363.	1.5	3
3	Deciphering the Association among Pathogenicity, Production and Polymorphisms of Capsule/Melanin in Clinical Isolates of Cryptococcus neoformans var. grubii VNI. Journal of Fungi (Basel, Switzerland), 2022, 8, 245.	1.5	3
4	Food for thought: Eating before saliva collection and interference with SARSâ€CoVâ€2 detection. Journal of Medical Virology, 2022, 94, 2471-2478.	2.5	6
5	Epidemiological Dynamics of SARS-CoV-2 Variants During Social Protests in Cali, Colombia. Frontiers in Medicine, 2022, 9, 863911.	1.2	4
6	Hotspots for SARS oVâ€2 Omicron variant spread: Lessons from New York City. Journal of Medical Virology, 2022, 94, 2911-2914.	2.5	6
7	Phylogenetic relationships and evolutionary patterns of the genus Psammolestes Bergroth, 1911 (Hemiptera: Reduviidae: Triatominae). Bmc Ecology and Evolution, 2022, 22, 30.	0.7	3
8	Evaluation of five different rapid immunochromatographic tests for canine leishmaniosis in Spain. Acta Tropica, 2022, 229, 106371.	0.9	5
9	Filling the gaps in <i>Leishmania naiffi</i> and <i>Leishmania guyanensis</i> genome plasticity. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	2
10	Robust clinical detection of SARS oVâ€2 variants by RTâ€PCR/MALDIâ€TOF multitarget approach. Journal of Medical Virology, 2022, 94, 1606-1616.	2.5	9
11	First report and genome sequencing of SARS-CoV-2 in a cat (Felis catus) in Colombia. Memorias Do Instituto Oswaldo Cruz, 2022, 117, e210375.	0.8	2
12	RT-PCR and Matrix-Assisted Laser Desorption-Ionization Time-of-Flight Mass Spectrometry Diagnostic Target Performance Reflects Circulating Severe Acute Respiratory Syndrome Coronavirus 2 Variant Diversity in New York City. Journal of Molecular Diagnostics, 2022, , .	1.2	3
13	Detangling the Crosstalk Between Ascaris, Trichuris and Gut Microbiota: WhatÂ's Next?. Frontiers in Cellular and Infection Microbiology, 2022, 12, .	1.8	5
14	The never-ending global emergence of viral zoonoses after COVID-19? The rising concern of monkeypox in Europe, North America and beyond. Travel Medicine and Infectious Disease, 2022, 49, 102362.	1.5	84
15	Genome plasticity driven by aneuploidy and loss of heterozygosity in Trypanosoma cruzi. Microbial Genomics, 2022, 8, .	1.0	5
16	Towards environmental detection of Chagas disease vectors and pathogen. Scientific Reports, 2022, 12,	1.6	3
17	Discrete typing units of Trypanosoma cruzi: Geographical and biological distribution in the Americas. Scientific Data, 2022, 9, .	2.4	18
18	Genomic Diversity of SARS-CoV-2 Omicron Variant in South American Countries. Viruses, 2022, 14, 1234.	1.5	7

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19	Pan-stage real-time PCR for quantitation of Trypanosoma cruzi parasitic loads in blood samples. International Journal of Infectious Diseases, 2022, 122, 310-312.	1.5	1
20	Safety and efficacy of convalescent plasma for severe COVID-19: a randomized, single blinded, parallel, controlled clinical study. BMC Infectious Diseases, 2022, 22, .	1.3	9
21	Estimating the genetic structure of Triatoma dimidiata (Hemiptera: Reduviidae) and the transmission dynamics of Trypanosoma cruzi in Boyacá, eastern Colombia. PLoS Neglected Tropical Diseases, 2022, 16, e0010534.	1.3	5
22	Latin America: Situation and preparedness facing the multi-country human monkeypox outbreak. The Lancet Regional Health Americas, 2022, 13, 100318.	1.5	18
23	Phylogenomic analysis of the monkeypox virus (MPXV) 2022 outbreak: Emergence of a novel viral lineage?. Travel Medicine and Infectious Disease, 2022, 49, 102402.	1.5	118
24	The arrival and spread of SARSâ€CoVâ€2 in Colombia. Journal of Medical Virology, 2021, 93, 1158-1163.	2.5	33
25	Microbial Communities' Characterization in Urban Recreational Surface Waters Using Next Generation Sequencing. Microbial Ecology, 2021, 81, 847-863.	1.4	12
26	Systematic review on the biology, ecology, genetic diversity and parasite transmission potential of Panstrongylus geniculatus (Latreille 1811) in Latin America. Memorias Do Instituto Oswaldo Cruz, 2021, 116, e200528.	0.8	11
27	Updating changes in human gut microbial communities associated with <i>Clostridioides difficile</i> infection. Gut Microbes, 2021, 13, 1966277.	4.3	5
28	Lemierre's syndrome associated with hypervirulent Klebsiella pneumoniae: A case report and genomic characterization of the isolate. IDCases, 2021, 25, e01173.	0.4	3
29	Association between physical activity and changes in intestinal microbiota composition: A systematic review. PLoS ONE, 2021, 16, e0247039.	1.1	66
30	Will the emergent SARSâ€CoV2 B.1.1.7 lineage affect molecular diagnosis of COVIDâ€19?. Journal of Medical Virology, 2021, 93, 2566-2568.	2.5	33
31	Gut microbiota profiles in diarrheic patients with co-occurrence of Clostridioides difficile and Blastocystis. PLoS ONE, 2021, 16, e0248185.	1.1	19
32	Phylogenomic Evidence of Reinfection and Persistence of SARS-CoV-2: First Report from Colombia. Vaccines, 2021, 9, 282.	2.1	14
33	Repeat-Driven Generation of Antigenic Diversity in a Major Human Pathogen,ÂTrypanosoma cruzi. Frontiers in Cellular and Infection Microbiology, 2021, 11, 614665.	1.8	25
34	Autoantibodies against the immunodominant sCha epitope discriminate the risk of sudden death in chronic Chagas cardiomyopathy. Annals of the New York Academy of Sciences, 2021, 1497, 27-38.	1.8	0
35	Deciphering the introduction and transmission of SARS-CoV-2 in the Colombian Amazon Basin. PLoS Neglected Tropical Diseases, 2021, 15, e0009327.	1.3	6
36	Characterizing SARS-CoV-2 genome diversity circulating in South American countries: Signatures of potentially emergent lineages?. International Journal of Infectious Diseases, 2021, 105, 329-332.	1.5	16

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37	Gut microbiota composition in health-care facility-and community-onset diarrheic patients with Clostridioides difficile infection. Scientific Reports, 2021, 11, 10849.	1.6	8
38	The Constant Threat of Zoonotic and Vector-Borne Emerging Tropical Diseases: Living on the Edge. Frontiers in Tropical Diseases, 2021, 2, 676905.	0.5	13
39	Evaluation of the diagnostic performance of nine commercial RTâ€PCR kits for the detection of SARSâ€CoVâ€2 in Colombia. Journal of Medical Virology, 2021, 93, 5618-5622.	2.5	14
40	RTâ€PCR/MALDIâ€TOF mass spectrometryâ€based detection of SARSâ€CoVâ€2 in saliva specimens. Journal of Medical Virology, 2021, 93, 5481-5486.	2.5	29
41	COVID-19 and helminth infection: Beyond the Th1/Th2 paradigm. PLoS Neglected Tropical Diseases, 2021, 15, e0009402.	1.3	14
42	Contrasting SARS-CoV-2 RNA copies and clinical symptoms in a large cohort of Colombian patients during the first wave of the COVID-19 pandemic. Annals of Clinical Microbiology and Antimicrobials, 2021, 20, 39.	1.7	10
43	Epidemiological and Molecular Characterization of Blastocystis Infection in Children Attending Daycare Centers in MedellÃn, Colombia. Biology, 2021, 10, 669.	1.3	31
44	Spatial and Temporal Variability of Visceral Leishmaniasis in Colombia, 2007 to 2018. American Journal of Tropical Medicine and Hygiene, 2021, 105, 144-155.	0.6	4
45	Clinical and Epidemiological Characterization of Acute Chagas Disease in Casanare, Eastern Colombia, 2012–2020. Frontiers in Medicine, 2021, 8, 681635.	1.2	12
46	Evolution and Epidemic Spread of SARS-CoV-2 in Colombia: A Year into the Pandemic. Vaccines, 2021, 9, 837.	2.1	11
47	Describing the intestinal microbiota of Holstein Fasciola-positive and -negative cattle from a hyperendemic area of fascioliasis in central Colombia. PLoS Neglected Tropical Diseases, 2021, 15, e0009658.	1.3	8
48	Cluster characterization of SARS-CoV-2 in military personnel deployed to Egypt and subsequent introduction of B.1.1.7 and C.36 lineages to Colombia. Journal of Travel Medicine, 2021, 28, .	1.4	1
49	Comparative analysis of the transcriptional responses of five Leishmania species to trivalent antimony. Parasites and Vectors, 2021, 14, 419.	1.0	3
50	Identification of Multiple Blastocystis Subtypes in Domestic Animals From Colombia Using Amplicon-Based Next Generation Sequencing. Frontiers in Veterinary Science, 2021, 8, 732129.	0.9	59
51	Genetic diversity and population structure of Rhipicephalus sanguineus sensu lato across different regions of Colombia. Parasites and Vectors, 2021, 14, 424.	1.0	13
52	Revisiting the heterogeneous global genomic population structure of Leishmania infantum. Microbial Genomics, 2021, 7, .	1.0	2
53	SARS-CoV-2 in Transit: Characterization of SARS-CoV-2 Genomes From Venezuelan Migrants in Colombia. International Journal of Infectious Diseases, 2021, 110, 410-416.	1.5	5
54	Poverty, Migration, and Chagas Disease. Current Tropical Medicine Reports, 2021, 8, 52-58.	1.6	20

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55	The potential risk of enzootic Trypanosoma cruzi transmission inside four training and re-training military battalions (BITER) in Colombia. Parasites and Vectors, 2021, 14, 519.	1.0	6
56	Development of an Amplicon-Based Next-Generation Sequencing Protocol to Identify <i>Leishmania </i> Species and Other Trypanosomatids in Leishmaniasis Endemic Areas. Microbiology Spectrum, 2021, 9, e0065221.	1.2	15
57	Editorial: Advances in the Molecular Biology of Trypanosomatid Pathogens: New Strategies Against Ancient Enemies. Frontiers in Cellular and Infection Microbiology, 2021, 11, 777008.	1.8	O
58	Human urogenital myiasis caused by the â€rat-tailed' larvae of Palpada scutellaris (Fabricius, 1805) in Santander, eastern Colombia: A case report. Parasitology International, 2021, 87, 102496.	0.6	2
59	Molecular and Clinical Aspects of Chronic Manifestations in Chagas Disease: A State-of-the-Art Review. Pathogens, 2021, 10, 1493.	1.2	12
60	Temporal Variation of the Presence of Rhodnius prolixus (Hemiptera: Reduviidae) Into Rural Dwellings in the Department of Casanare, Eastern Colombia. Journal of Medical Entomology, 2020, 57, 173-180.	0.9	7
61	Genomic analyses reveal moderate levels of ploidy, high heterozygosity and structural variations in a Colombian isolate of Leishmania (Leishmania) amazonensis. Acta Tropica, 2020, 203, 105296.	0.9	13
62	Microbiota characterization in Blastocystis-colonized and Blastocystis-free school-age children from Colombia. Parasites and Vectors, 2020, 13, 521.	1.0	15
63	Complex ecological interactions across a focus of cutaneous leishmaniasis in Eastern Colombia: novel description of <i>Leishmania</i> species, hosts and phlebotomine fauna. Royal Society Open Science, 2020, 7, 200266.	1.1	10
64	Development of a Multilocus Sequence Typing Scheme for Giardia intestinalis. Genes, 2020, 11, 764.	1.0	5
65	Understanding the oral transmission of Trypanosoma cruzi as a veterinary and medical foodborne zoonosis. Research in Veterinary Science, 2020, 132, 448-461.	0.9	24
66	Human Chagas-Flow ATE-lgG1 for advanced universal and Trypanosoma cruzi Discrete Typing Units-specific serodiagnosis of Chagas disease. Scientific Reports, 2020, 10, 13296.	1.6	4
67	Genetic Diversity Among SARS-CoV2 Strains in South America may Impact Performance of Molecular Detection. Pathogens, 2020, 9, 580.	1.2	28
68	Transcriptional remodeling during metacyclogenesis in Trypanosoma cruzi I. Virulence, 2020, 11, 968-979.	1.8	11
69	Genomic Diversification, Structural Plasticity, and Hybridization in Leishmania (Viannia) braziliensis. Frontiers in Cellular and Infection Microbiology, 2020, 10, 582192.	1.8	21
70	Identification of blood-feeding sources in Panstrongylus, Psammolestes, Rhodnius and Triatoma using amplicon-based next-generation sequencing. Parasites and Vectors, 2020, 13, 434.	1.0	24
71	Identification of Aedes (Diptera: Culicidae) Species and Arboviruses Circulating in Arauca, Eastern Colombia. Frontiers in Ecology and Evolution, 2020, 8, .	1.1	9
72	Succinate dehydrogenase gene as a marker for studying Blastocystis genetic diversity. Heliyon, 2020, 6, e05387.	1.4	4

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73	Epidemiological characterisation of asymptomatic carriers of COVID-19 in Colombia: a cross-sectional study. BMJ Open, 2020, 10, e042122.	0.8	9
74	Distribution, treatment outcome and genetic diversity of Leishmania species in military personnel from Colombia with cutaneous leishmaniasis. BMC Infectious Diseases, 2020, 20, 938.	1.3	13
75	SARS-CoV-2 spread across the Colombian-Venezuelan border. Infection, Genetics and Evolution, 2020, 86, 104616.	1.0	16
76	Slight temperature changes cause rapid transcriptomic responses in Trypanosoma cruzi metacyclic trypomastigotes. Parasites and Vectors, 2020, 13, 255.	1.0	11
77	Potential negative effects of the free use of chloroquine to manage COVIDâ€19 in Colombia. Journal of Medical Virology, 2020, 92, 2254-2256.	2.5	3
78	Taxonomy, Evolution, and Biogeography of the Rhodniini Tribe (Hemiptera: Reduviidae). Diversity, 2020, 12, 97.	0.7	12
79	Intraspecific Genomic Divergence and Minor Structural Variations in Leishmania (Viannia) panamensis. Genes, 2020, 11, 252.	1.0	17
80	An interactive database of Leishmania species distribution in the Americas. Scientific Data, 2020, 7, 110.	2.4	37
81	Occurrence of Blastocystis in Patients with Clostridioides difficile Infection. Pathogens, 2020, 9, 283.	1.2	13
82	Human Papillomavirus (HPV69/HPV73) Coinfection associated with Simultaneous Squamous Cell Carcinoma of the Anus and Presumed Lung Metastasis. Viruses, 2020, 12, 349.	1.5	3
83	Presumptive asymptomatic COVID-19 carriers' estimation and expected person-to-person spreading among repatriated passengers returning from China. Travel Medicine and Infectious Disease, 2020, 37, 101688.	1.5	7
84	Usefulness of autocidal gravid ovitraps for the surveillance and control of Aedes (Stegomyia) aegypti (Diptera: Culicidae) in eastern Colombia. Medical and Veterinary Entomology, 2020, 34, 379-384.	0.7	3
85	Culture-free genome-wide locus sequence typing (GLST) provides new perspectives on Trypanosoma cruzi dispersal and infection complexity. PLoS Genetics, 2020, 16, e1009170.	1.5	7
86	SARS-CoV-2 in the Amazon region: A harbinger of doom for Amerindians. PLoS Neglected Tropical Diseases, 2020, 14, e0008686.	1.3	22
87	Species-dependent variation of the gut bacterial communities across Trypanosoma cruzi insect vectors. PLoS ONE, 2020, 15, e0240916.	1.1	6
88	Minor temperature shifts do not affect chromosomal ploidy but cause transcriptomic changes in Leishmania braziliensis promastigotes in vitro. Memorias Do Instituto Oswaldo Cruz, 2020, 115, e190413.	0.8	1
89	Persistence of clonal azole-resistant isolates of Candida albicans from a patient with chronic mucocutaneous candidiasis in Colombia. Journal of Global Infectious Diseases, 2020, 12, 16.	0.2	8
90	Molecular detection and genotyping of intestinal protozoa from different biogeographical regions of Colombia. PeerJ, 2020, 8, e8554.	0.9	38

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91	Transcriptomic changes across the life cycle of <i>Trypanosoma cruzi II</i> . PeerJ, 2020, 8, e8947.	0.9	8
92	Integrated genomic epidemiology and phenotypic profiling of Clostridium difficile across intra-hospital and community populations in Colombia. Scientific Reports, 2019, 9, 11293.	1.6	12
93	Ecological niche modelling for predicting the risk of cutaneous leishmaniasis in the Neotropical moist forest biome. PLoS Neglected Tropical Diseases, 2019, 13, e0007629.	1.3	29
94	Major changes in chromosomal somy, gene expression and gene dosage driven by SbIII in Leishmania braziliensis and Leishmania panamensis. Scientific Reports, 2019, 9, 9485.	1.6	42
95	Transcriptional responses of Leishmania (Leishmania) amazonensis in the presence of trivalent sodium stibogluconate. Parasites and Vectors, 2019, 12, 348.	1.0	25
96	Comparative genomics identifies potential virulence factors in <i>Clostridium tertium</i> and <i>C. paraputrificum</i> Virulence, 2019, 10, 657-676.	1.8	13
97	Dissecting the Heterogeneous Population Genetic Structure of Candida albicans: Limitations and Constraints of the Multilocus Sequence Typing Scheme. Frontiers in Microbiology, 2019, 10, 1052.	1.5	9
98	Genetic diversification of Panstrongylus geniculatus (Reduviidae: Triatominae) in northern South America. PLoS ONE, 2019, 14, e0223963.	1.1	11
99	Genomic epidemiology supports multiple introductions and cryptic transmission of Zika virus in Colombia. BMC Infectious Diseases, 2019, 19, 963.	1.3	12
100	Evaluation of four rapid diagnostic tests for canine and human visceral Leishmaniasis in Colombia. BMC Infectious Diseases, 2019, 19, 747.	1.3	15
101	A summary of Blastocystis subtypes in North and South America. Parasites and Vectors, 2019, 12, 376.	1.0	96
102	Development of a Digital Droplet Polymerase Chain Reaction (ddPCR) assay to detect Leishmania DNA in samples from Cutaneous Leishmaniasis patients. International Journal of Infectious Diseases, 2019, 79, 1-3.	1.5	13
103	High frequency of toxigenic Clostridium difficile and Clostridium perfringens coinfection among diarrheic patients at health care facility-onset (HCFO) and community-onset (CO) centers in Bogot $\tilde{A}_i$ , Colombia. Gut Pathogens, 2019, 11, 27.	1.6	5
104	Evaluation of the multispecies coalescent method to explore intra- <i>Trypanosoma cruzi</i> I relationships and genetic diversity. Parasitology, 2019, 146, 1063-1074.	0.7	8
105	Resurgence of Vaccine-Preventable Diseases in Venezuela as a Regional Public Health Threat in the Americas. Emerging Infectious Diseases, 2019, 25, 625-632.	2.0	87
106	Molecular and descriptive epidemiology of intestinal protozoan parasites of children and their pets in Cauca, Colombia: a cross-sectional study. BMC Infectious Diseases, 2019, 19, 190.	1.3	57
107	Taxonomical over splitting in the Rhodnius prolixus (Insecta: Hemiptera: Reduviidae) clade: Are R. taquarussuensis (da Rosa et al., 2017) and R. neglectus (Lent, 1954) the same species? PLoS ONE, 2019, 14, e0211285.	1.1	46
108	Trypanosoma cruzi infection, discrete typing units and feeding sources among Psammolestes arthuri (Reduviidae: Triatominae) collected in eastern Colombia. Parasites and Vectors, 2019, 12, 157.	1.0	19

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109	Venezuela's humanitarian crisis, resurgence of vector-borne diseases, and implications for spillover in the region. Lancet Infectious Diseases, The, 2019, 19, e149-e161.	4.6	138
110	A systematic review of the $\langle i \rangle$ Trypanosoma cruzi $\langle i \rangle$ genetic heterogeneity, host immune response and genetic factors as plausible drivers of chronic chagasic cardiomyopathy. Parasitology, 2019, 146, 269-283.	0.7	20
111	Molecular epidemiology of dengue, yellow fever, Zika and Chikungunya arboviruses: An update. Acta Tropica, 2019, 190, 99-111.	0.9	52
112	Comparison of parasite loads in serum and blood samples from patients in acute and chronic phases of Chagas disease. Parasitology, 2018, 145, 1837-1843.	0.7	11
113	Identification of bat trypanosomes from Minas Gerais state, Brazil, based on 18S rDNA and Cathepsin-L-like targets. Parasitology Research, 2018, 117, 737-746.	0.6	11
114	Trypanosoma cruzi I: Towards the need of genetic subdivision?, Part II. Acta Tropica, 2018, 184, 53-58.	0.9	18
115	The Colombian peace deal and its impact on the evolution of tropical diseases agents. Infection, Genetics and Evolution, 2018, 57, 145-150.	1.0	5
116	Evaluation of the analytical and diagnostic performance of a digital droplet polymerase chain reaction (ddPCR) assay to detect Trypanosoma cruzi DNA in blood samples. PLoS Neglected Tropical Diseases, 2018, 12, e0007063.	1.3	21
117	Unveiling the Multilocus Sequence Typing (MLST) Schemes and Core Genome Phylogenies for Genotyping Chlamydia trachomatis. Frontiers in Microbiology, 2018, 9, 1854.	1.5	23
118	Molecular detection and genotyping of pathogenic protozoan parasites in raw and treated water samples from southwest Colombia. Parasites and Vectors, 2018, 11, 563.	1.0	23
119	Geospatial-temporal distribution of Tegumentary Leishmaniasis in Colombia (2007–2016). PLoS Neglected Tropical Diseases, 2018, 12, e0006419.	1.3	12
120	Description of Leishmania species among dogs and humans in Colombian Visceral Leishmaniasis outbreaks. Infection, Genetics and Evolution, 2018, 64, 135-138.	1.0	7
121	Estimating the Intra-taxa Diversity, Population Genetic Structure, and Evolutionary Pathways of Cryptococcus neoformans and Cryptococcus gattii. Frontiers in Genetics, 2018, 9, 148.	1.1	30
122	New Insights into Clostridium difficile (CD) Infection in Latin America: Novel Description of Toxigenic Profiles of Diarrhea-Associated to CD in Bogot $\tilde{A}_i$ , Colombia. Frontiers in Microbiology, 2018, 9, 74.	1.5	14
123	The effect of temperature increase on the development of Rhodnius prolixus and the course of Trypanosoma cruzi metacyclogenesis. PLoS Neglected Tropical Diseases, 2018, 12, e0006735.	1.3	29
124	Analytical Performance of a Loop-Mediated Isothermal Amplification Assay for Leishmania DNA Detection in Sandflies and Direct Smears of Patients with Cutaneous Leishmaniasis. American Journal of Tropical Medicine and Hygiene, 2018, 98, 1325-1331.	0.6	9
125	Ecology of Trypanosoma cruzi I genotypes across Rhodnius prolixus captured in Attalea butyracea palms. Infection, Genetics and Evolution, 2017, 49, 146-150.	1.0	3
126	RNA-seq in kinetoplastids: A powerful tool for the understanding of the biology and host-pathogen interactions. Infection, Genetics and Evolution, 2017, 49, 273-282.	1.0	30

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127	Evaluation of a Multilocus Sequence Typing (MLST) scheme for Leishmania (Viannia) braziliensis and Leishmania (Viannia) panamensis in Colombia. Parasites and Vectors, 2017, 10, 236.	1.0	36
128	Molecular and serological detection of Trypanosoma cruzi in dogs (Canis lupus familiaris) suggests potential transmission risk in areas of recent acute Chagas disease outbreaks in Colombia. Preventive Veterinary Medicine, 2017, 141, 1-6.	0.7	22
129	<i>Leishmania</i> infection in bats from a non-endemic region of Leishmaniasis in Brazil. Parasitology, 2017, 144, 1980-1986.	0.7	22
130	Purification of Trypanosoma cruzi metacyclic trypomastigotes by ion exchange chromatography in sepharose-DEAE, a novel methodology for host-pathogen interaction studies. Journal of Microbiological Methods, 2017, 142, 27-32.	0.7	15
131	Determining Clostridium difficile intra-taxa diversity by mining multilocus sequence typing databases. BMC Microbiology, 2017, 17, 62.	1.3	44
132	Molecular and morphological characterization of Acanthamoeba isolated from corneal scrapes and contact lens wearers in Argentina. Infection, Genetics and Evolution, 2017, 54, 170-175.	1.0	10
133	Murine models susceptibility to distinct <i>Trypanosoma cruzi</i> I genotypes infection. Parasitology, 2017, 144, 512-519.	0.7	17
134	Molecular Epidemiology of Giardia, Blastocystis and Cryptosporidium among Indigenous Children from the Colombian Amazon Basin. Frontiers in Microbiology, 2017, 8, 248.	1.5	99
135	Analytical Performance of Four Polymerase Chain Reaction (PCR) and Real Time PCR (qPCR) Assays for the Detection of Six Leishmania Species DNA in Colombia. Frontiers in Microbiology, 2017, 8, 1907.	1.5	33
136	Community-acquired infection with hypervirulent Clostridium difficile isolates that carry different toxin and antibiotic resistance loci: a case report. Gut Pathogens, 2017, 9, 63.	1.6	4
137	Spatial distribution, Leishmania species and clinical traits of Cutaneous Leishmaniasis cases in the Colombian army. PLoS Neglected Tropical Diseases, 2017, 11, e0005876.	1.3	53
138	Blastocystis subtyping and its association with intestinal parasites in children from different geographical regions of Colombia. PLoS ONE, 2017, 12, e0172586.	1.1	55
139	First Colombian consensus on congenital Chagas and clinical approach for women of child-bearing age diagnosed with Chagas. Infectio, 2017, 21, .	0.4	2
140	Importation of Hybrid Human-Associated <i>Trypanosoma cruzi </i> Strains of Southern South American Origin, Colombia. Emerging Infectious Diseases, 2016, 22, 1452-1455.	2.0	13
141	Host and Toxoplasma gondii genetic and non-genetic factors influencing the development of ocular toxoplasmosis: A systematic review. Infection, Genetics and Evolution, 2016, 44, 199-209.	1.0	14
142	Taxonomy, diversity, temporal and geographical distribution of Cutaneous Leishmaniasis in Colombia: A retrospective study. Scientific Reports, 2016, 6, 28266.	1.6	86
143	Untangling the transmission dynamics of primary and secondary vectors of Trypanosoma cruzi in Colombia: parasite infection, feeding sources and discrete typing units. Parasites and Vectors, 2016, 9, 620.	1.0	55
144	Geographic distribution of human Blastocystis subtypes in South America. Infection, Genetics and Evolution, 2016, 41, 32-35.	1.0	174

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145	Host-Protozoan Interactions Protect from Mucosal Infections through Activation of the Inflammasome. Cell, 2016, 167, 444-456.e14.	13.5	251
146	High-Resolution Molecular Typing of <i>Trypanosoma cruzi &lt; /i&gt;in 2 Large Outbreaks of Acute Chagas Disease in Colombia. Journal of Infectious Diseases, 2016, 214, 1252-1255.</i>	1.9	34
147	Prevalence of Trypanosoma cruzi's Discrete Typing Units in a cohort of Latin American migrants in Spain. Acta Tropica, 2016, 157, 145-150.	0.9	37
148	Molecular Diagnosis of Chagas Disease in Colombia: Parasitic Loads and Discrete Typing Units in Patients from Acute and Chronic Phases. PLoS Neglected Tropical Diseases, 2016, 10, e0004997.	1.3	56
149	Chlamydia trachomatis Frequency in a Cohort of HPV-Infected Colombian Women. PLoS ONE, 2016, 11, e0147504.	1.1	12
150	Response to Tibayrenc and Ayala: reproductive clonality in protozoan pathogens – truth or artefact?. Molecular Ecology, 2015, 24, 5782-5784.	2.0	14
151	Risks associated with dispersive nocturnal flights of sylvatic Triatominae to artificial lights in a model house in the northeastern plains of Colombia. Parasites and Vectors, 2015, 8, 600.	1.0	28
152	Molecular Epidemiology of Entamoeba: First Description of Entamoeba moshkovskii in a Rural Area from Central Colombia. PLoS ONE, 2015, 10, e0140302.	1.1	26
153	Retrospective distribution of Trypanosoma cruzi I genotypes in Colombia. Memorias Do Instituto Oswaldo Cruz, 2015, 110, 387-393.	0.8	27
154	Detection of Entamoeba histolytica by Recombinase Polymerase Amplification. American Journal of Tropical Medicine and Hygiene, 2015, 93, 591-595.	0.6	31
155	Follow-up of an Asymptomatic Chagas Disease Population of Children after Treatment with Nifurtimox (Lampit) in a Sylvatic Endemic Transmission Area of Colombia. PLoS Neglected Tropical Diseases, 2015, 9, e0003465.	1.3	41
156	Agreement of the Kato-Katz test established by the WHO with samples fixed with sodium acetate analyzed at 6 months to diagnose intestinal geohelminthes. Acta Tropica, 2015, 146, 42-44.	0.9	11
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