

Jean-Claude Dujardin

List of Publications by Year in descending order

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citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptional Shift and Metabolic Adaptations during <i>Leishmania</i> Quiescence Using Stationary Phase and Drug Pressure as Models. <i>Microorganisms</i> , 2022, 10, 97.	3.6	7
2	Genomic and Phenotypic Characterization of Experimentally Selected Resistant <i>Leishmania donovani</i> Reveals a Role for Dynamin-1-Like Protein in the Mechanism of Resistance to a Novel Antileishmanial Compound. <i>MBio</i> , 2022, 13, e0326421.	4.1	5
3	High throughput single-cell genome sequencing gives insights into the generation and evolution of mosaic aneuploidy in <i>Leishmania donovani</i> . <i>Nucleic Acids Research</i> , 2022, 50, 293-305.	14.5	14
4	Application of CRISPR/Cas9-Based Reverse Genetics in <i>Leishmania braziliensis</i> : Conserved Roles for HSP100 and HSP23. <i>Genes</i> , 2020, 11, 1159.	2.4	9
5	Ecological divergence and hybridization of Neotropical <i>Leishmania</i> parasites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 25159-25168.	7.1	60
6	The Absence of C-5 DNA Methylation in <i>Leishmania donovani</i> Allows DNA Enrichment from Complex Samples. <i>Microorganisms</i> , 2020, 8, 1252.	3.6	9
7	Evaluation of whole genome amplification and bioinformatic methods for the characterization of <i>Leishmania</i> genomes at a single cell level. <i>Scientific Reports</i> , 2020, 10, 15043.	3.3	20
8	Next-Generation Molecular Surveillance of TriTryp Diseases. <i>Trends in Parasitology</i> , 2020, 36, 356-367.	3.3	10
9	Non- <i>Leishmania</i> Parasite in Fatal Visceral Leishmaniasis-like Disease, Brazil. <i>Emerging Infectious Diseases</i> , 2020, 26, 388-388.	4.3	4
10	Global genome diversity of the <i>Leishmania donovani</i> complex. <i>ELife</i> , 2020, 9, .	6.0	90
11	ISC1, a new <i>Leishmania donovani</i> population emerging in the Indian sub-continent: Vector competence of <i>Phlebotomus argentipes</i> . <i>Infection, Genetics and Evolution</i> , 2019, 76, 104073.	2.3	6
12	Genomes of <i>Leishmania</i> parasites directly sequenced from patients with visceral leishmaniasis in the Indian subcontinent. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007900.	3.0	48
13	Integrated genomic and metabolomic profiling of ISC1, an emerging <i>Leishmania donovani</i> population in the Indian subcontinent. <i>Infection, Genetics and Evolution</i> , 2018, 62, 170-178.	2.3	32
14	<i>Leishmania</i> Genome Dynamics during Environmental Adaptation Reveal Strain-Specific Differences in Gene Copy Number Variation, Karyotype Instability, and Telomeric Amplification. <i>MBio</i> , 2018, 9, .	4.1	82
15	Epidemiology of Leishmaniasis in the Time of Drug Resistance (the Miltefosine Era). , 2018, , 85-107.		3
16	Importance of secondary screening with clinical isolates for anti-leishmania drug discovery. <i>Scientific Reports</i> , 2018, 8, 11765.	3.3	21
17	Exploiting Knowledge on <i>Leishmania</i> Drug Resistance to Support the Quest for New Drugs. <i>Trends in Parasitology</i> , 2017, 33, 162-174.	3.3	105
18	Discovery and genomic analyses of hybridization between divergent lineages of <i>Trypanosoma congolense</i> , causative agent of Animal African Trypanosomiasis. <i>Molecular Ecology</i> , 2017, 26, 6524-6538.	3.9	50

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19	Haplotype selection as an adaptive mechanism in the protozoan pathogen <i>Leishmania donovani</i> . <i>Nature Ecology and Evolution</i> , 2017, 1, 1961-1969.	7.8	95
20	Macromolecular biosynthetic parameters and metabolic profile in different life stages of <i>Leishmania braziliensis</i> : Amastigotes as a functionally less active stage. <i>PLoS ONE</i> , 2017, 12, e0180532.	2.5	35
21	Single locus genotyping to track <i>Leishmania donovani</i> in the Indian subcontinent: Application in Nepal. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005420.	3.0	19
22	Alice in microbes' land: adaptations and counter-adaptations of vector-borne parasitic protozoa and their hosts. <i>FEMS Microbiology Reviews</i> , 2016, 40, 664-685.	8.6	24
23	Association of the Endobiont Double-Stranded RNA Virus LRV1 With Treatment Failure for Human Leishmaniasis Caused by <i>Leishmania braziliensis</i> in Peru and Bolivia. <i>Journal of Infectious Diseases</i> , 2016, 213, 112-121.	4.0	114
24	Genomic and Molecular Characterization of Miltefosine Resistance in <i>Leishmania infantum</i> Strains with Either Natural or Acquired Resistance through Experimental Selection of Intracellular Amastigotes. <i>PLoS ONE</i> , 2016, 11, e0154101.	2.5	80
25	Evolutionary genomics of epidemic visceral leishmaniasis in the Indian subcontinent. <i>ELife</i> , 2016, 5, .	6.0	147
26	Species Typing in Dermal Leishmaniasis. <i>Clinical Microbiology Reviews</i> , 2015, 28, 265-294.	13.6	121
27	A novel marker, ARM58, confers antimony resistance to <i>Leishmania</i> spp.. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2014, 4, 37-47.	3.4	23
28	Mosaic aneuploidy in <i>Leishmania</i> : the perspective of whole genome sequencing. <i>Trends in Parasitology</i> , 2014, 30, 554-555.	3.3	18
29	Epidemiology of Leishmaniasis in the Time of Drug Resistance. , 2013, , 65-83.		4
30	In vitro Susceptibility of <i>Leishmania donovani</i> to Miltefosine in Indian Visceral Leishmaniasis. <i>American Journal of Tropical Medicine and Hygiene</i> , 2013, 89, 750-754.	1.4	46
31	Evolution of the <i>Leishmania braziliensis</i> species complex from amplified fragment length polymorphisms, and clinical implications. <i>Infection, Genetics and Evolution</i> , 2012, 12, 1994-2002.	2.3	38
32	Adaptive mechanisms in pathogens: universal aneuploidy in <i>Leishmania</i> . <i>Trends in Parasitology</i> , 2012, 28, 370-376.	3.3	120
33	Natural <i>Leishmania donovani/Leishmania aethiopia</i> hybrids identified from Ethiopia. <i>Infection, Genetics and Evolution</i> , 2011, 11, 2113-2118.	2.3	49
34	Whole genome sequencing of multiple <i>Leishmania donovani</i> clinical isolates provides insights into population structure and mechanisms of drug resistance. <i>Genome Research</i> , 2011, 21, 2143-2156.	5.5	381
35	Chromosome and gene copy number variation allow major structural change between species and strains of <i>Leishmania</i> . <i>Genome Research</i> , 2011, 21, 2129-2142.	5.5	380
36	Domestic Animals and Epidemiology of Visceral Leishmaniasis, Nepal. <i>Emerging Infectious Diseases</i> , 2010, 16, 231-237.	4.3	82

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37	Extreme inbreeding in <i>Leishmania braziliensis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 10224-10229.	7.1	158
38	Leishmaniasis in the Mediterranean in the era of molecular epidemiology. Trends in Parasitology, 2008, 24, 135-142.	3.3	86
39	Influence of <i>Leishmania</i> (Viannia) Species on the Response to Antimonial Treatment in Patients with American Tegumentary Leishmaniasis. Journal of Infectious Diseases, 2007, 195, 1846-1851.	4.0	212
40	Evolutionary and geographical history of the <i>Leishmania donovani</i> complex with a revision of current taxonomy. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 9375-9380.	7.1	358
41	Cutaneous leishmaniasis. Lancet Infectious Diseases, The, 2007, 7, 581-596.	9.1	1,130
42	American Tegumentary Leishmaniasis: Is Antimonial Treatment Outcome Related to Parasite Drug Susceptibility?. Journal of Infectious Diseases, 2006, 194, 1168-1175.	4.0	92
43	THE SENSITIVITY OF CLINICAL ISOLATES OF LEISHMANIA FROM PERU AND NEPAL TO MILTEFOSINE. American Journal of Tropical Medicine and Hygiene, 2005, 73, 272-275.	1.4	99
44	The sensitivity of clinical isolates of <i>Leishmania</i> from Peru and Nepal to miltefosine. American Journal of Tropical Medicine and Hygiene, 2005, 73, 272-5.	1.4	40
45	Is <i>Leishmania</i> (Viannia) <i>peruviana</i> a Distinct Species? A MLEE/RAPD Evolutionary Genetics Answer. Journal of Eukaryotic Microbiology, 2000, 47, 197-207.	1.7	37
46	Putative <i>Leishmania</i> hybrids in the Eastern Andean valley of Huanuco, Peru. Acta Tropica, 1995, 59, 293-307.	2.0	96