

Gert Van der Auwera

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

3,700
citations

236925

25
h-index

161849

54
g-index

58
all docs

58
docs citations

58
times ranked

4532
citing authors

#	ARTICLE	IF	CITATIONS
1	Cutaneous leishmaniasis. <i>Lancet Infectious Diseases</i> , The, 2007, 7, 581-596.	9.1	1,130
2	Drug resistance and treatment failure in leishmaniasis: A 21st century challenge. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0006052.	3.0	571
3	Culture-Independent Species Typing of Neotropical <i>Leishmania</i> for Clinical Validation of a PCR-Based Assay Targeting Heat Shock Protein 70 Genes. <i>Journal of Clinical Microbiology</i> , 2004, 42, 2294-2297.	3.9	174
4	Phylogeny of <i>Leishmania</i> species based on the heat-shock protein 70 gene. <i>Infection, Genetics and Evolution</i> , 2010, 10, 238-245.	2.3	157
5	Evolutionary genomics of epidemic visceral leishmaniasis in the Indian subcontinent. <i>ELife</i> , 2016, 5, .	6.0	147
6	Species Typing in Dermal Leishmaniasis. <i>Clinical Microbiology Reviews</i> , 2015, 28, 265-294.	13.6	121
7	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
8	Multilocus microsatellite typing (MLMT) reveals genetic homogeneity of <i>Leishmania donovani</i> strains in the Indian subcontinent. <i>Infection, Genetics and Evolution</i> , 2009, 9, 24-31.	2.3	81
9	Diagnostic accuracy of a new <i>Leishmania</i> PCR for clinical visceral leishmaniasis in Nepal and its role in diagnosis of disease. <i>Tropical Medicine and International Health</i> , 2008, 13, 1378-1383.	2.3	76
10	Evaluation of Four Single-Locus Markers for <i>Leishmania</i> Species Discrimination by Sequencing. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1098-1104.	3.9	61
11	Detection of <i>Leptomonas</i> sp. parasites in clinical isolates of Kala-azar patients from India. <i>Infection, Genetics and Evolution</i> , 2010, 10, 1145-1150.	2.3	53
12	Antimony-Resistant <i>Leishmania donovani</i> Exploits miR-466i To Deactivate Host MyD88 for Regulating IL-10/IL-12 Levels during Early Hours of Infection. <i>Journal of Immunology</i> , 2015, 195, 2731-2742.	0.8	50
13	Epidemiological dynamics of antimonial resistance in <i>Leishmania donovani</i> : Genotyping reveals a polyclonal population structure among naturally-resistant clinical isolates from Nepal. <i>Infection, Genetics and Evolution</i> , 2007, 7, 206-212.	2.3	49
14	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
15	Experimental Resistance to Drug Combinations in <i>Leishmania donovani</i> : Metabolic and Phenotypic Adaptations. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 2242-2255.	3.2	47
16	Transmission of <i>Leishmania donovani</i> in the Hills of Eastern Nepal, an Outbreak Investigation in Okhaldhunga and Bhojpur Districts. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003966.	3.0	46
17	American tegumentary leishmaniasis: direct species identification of <i>Leishmania</i> in non-invasive clinical samples. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2007, 101, 368-371.	1.8	45
18	Accurate and rapid species typing from cutaneous and mucocutaneous leishmaniasis lesions of the New World. <i>Diagnostic Microbiology and Infectious Disease</i> , 2012, 74, 142-150.	1.8	40

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19	LC-MS METABOLOMICS FROM STUDY DESIGN TO DATA-ANALYSIS “ USING A VERSATILE PATHOGEN AS A TEST CASE. Computational and Structural Biotechnology Journal, 2013, 4, e201301002.	4.1	39
20	Model-Based Investigations of Different Vector-Related Intervention Strategies to Eliminate Visceral Leishmaniasis on the Indian Subcontinent. PLoS Neglected Tropical Diseases, 2014, 8, e2810.	3.0	37
21	Macromolecular biosynthetic parameters and metabolic profile in different life stages of Leishmania braziliensis: Amastigotes as a functionally less active stage. PLoS ONE, 2017, 12, e0180532.	2.5	35
22	Quantification of Leishmania (Viannia) Kinetoplast DNA in Ulcers of Cutaneous Leishmaniasis Reveals Inter-site and Inter-sampling Variability in Parasite Load. PLoS Neglected Tropical Diseases, 2015, 9, e0003936.	3.0	34
23	Tegumentary leishmaniasis and coinfections other than HIV. PLoS Neglected Tropical Diseases, 2018, 12, e0006125.	3.0	33
24	Integrated genomic and metabolomic profiling of ISC1, an emerging Leishmania donovani population in the Indian subcontinent. Infection, Genetics and Evolution, 2018, 62, 170-178.	2.3	32
25	Differentiation of Leishmania (Viannia) panamensis and Leishmania (V.) guyanensis using BclI for hsp70 PCR-RFLP. Transactions of the Royal Society of Tropical Medicine and Hygiene, 2010, 104, 364-367.	1.8	27
26	Detection and identification of Leishmania spp.: application of two hsp70-based PCR-RFLP protocols to clinical samples from the New World. Parasitology Research, 2017, 116, 1843-1848.	1.6	26
27	Identification of Old World Leishmania spp. by specific polymerase chain reaction amplification of cysteine proteinase B genes and rapid dipstick detection. Diagnostic Microbiology and Infectious Disease, 2009, 63, 173-181.	1.8	24
28	Alice in microbes' land: adaptations and counter-adaptations of vector-borne parasitic protozoa and their hosts. FEMS Microbiology Reviews, 2016, 40, 664-685.	8.6	24
29	Leishmania AFLP: Paving the way towards improved molecular assays and markers of diversity. Infection, Genetics and Evolution, 2011, 11, 960-967.	2.3	23
30	Comparative Fitness of a Parent Leishmania donovani Clinical Isolate and Its Experimentally Derived Paromomycin-Resistant Strain. PLoS ONE, 2015, 10, e0140139.	2.5	21
31	Ecology and seasonality of sandflies and potential reservoirs of cutaneous leishmaniasis in Ochollo, a hotspot in southern Ethiopia. PLoS Neglected Tropical Diseases, 2019, 13, e0007667.	3.0	21
32	HIV-1 genetic variability in Cameroon. Aids, 2000, 14, 1862-1864.	2.2	21
33	Structure of the Large Subunit rDNA from a Diatom, and Comparison Between Small and Large Subunit Ribosomal RNA for Studying Stramenopile Evolution. Journal of Eukaryotic Microbiology, 1998, 45, 521-527.	1.7	20
34	HindIII and SduI digests of heat-shock protein 70 PCR for Leishmania typing. Diagnostic Microbiology and Infectious Disease, 2013, 77, 245-247.	1.8	20
35	Direct Leishmania species typing in Old World clinical samples: evaluation of 3 sensitive methods based on the heat-shock protein 70 gene. Diagnostic Microbiology and Infectious Disease, 2014, 80, 35-39.	1.8	20
36	Species- and Strain-Specific Adaptation of the HSP70 Super Family in Pathogenic Trypanosomatids. Genome Biology and Evolution, 2016, 8, 1980-1995.	2.5	20

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37	Evaluation of whole genome amplification and bioinformatic methods for the characterization of Leishmania genomes at a single cell level. <i>Scientific Reports</i> , 2020, 10, 15043.	3.3	20
38	Longitudinal evaluation of asymptomatic Leishmania infection in HIV-infected individuals in North-West Ethiopia: A pilot study. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007765.	3.0	19
39	Single locus genotyping to track Leishmania donovani in the Indian subcontinent: Application in Nepal. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005420.	3.0	19
40	Mosaic aneuploidy in Leishmania: the perspective of whole genome sequencing. <i>Trends in Parasitology</i> , 2014, 30, 554-555.	3.3	18
41	Apolipoprotein L1 Variant Associated with Increased Susceptibility to Trypanosome Infection. <i>MBio</i> , 2016, 7, e02198-15.	4.1	18
42	HIV-1 subtype H near-full length genome reference strains and analysis of subtype-H-containing inter-subtype recombinants. <i>Aids</i> , 2000, 14, 1533-1543.	2.2	13
43	Epidemiology, clinical pattern and impact of species-specific molecular diagnosis on management of leishmaniasis in Belgium, 2010–2018: A retrospective study. <i>Travel Medicine and Infectious Disease</i> , 2020, 38, 101885.	3.0	13
44	Identification of Leishmania tropica from micro-foci of cutaneous leishmaniasis in the Kenyan Rift Valley. <i>Pathogens and Global Health</i> , 2012, 106, 159-165.	2.3	12
45	Phylogenetic analysis of the Trypanosoma genus based on the heat-shock protein 70 gene. <i>Infection, Genetics and Evolution</i> , 2016, 43, 165-172.	2.3	12
46	Clinical diversity and treatment results in Tegumentary Leishmaniasis: A European clinical report in 459 patients. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009863.	3.0	12
47	Next-Generation Molecular Surveillance of TriTryp Diseases. <i>Trends in Parasitology</i> , 2020, 36, 356-367.	3.3	10
48	Inpatient Variability of HIV Type 1 Group O ANT70 during a 10-Year Follow-up. <i>AIDS Research and Human Retroviruses</i> , 1999, 15, 1325-1332.	1.1	8
49	Transcriptional Shift and Metabolic Adaptations during Leishmania Quiescence Using Stationary Phase and Drug Pressure as Models. <i>Microorganisms</i> , 2022, 10, 97.	3.6	7
50	Reanalysis of Full-Length HIV Type 1 Group M Subtype K and Sub-Subtype F2 with an MS-DOS Bootscanning Program. <i>AIDS Research and Human Retroviruses</i> , 2001, 17, 185-189.	1.1	6
51	ISC1, a new Leishmania donovani population emerging in the Indian sub-continent: Vector competence of Phlebotomus argentipes. <i>Infection, Genetics and Evolution</i> , 2019, 76, 104073.	2.3	6
52	Differentiation between <i>Trypanosoma cruzi</i> and <i>Trypanosoma rangeli</i> using heat-shock protein 70 polymorphisms. <i>Tropical Medicine and International Health</i> , 2014, 19, 195-206.	2.3	4
53	Epidemiology of Leishmaniasis in the Time of Drug Resistance (the Miltefosine Era). , 2018, , 85-107.		3
54	Remarks on identification of amplified fragment length polymorphisms linked to SAG resistance in Leishmania. <i>Acta Tropica</i> , 2010, 113, 92-93.	2.0	2

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55	Treatment outcome of imported cutaneous leishmaniasis among travelers and migrants infected with <i>Leishmania major</i> and <i>Leishmania tropica</i> : a retrospective study in European centers 2013 to 2019. <i>International Journal of Infectious Diseases</i> , 2022, 122, 375-381.	3.3	1