Manu Vanaerschot

List of Publications by Year
in descending order

48	2,973	31	48
papers	citations	h-index	g-index
		147801	206112

53	53	53	3854
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Whole genome sequencing of multiple <i>Leishmania donovani</i> clinical isolates provides insights into population structure and mechanisms of drug resistance. Genome Research, 2011, 21, 2143-2156.	5.5	381
2	Increasing Failure of Miltefosine in the Treatment of Kala-azar in Nepal and the Potential Role of Parasite Drug Resistance, Reinfection, or Noncompliance. Clinical Infectious Diseases, 2013, 56, 1530-1538.	5.8	276
3	Mapping the malaria parasite druggable genome by using in vitro evolution and chemogenomics. Science, 2018, 359, 191-199.	12.6	194
4	Modulation of Aneuploidy in <i>Leishmania donovani</i> during Adaptation to Different <i>In Vitro</i> and <i>In Vivo</i> Environments and Its Impact on Gene Expression. MBio, 2017, 8, .	4.1	157
5	Evolutionary genomics of epidemic visceral leishmaniasis in the Indian subcontinent. ELife, 2016, 5, .	6.0	147
6	Open-source discovery of chemical leads for next-generation chemoprotective antimalarials. Science, 2018, 362, .	12.6	99
7	Evaluation of Normalization Methods to Pave the Way Towards Large-Scale LC-MS-Based Metabolomics Profiling Experiments. OMICS A Journal of Integrative Biology, 2013, 17, 473-485.	2.0	89
8	Molecular Mechanisms of Drug Resistance in Natural Leishmania Populations Vary with Genetic Background. PLoS Neglected Tropical Diseases, 2012, 6, e1514.	3.0	79
9	Linking In Vitro and In Vivo Survival of Clinical Leishmania donovani Strains. PLoS ONE, 2010, 5, e12211.	2.5	70
10	Identification of a Polymorphism in the N Gene of SARS-CoV-2 That Adversely Impacts Detection by Reverse Transcription-PCR. Journal of Clinical Microbiology, 2020, 59, .	3.9	66
11	Treatment failure in leishmaniasis: drug-resistance or another (epi-) phenotype?. Expert Review of Anti-Infective Therapy, 2014, 12, 937-946.	4.4	64
12	Antileishmanial Activity of a Series of <i>N</i>²,<i>N</i>⁴-Disubstituted Quinazoline-2,4-diamines. Journal of Medicinal Chemistry, 2014, 57, 5141-5156.	6.4	59
13	Relapse after Treatment with Miltefosine for Visceral Leishmaniasis Is Associated with Increased Infectivity of the Infecting Leishmania donovani Strain. MBio, 2013, 4, e00611-13.	4.1	57
14	Inhibition of Resistance-Refractory P. falciparum Kinase PKG Delivers Prophylactic, Blood Stage, and Transmission-Blocking Antiplasmodial Activity. Cell Chemical Biology, 2020, 27, 806-816.e8.	5.2	56
15	Defining the Determinants of Specificity of <i>Plasmodium</i> Proteasome Inhibitors. Journal of the American Chemical Society, 2018, 140, 11424-11437.	13.7	54
16	Combining Stage Specificity and Metabolomic Profiling to Advance Antimalarial Drug Discovery. Cell Chemical Biology, 2020, 27, 158-171.e3.	5.2	54
17	Detection of Leptomonas sp. parasites in clinical isolates of Kala-azar patients from India. Infection, Genetics and Evolution, 2010, 10, 1145-1150.	2.3	53
18	Antimonial Resistance in Leishmania donovani Is Associated with Increased In Vivo Parasite Burden. PLoS ONE, 2011, 6, e23120.	2.5	52

#	Article	IF	Citations
19	Genome-wide SNP and microsatellite variation illuminate population-level epidemiology in the Leishmania donovani species complex. Infection, Genetics and Evolution, 2012, 12, 149-159.	2.3	50
20	Treatment of Visceral Leishmaniasis: Model-Based Analyses on the Spread of Antimony-Resistant L. donovani in Bihar, India. PLoS Neglected Tropical Diseases, 2012, 6, e1973.	3.0	49
21	Metabolic adaptations of <i><scp>L</scp>eishmania donovani</i> in relation to differentiation, drug resistance, and drug pressure. Molecular Microbiology, 2013, 90, 428-442.	2.5	48
22	Genomes of Leishmania parasites directly sequenced from patients with visceral leishmaniasis in the Indian subcontinent. PLoS Neglected Tropical Diseases, 2019, 13, e0007900.	3.0	48
23	Experimental Resistance to Drug Combinations in Leishmania donovani: Metabolic and Phenotypic Adaptations. Antimicrobial Agents and Chemotherapy, 2015, 59, 2242-2255.	3.2	47
24	Hexahydroquinolines are antimalarial candidates with potent blood-stage and transmission-blocking activity. Nature Microbiology, 2017, 2, 1403-1414.	13.3	47
25	In vitro Susceptibility of Leishmania donovani to Miltefosine in Indian Visceral Leishmaniasis. American Journal of Tropical Medicine and Hygiene, 2013, 89, 750-754.	1.4	46
26	Increased metacyclogenesis of antimony-resistant <i>Leishmania donovani</i> clinical lines. Parasitology, 2011, 138, 1392-1399.	1.5	45
27	Drug resistance in vectorborne parasites: multiple actors and scenarios for an evolutionary arms race. FEMS Microbiology Reviews, 2014, 38, 41-55.	8.6	43
28	UCT943, a Next-Generation Plasmodium falciparum PI4K Inhibitor Preclinical Candidate for the Treatment of Malaria. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	40
29	LC-MS METABOLOMICS FROM STUDY DESIGN TO DATA-ANALYSIS â€" USING A VERSATILE PATHOGEN AS A TEST CASE. Computational and Structural Biotechnology Journal, 2013, 4, e201301002.	4.1	39
30	Chemogenomics identifies acetyl-coenzyme A synthetase as a target for malaria treatment and prevention. Cell Chemical Biology, 2022, 29, 191-201.e8.	5.2	39
31	Comparison of gene expression patterns among<i>Leishmania braziliensis</i>clinical isolates showing a different<i>in vitro</i>susceptibility to pentavalent antimony. Parasitology, 2011, 138, 183-193.	1.5	37
32	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
33	Drug-resistant microorganisms with a higher fitness â€" can medicines boost pathogens?. Critical Reviews in Microbiology, 2013, 39, 384-394.	6.1	33
34	Complete Genome Sequence of a Novel Coronavirus (SARS-CoV-2) Isolate from Bangladesh. Microbiology Resource Announcements, 2020, 9, .	0.6	31
35	(Post-) Genomic approaches to tackle drug resistance in <i>Leishmania</i>. Parasitology, 2013, 140, 1492-1505.	1.5	29
36	Probing the Open Global Health Chemical Diversity Library for Multistage-Active Starting Points for Next-Generation Antimalarials. ACS Infectious Diseases, 2020, 6, 613-628.	3.8	26

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37	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
38	Multiplexed Spliced-Leader Sequencing: A high-throughput, selective method for RNA-seq in Trypanosomatids. Scientific Reports, 2017, 7, 3725.	3.3	24
39	Gene expression profiling ofLeishmania (Leishmania) donovani: overcoming technical variation and exploiting biological variation. Parasitology, 2008, 135, 183-194.	1.5	23
40	Genetic Markers for SSG Resistance in Leishmania donovani and SSG Treatment Failure in Visceral Leishmaniasis Patients of the Indian Subcontinent. Journal of Infectious Diseases, 2012, 206, 752-755.	4.0	23
41	Comparative Gene Expression Analysis throughout the Life Cycle of Leishmania braziliensis: Diversity of Expression Profiles among Clinical Isolates. PLoS Neglected Tropical Diseases, 2011, 5, e1021.	3.0	21
42	Evaluation of whole genome amplification and bioinformatic methods for the characterization of Leishmania genomes at a single cell level. Scientific Reports, 2020, 10, 15043.	3.3	20
43	Single locus genotyping to track Leishmania donovani in the Indian subcontinent: Application in Nepal. PLoS Neglected Tropical Diseases, 2017, 11, e0005420.	3.0	19
44	Rapid deployment of SARS-CoV-2 testing: The CLIAHUB. PLoS Pathogens, 2020, 16, e1008966.	4.7	18
45	The Plasmodium falciparum ABC transporter ABCI3 confers parasite strain-dependent pleiotropic antimalarial drug resistance. Cell Chemical Biology, 2022, 29, 824-839.e6.	5.2	14
46	The antimalarial efficacy and mechanism of resistance of the novel chemotype DDD01034957. Scientific Reports, 2021, 11, 1888.	3.3	10
47	Reply to Das. Clinical Infectious Diseases, 2013, 57, 1365-1366.	5.8	1
48	The Concept of Fitness in Leishmania. , 2018, , 341-366.		0