Manu Vanaerschot

List of Publications by Year
in descending order

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48 papers	2,973 citations	147801 31 h-index	206112 48 g-index
53 all docs	53 docs citations	53 times ranked	3854 citing authors

#	Article	IF	Citations
1	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
2	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
3	The antimalarial efficacy and mechanism of resistance of the novel chemotype DDD01034957. Scientific Reports, 2021, 11, 1888.	3.3	10
4	Combining Stage Specificity and Metabolomic Profiling to Advance Antimalarial Drug Discovery. Cell Chemical Biology, 2020, 27, 158-171.e3.	5.2	54
5	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
6	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
7	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
8	Complete Genome Sequence of a Novel Coronavirus (SARS-CoV-2) Isolate from Bangladesh. Microbiology Resource Announcements, 2020, 9, .	0.6	31
9	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
10	Rapid deployment of SARS-CoV-2 testing: The CLIAHUB. PLoS Pathogens, 2020, 16, e1008966.	4.7	18
11	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
12	Mapping the malaria parasite druggable genome by using in vitro evolution and chemogenomics. Science, 2018, 359, 191-199.	12.6	194
13	Open-source discovery of chemical leads for next-generation chemoprotective antimalarials. Science, 2018, 362, .	12.6	99
14	UCT943, a Next-Generation Plasmodium falciparum PI4K Inhibitor Preclinical Candidate for the Treatment of Malaria. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	40
15	The Concept of Fitness in Leishmania. , 2018, , 341-366.		0
16	Defining the Determinants of Specificity of Plasmodium Proteasome Inhibitors. Journal of the American Chemical Society, 2018, 140, 11424-11437.	13.7	54
17	Multiplexed Spliced-Leader Sequencing: A high-throughput, selective method for RNA-seq in Trypanosomatids. Scientific Reports, 2017, 7, 3725.	3.3	24
18	Modulation of Aneuploidy in Leishmania donovani during Adaptation to Different In Vitro and In Vivo Environments and Its Impact on Gene Expression. MBio, 2017, 8, .	4.1	157

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19	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
20	Hexahydroquinolines are antimalarial candidates with potent blood-stage and transmission-blocking activity. Nature Microbiology, 2017, 2, 1403-1414.	13.3	47
21	Single locus genotyping to track Leishmania donovani in the Indian subcontinent: Application in Nepal. PLoS Neglected Tropical Diseases, 2017, 11, e0005420.	3.0	19
22	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
23	Evolutionary genomics of epidemic visceral leishmaniasis in the Indian subcontinent. ELife, 2016, 5, .	6.0	147
24	Experimental Resistance to Drug Combinations in Leishmania donovani: Metabolic and Phenotypic Adaptations. Antimicrobial Agents and Chemotherapy, 2015, 59, 2242-2255.	3.2	47
25	Drug resistance in vectorborne parasites: multiple actors and scenarios for an evolutionary arms race. FEMS Microbiology Reviews, 2014, 38, 41-55.	8.6	43
26	Antileishmanial Activity of a Series of N²,N⁴-Disubstituted Quinazoline-2,4-diamines. Journal of Medicinal Chemistry, 2014, 57, 5141-5156.	6.4	59
27	Treatment failure in leishmaniasis: drug-resistance or another (epi-) phenotype?. Expert Review of Anti-Infective Therapy, 2014, 12, 937-946.	4.4	64
28	Metabolic adaptations of <scp>L</scp>eishmania donovani in relation to differentiation, drug resistance, and drug pressure. Molecular Microbiology, 2013, 90, 428-442.	2.5	48
29	Drug-resistant microorganisms with a higher fitness â€“ can medicines boost pathogens?. Critical Reviews in Microbiology, 2013, 39, 384-394.	6.1	33
30	(Post-) Genomic approaches to tackle drug resistance in Leishmania. Parasitology, 2013, 140, 1492-1505.	1.5	29
31	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
32	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
33	Reply to Das. Clinical Infectious Diseases, 2013, 57, 1365-1366.	5.8	1
34	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
35	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
36	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

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37	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
38	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
39	Molecular Mechanisms of Drug Resistance in Natural Leishmania Populations Vary with Genetic Background. PLoS Neglected Tropical Diseases, 2012, 6, e1514.	3.0	79
40	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
41	Comparison of gene expression patterns amongLeishmania braziliensisclinical isolates showing a differentin vitrosusceptibility to pentavalent antimony. Parasitology, 2011, 138, 183-193.	1.5	37
42	Increased metacyclogenesis of antimony-resistant Leishmania donovani clinical lines. Parasitology, 2011, 138, 1392-1399.	1.5	45
43	Whole genome sequencing of multiple Leishmania donovani clinical isolates provides insights into population structure and mechanisms of drug resistance. Genome Research, 2011, 21, 2143-2156.	5.5	381
44	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
45	Antimonial Resistance in Leishmania donovani Is Associated with Increased In Vivo Parasite Burden. PLoS ONE, 2011, 6, e23120.	2.5	52
46	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
47	Linking In Vitro and In Vivo Survival of Clinical Leishmania donovani Strains. PLoS ONE, 2010, 5, e12211.	2.5	70
48	Gene expression profiling ofLeishmania (Leishmania) donovani: overcoming technical variation and exploiting biological variation. Parasitology, 2008, 135, 183-194.	1.5	23