

Frederik Van den Broeck

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

1,024
citations

471061

17
h-index

476904

29
g-index

38
all docs

38
docs citations

38
times ranked

1464
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	6.5	14
2	Molecular Analysis of Trypanosome Infections in Algerian Camels. <i>Acta Parasitologica</i> , 2022, 67, 1246-1253.	0.4	2
3	The phylodynamics of SARS-CoV-2 during 2020 in Finland. <i>Communications Medicine</i> , 2022, 2, .	1.9	5
4	Population genetics of African <i>Schistosoma</i> species. <i>Infection, Genetics and Evolution</i> , 2021, 89, 104727.	1.0	24
5	Untangling introductions and persistence in COVID-19 resurgence in Europe. <i>Nature</i> , 2021, 595, 713-717.	13.7	133
6	rKOMICS: an R package for processing mitochondrial minicircle assemblies in population-scale genome projects. <i>BMC Bioinformatics</i> , 2021, 22, 468.	1.2	7
7	Genomic population structure associated with repeated escape of <i>Salmonella enterica</i> ATCC14028s from the laboratory into nature. <i>PLoS Genetics</i> , 2021, 17, e1009820.	1.5	8
8	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.	3.3	60
9	Meiotic sex in Chagas disease parasite <i>Trypanosoma cruzi</i> . <i>Nature Communications</i> , 2019, 10, 3972.	5.8	58
10	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.	1.3	48
11	Barcoding hybrids: heterogeneous distribution of <i>Schistosoma haematobium</i> – <i>Schistosoma bovis</i> hybrids across the Senegal River Basin. <i>Parasitology</i> , 2018, 145, 634-645.	0.7	27
12	Evolutionary epidemiology of schistosomiasis: linking parasite genetics with disease phenotype in humans. <i>International Journal for Parasitology</i> , 2018, 48, 107-115.	1.3	7
13	Mitonuclear genomics challenges the theory of clonality in <i>Trypanosoma congolense</i> : Reply to Tibayrenc and Ayala. <i>Molecular Ecology</i> , 2018, 27, 3425-3431.	2.0	14
14	Population genetics of the <i>Schistosoma</i> snail host <i>Bulinus truncatus</i> in Egypt. <i>Acta Tropica</i> , 2017, 172, 36-43.	0.9	12
15	Genome-Wide SNP Analysis Reveals Distinct Origins of <i>Trypanosoma evansi</i> and <i>Trypanosoma equiperdum</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 1990-1997.	1.1	33
16	Genomic analysis of Isometamidium Chloride resistance in <i>Trypanosoma congolense</i> . <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2017, 7, 350-361.	1.4	48
17	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.	2.0	50
18	Apolipoprotein L1 Variant Associated with Increased Susceptibility to Trypanosome Infection. <i>MBio</i> , 2016, 7, e02198-15.	1.8	18

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19	Evolutionary genomics of epidemic visceral leishmaniasis in the Indian subcontinent. <i>ELife</i> , 2016, 5, .	2.8	147
20	Reconstructing Colonization Dynamics of the Human Parasite <i>Schistosoma mansoni</i> following Anthropogenic Environmental Changes in Northwest Senegal. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003998.	1.3	23
21	Drug resistance in vectorborne parasites: multiple actors and scenarios for an evolutionary arms race. <i>FEMS Microbiology Reviews</i> , 2014, 38, 41-55.	3.9	43
22	Inbreeding within human <i>Schistosoma mansoni</i> : do host-specific factors shape the genetic composition of parasite populations?. <i>Heredity</i> , 2014, 113, 32-41.	1.2	28
23	Hybridisation between the two major African schistosome species of humans. <i>International Journal for Parasitology</i> , 2013, 43, 687-689.	1.3	56
24	Regular treatments of praziquantel do not impact on the genetic make-up of <i>Schistosoma mansoni</i> in Northern Senegal. <i>Infection, Genetics and Evolution</i> , 2013, 18, 100-105.	1.0	21
25	Micro-Geographical Heterogeneity in <i>Schistosoma mansoni</i> and <i>S. haematobium</i> Infection and Morbidity in a Co-Endemic Community in Northern Senegal. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2608.	1.3	36
26	Panmictic Structure of the <i>Cryptosporidium parvum</i> Population in Irish Calves: Influence of Prevalence and Host Movement. <i>Applied and Environmental Microbiology</i> , 2013, 79, 2534-2541.	1.4	25
27	Quantifying population structure on short timescales. <i>Molecular Ecology</i> , 2012, 21, 3458-3473.	2.0	13
28	Multilocus genotyping reveals a polyphyletic pattern among naturally antimony-resistant <i>Leishmania braziliensis</i> isolates from Peru. <i>Infection, Genetics and Evolution</i> , 2011, 11, 1873-1880.	1.0	16
29	Optimal sample storage and extraction protocols for reliable multilocus genotyping of the human parasite <i>Schistosoma mansoni</i> . <i>Infection, Genetics and Evolution</i> , 2011, 11, 1413-1418.	1.0	30