

Magnus Manske

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

4,203
citations

236925

25
h-index

361022

35
g-index

41
all docs

41
docs citations

41
times ranked

6272
citing authors

#	ARTICLE	IF	CITATIONS
1	An open dataset of Plasmodium falciparum genome variation in 7,000 worldwide samples. Wellcome Open Research, 2021, 6, 42.	1.8	97
2	An open dataset of Plasmodium falciparum genome variation in 7,000 worldwide samples. Wellcome Open Research, 2021, 6, 42.	1.8	51
3	Wikidata as a knowledge graph for the life sciences. ELife, 2020, 9, .	6.0	76
4	GeneDB and Wikidata. Wellcome Open Research, 2019, 4, 114.	1.8	2
5	GeneDB and Wikidata. Wellcome Open Research, 2019, 4, 114.	1.8	0
6	A forward genetic screen reveals a primary role for Plasmodium falciparum Reticulocyte Binding Protein Homologue 2a and 2b in determining alternative erythrocyte invasion pathways. PLoS Pathogens, 2018, 14, e1007436.	4.7	15
7	Human candidate gene polymorphisms and risk of severe malaria in children in Kilifi, Kenya: a case-control association study. Lancet Haematology, the, 2018, 5, e333-e345.	4.6	90
8	Plasmodium malariae and P. ovale genomes provide insights into malaria parasite evolution. Nature, 2017, 542, 101-104.	27.8	150
9	Estimating Geographical Variation in the Risk of Zoonotic Plasmodium knowlesi Infection in Countries Eliminating Malaria. PLoS Neglected Tropical Diseases, 2016, 10, e0004915.	3.0	76
10	Whole genome sequencing of Plasmodium falciparum from dried blood spots using selective whole genome amplification. Malaria Journal, 2016, 15, 597.	2.3	129
11	Genomic analysis of local variation and recent evolution in Plasmodium vivax. Nature Genetics, 2016, 48, 959-964.	21.4	169
12	Genetic architecture of artemisinin-resistant Plasmodium falciparum. Nature Genetics, 2015, 47, 226-234.	21.4	515
13	Optimized Whole-Genome Amplification Strategy for Extremely AT-Biased Template. DNA Research, 2014, 21, 661-671.	3.4	27
14	Adaptive introgression between Anopheles sibling species eliminates a major genomic island but not reproductive isolation. Nature Communications, 2014, 5, 4248.	12.8	143
15	A Genome Wide Association Study of Plasmodium falciparum Susceptibility to 22 Antimalarial Drugs in Kenya. PLoS ONE, 2014, 9, e96486.	2.5	27
16	Multiple populations of artemisinin-resistant Plasmodium falciparum in Cambodia. Nature Genetics, 2013, 45, 648-655.	21.4	424
17	The NGS WikiBook: a dynamic collaborative online training effort with long-term sustainability. Briefings in Bioinformatics, 2013, 14, 548-555.	6.5	8
18	<i>Plasmodium falciparum</i> -like parasites infecting wild apes in southern Cameroon do not represent a recurrent source of human malaria. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 7020-7025.	7.1	53

#	ARTICLE	IF	CITATIONS
19	Efficient Depletion of Host DNA Contamination in Malaria Clinical Sequencing. <i>Journal of Clinical Microbiology</i> , 2013, 51, 745-751.	3.9	63
20	Genome-wide screen identifies new candidate genes associated with artemisinin susceptibility in <i>Plasmodium falciparum</i> in Kenya. <i>Scientific Reports</i> , 2013, 3, 3318.	3.3	75
21	Effective Preparation of <i>Plasmodium vivax</i> Field Isolates for High-Throughput Whole Genome Sequencing. <i>PLoS ONE</i> , 2013, 8, e53160.	2.5	26
22	Population Genomic Scan for Candidate Signatures of Balancing Selection to Guide Antigen Characterization in Malaria Parasites. <i>PLoS Genetics</i> , 2012, 8, e1002992.	3.5	167
23	VarB: a variation browsing and analysis tool for variants derived from next-generation sequencing data. <i>Bioinformatics</i> , 2012, 28, 2983-2985.	4.1	8
24	Characterization of Within-Host <i>Plasmodium falciparum</i> Diversity Using Next-Generation Sequence Data. <i>PLoS ONE</i> , 2012, 7, e32891.	2.5	102
25	Analysis of <i>Plasmodium falciparum</i> diversity in natural infections by deep sequencing. <i>Nature</i> , 2012, 487, 375-379.	27.8	450
26	Optimizing illumina next-generation sequencing library preparation for extremely at-biased genomes. <i>BMC Genomics</i> , 2012, 13, 1.	2.8	772
27	An In-Solution Hybridisation Method for the Isolation of Pathogen DNA from Human DNA-rich Clinical Samples for Analysis by NGS. <i>The Open Genomics Journal</i> , 2012, 5, 18-29.	0.5	12
28	An optimized microarray platform for assaying genomic variation in <i>Plasmodium falciparum</i> field populations. <i>Genome Biology</i> , 2011, 12, R35.	9.6	26
29	An Effective Method to Purify <i>Plasmodium falciparum</i> DNA Directly from Clinical Blood Samples for Whole Genome High-Throughput Sequencing. <i>PLoS ONE</i> , 2011, 6, e22213.	2.5	68
30	Drug-Resistant Genotypes and Multi-Clonality in <i>Plasmodium falciparum</i> Analysed by Direct Genome Sequencing from Peripheral Blood of Malaria Patients. <i>PLoS ONE</i> , 2011, 6, e23204.	2.5	41
31	Ten Simple Rules for Editing Wikipedia. <i>PLoS Computational Biology</i> , 2010, 6, e1000941.	3.2	36
32	LookSeq: A browser-based viewer for deep sequencing data. <i>Genome Research</i> , 2009, 19, 2125-2132.	5.5	56
33	SNP-o-matic. <i>Bioinformatics</i> , 2009, 25, 2434-2435.	4.1	23
34	SnoopCGH: software for visualizing comparative genomic hybridization data. <i>Bioinformatics</i> , 2009, 25, 2732-2733.	4.1	9
35	A global network for investigating the genomic epidemiology of malaria. <i>Nature</i> , 2008, 456, 732-737.	27.8	148
36	The RNA WikiProject: Community annotation of RNA families. <i>Rna</i> , 2008, 14, 2462-2464.	3.5	66