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List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

1,624
citations

687363

13
h-index

752698

20
g-index

25
all docs

25
docs citations

25
times ranked

2696
citing authors

#	ARTICLE	IF	CITATIONS
1	Malaria protection due to sickle haemoglobin depends on parasite genotype. <i>Nature</i> , 2022, 602, 106-111.	27.8	36
2	High-throughput genotyping assays for identification of glycoprotein B deletion variants in population studies. <i>Experimental Biology and Medicine</i> , 2021, 246, 916-928.	2.4	2
3	An open dataset of <i>Plasmodium falciparum</i> genome variation in 7,000 worldwide samples. <i>Wellcome Open Research</i> , 2021, 6, 42.	1.8	97
4	An open dataset of <i>Plasmodium falciparum</i> genome variation in 7,000 worldwide samples. <i>Wellcome Open Research</i> , 2021, 6, 42.	1.8	51
5	Genetic surveillance in the Greater Mekong subregion and South Asia to support malaria control and elimination. <i>ELife</i> , 2021, 10, .	6.0	53
6	Haplotype heterogeneity and low linkage disequilibrium reduce reliable prediction of genotypes for the α^+ form of β -thalassaemia using genome-wide microarray data. <i>Wellcome Open Research</i> , 2020, 5, 287.	1.8	3
7	Haplotype heterogeneity and low linkage disequilibrium reduce reliable prediction of genotypes for the α^+ form of β -thalassaemia using genome-wide microarray data. <i>Wellcome Open Research</i> , 2020, 5, 287.	1.8	4
8	Host genetic polymorphisms and serological response against malaria in a selected population in Sri Lanka. <i>Malaria Journal</i> , 2018, 17, 473.	2.3	3
9	Human candidate gene polymorphisms and risk of severe malaria in children in Kilifi, Kenya: a case-control association study. <i>Lancet Haematology</i> , 2018, 5, e333-e345.	4.6	90
10	Resistance to malaria through structural variation of red blood cell invasion receptors. <i>Science</i> , 2017, 356, .	12.6	135
11	Malaria Host Candidate Genes Validated by Association With Current, Recent, and Historical Measures of Transmission Intensity. <i>Journal of Infectious Diseases</i> , 2017, 216, 45-54.	4.0	13
12	THE REAL McCOIL: A method for the concurrent estimation of the complexity of infection and SNP allele frequency for malaria parasites. <i>PLoS Computational Biology</i> , 2017, 13, e1005348.	3.2	93
13	Characterisation of the opposing effects of G6PD deficiency on cerebral malaria and severe malarial anaemia. <i>ELife</i> , 2017, 6, .	6.0	64
14	Geographic-genetic analysis of <i>Plasmodium falciparum</i> parasite populations from surveys of primary school children in Western Kenya. <i>Wellcome Open Research</i> , 2017, 2, 29.	1.8	14
15	Heterogeneous alleles comprising G6PD deficiency trait in West Africa exert contrasting effects on two major clinical presentations of severe malaria. <i>Malaria Journal</i> , 2016, 15, 13.	2.3	25
16	Conjunctival fibrosis and the innate barriers to <i>Chlamydia trachomatis</i> intracellular infection: a genome wide association study. <i>Scientific Reports</i> , 2015, 5, 17447.	3.3	11
17	Genetic determinants of anti-malarial acquired immunity in a large multi-centre study. <i>Malaria Journal</i> , 2015, 14, 333.	2.3	26
18	Imputation-Based Meta-Analysis of Severe Malaria in Three African Populations. <i>PLoS Genetics</i> , 2013, 9, e1003509.	3.5	95

#	ARTICLE	IF	CITATIONS
19	Analysis of Plasmodium falciparum diversity in natural infections by deep sequencing. Nature, 2012, 487, 375-379.	27.8	450
20	Genome-wide and fine-resolution association analysis of malaria in West Africa. Nature Genetics, 2009, 41, 657-665.	21.4	345
21	Geographic-genetic analysis of Plasmodium falciparum parasite populations from surveys of primary school children in Western Kenya. Wellcome Open Research, 0, 2, 29.	1.8	10