

Christina Hubbart

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2192004/publications.pdf>

Version: 2024-02-01

27
papers

1,961
citations

516561

16
h-index

580701

25
g-index

32
all docs

32
docs citations

32
times ranked

2933
citing authors

#	ARTICLE	IF	CITATIONS
1	Analysis of Plasmodium falciparum diversity in natural infections by deep sequencing. Nature, 2012, 487, 375-379.	13.7	450
2	Multiple populations of artemisinin-resistant Plasmodium falciparum in Cambodia. Nature Genetics, 2013, 45, 648-655.	9.4	424
3	Genomic analysis of local variation and recent evolution in Plasmodium vivax. Nature Genetics, 2016, 48, 959-964.	9.4	169
4	Resistance to malaria through structural variation of red blood cell invasion receptors. Science, 2017, 356, .	6.0	135
5	An open dataset of Plasmodium falciparum genome variation in 7,000 worldwide samples. Wellcome Open Research, 2021, 6, 42.	0.9	97
6	Imputation-Based Meta-Analysis of Severe Malaria in Three African Populations. PLoS Genetics, 2013, 9, e1003509.	1.5	95
7	THE REAL McCOIL: A method for the concurrent estimation of the complexity of infection and SNP allele frequency for malaria parasites. PLoS Computational Biology, 2017, 13, e1005348.	1.5	93
8	Human candidate gene polymorphisms and risk of severe malaria in children in Kilifi, Kenya: a case-control association study. Lancet Haematology, 2018, 5, e333-e345.	2.2	90
9	Characterisation of the opposing effects of G6PD deficiency on cerebral malaria and severe malarial anaemia. ELife, 2017, 6, .	2.8	64
10	Genetic surveillance in the Greater Mekong subregion and South Asia to support malaria control and elimination. ELife, 2021, 10, .	2.8	53
11	An open dataset of Plasmodium falciparum genome variation in 7,000 worldwide samples. Wellcome Open Research, 2021, 6, 42.	0.9	51
12	A high throughput multi-locus insecticide resistance marker panel for tracking resistance emergence and spread in Anopheles gambiae. Scientific Reports, 2019, 9, 13335.	1.6	41
13	Malaria protection due to sickle haemoglobin depends on parasite genotype. Nature, 2022, 602, 106-111.	13.7	36
14	Micro-epidemiological structuring of Plasmodium falciparum parasite populations in regions with varying transmission intensities in Africa. Wellcome Open Research, 2017, 2, 10.	0.9	27
15	Genetic determinants of anti-malarial acquired immunity in a large multi-centre study. Malaria Journal, 2015, 14, 333.	0.8	26
16	Heterogeneous alleles comprising G6PD deficiency trait in West Africa exert contrasting effects on two major clinical presentations of severe malaria. Malaria Journal, 2016, 15, 13.	0.8	25
17	Evaluating the Performance of Malaria Genetics for Inferring Changes in Transmission Intensity Using Transmission Modeling. Molecular Biology and Evolution, 2021, 38, 274-289.	3.5	17
18	Geographic-genetic analysis of Plasmodium falciparum parasite populations from surveys of primary school children in Western Kenya. Wellcome Open Research, 2017, 2, 29.	0.9	14

#	ARTICLE	IF	CITATIONS
19	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.	1.9	13
20	Geographic-genetic analysis of <i>Plasmodium falciparum</i> parasite populations from surveys of primary school children in Western Kenya. <i>Wellcome Open Research</i> , 0, 2, 29.	0.9	10
21	Novel genotyping approaches to easily detect genomic admixture between the major Afrotropical malaria vector species, <i>Anopheles coluzzii</i> and <i>An. gambiae</i> . <i>Molecular Ecology Resources</i> , 2021, 21, 1504-1516.	2.2	7
22	Micro-epidemiological structuring of <i>Plasmodium falciparum</i> parasite populations in regions with varying transmission intensities in Africa.. <i>Wellcome Open Research</i> , 0, 2, 10.	0.9	7
23	High-throughput genotyping of <i>Anopheles</i> mosquitoes using intact legs by <i>genosciences</i> iPLEX. <i>Molecular Ecology Resources</i> , 2016, 16, 480-486.	2.2	5
24	Haplotype heterogeneity and low linkage disequilibrium reduce reliable prediction of genotypes for the β^0/β^0 form of β^0 -thalassaemia using genome-wide microarray data. <i>Wellcome Open Research</i> , 2020, 5, 287.	0.9	4
25	Haplotype heterogeneity and low linkage disequilibrium reduce reliable prediction of genotypes for the β^0/β^0 form of β^0 -thalassaemia using genome-wide microarray data. <i>Wellcome Open Research</i> , 2020, 5, 287.	0.9	3
26	Investigating the drivers of the spatio-temporal patterns of genetic differences between <i>Plasmodium falciparum</i> malaria infections in Kilifi County, Kenya. <i>Scientific Reports</i> , 2019, 9, 19018.	1.6	2
27	High-throughput genotyping assays for identification of glycoporphin B deletion variants in population studies. <i>Experimental Biology and Medicine</i> , 2021, 246, 916-928.	1.1	2