# Christina Hubbart

List of Publications by Year
in descending order



| | | | |
|---|---|---|---|
| 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 | Malaria protection due to sickle haemoglobin depends on parasite genotype. Nature, 2022, 602, 106-111. | 13.7 | 36 |
| 2 | High-throughput genotyping assays for identification of glycophorin B deletion variants in population studies. Experimental Biology and Medicine, 2021, 246, 916-928. | 1.1 | 2 |
| 3 | 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 |
| 4 | An open dataset of Plasmodium falciparum genome variation in 7,000 worldwide samples. Wellcome Open Research, 2021, 6, 42. | 0.9 | 97 |
| 5 | Novel genotyping approaches to easily detect genomic admixture between the major Afrotropical malaria vector species, Anopheles coluzzii and An. gambiae. Molecular Ecology Resources, 2021, 21, 1504-1516. | 2.2 | 7 |
| 6 | An open dataset of Plasmodium falciparum genome variation in 7,000 worldwide samples. Wellcome Open Research, 2021, 6, 42. | 0.9 | 51 |
| 7 | Genetic surveillance in the Greater Mekong subregion and South Asia to support malaria control and elimination. ELife, 2021, 10, . | 2.8 | 53 |
| 8 | Haplotype heterogeneity and low linkage disequilibrium reduce reliable prediction of genotypes for the â€Î±3.7I form of Î±-thalassaemia using genome-wide microarray data. Wellcome Open Research, 2020, 5, 287. | 0.9 | 3 |
| 9 | Haplotype heterogeneity and low linkage disequilibrium reduce reliable prediction of genotypes for the â€Î±3.7I form of Î±-thalassaemia using genome-wide microarray data. Wellcome Open Research, 2020, 5, 287. | 0.9 | 4 |
| 10 | 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 |
| 11 | Investigating the drivers of the spatio-temporal patterns of genetic differences between Plasmodium falciparum malaria infections in Kilifi County, Kenya. Scientific Reports, 2019, 9, 19018. | 1.6 | 2 |
| 12 | 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. | 2.2 | 90 |
| 13 | Resistance to malaria through structural variation of red blood cell invasion receptors. Science, 2017, 356, . | 6.0 | 135 |
| 14 | Malaria Host Candidate Genes Validated by Association With Current, Recent, and Historical Measures of Transmission Intensity. Journal of Infectious Diseases, 2017, 216, 45-54. | 1.9 | 13 |
| 15 | 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 |
| 16 | Characterisation of the opposing effects of G6PD deficiency on cerebral malaria and severe malarial anaemia. ELife, 2017, 6, . | 2.8 | 64 |
| 17 | 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 |
| 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 | Highâ€throughput genotyping of <scp>A</scp>nopheles mosquitoes using intact legs by <scp>A</scp>gena <scp>B</scp>iosciences i<scp>PLEX</scp>. Molecular Ecology Resources, 2016, 16, 480-486. | 2.2 | 5 |
| 20 | 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 |
| 21 | Genomic analysis of local variation and recent evolution in Plasmodium vivax. Nature Genetics, 2016, 48, 959-964. | 9.4 | 169 |
| 22 | Genetic determinants of anti-malarial acquired immunity in a large multi-centre study. Malaria Journal, 2015, 14, 333. | 0.8 | 26 |
| 23 | Multiple populations of artemisinin-resistant Plasmodium falciparum in Cambodia. Nature Genetics, 2013, 45, 648-655. | 9.4 | 424 |
| 24 | Imputation-Based Meta-Analysis of Severe Malaria in Three African Populations. PLoS Genetics, 2013, 9, e1003509. | 1.5 | 95 |
| 25 | Analysis of Plasmodium falciparum diversity in natural infections by deep sequencing. Nature, 2012, 487, 375-379. | 13.7 | 450 |
| 26 | Geographic-genetic analysis of Plasmodium falciparum parasite populations from surveys of primary school children in Western Kenya. Wellcome Open Research, 0, 2, 29. | 0.9 | 10 |
| 27 | Micro-epidemiological structuring of Plasmodium falciparum parasite populations in regions with varying transmission intensities in Africa.. Wellcome Open Research, 0, 2, 10. | 0.9 | 7 |