

Kirk A Rockett

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5444173/publications.pdf>

Version: 2024-02-01

68
papers

5,170
citations

147801

31
h-index

106344

65
g-index

81
all docs

81
docs citations

81
times ranked

7315
citing authors

#	ARTICLE	IF	CITATIONS
1	The African Genome Variation Project shapes medical genetics in Africa. <i>Nature</i> , 2015, 517, 327-332.	27.8	473
2	Analysis of <i>Plasmodium falciparum</i> diversity in natural infections by deep sequencing. <i>Nature</i> , 2012, 487, 375-379.	27.8	450
3	Multiple populations of artemisinin-resistant <i>Plasmodium falciparum</i> in Cambodia. <i>Nature Genetics</i> , 2013, 45, 648-655.	21.4	424
4	Severe Anemia in Malawian Children. <i>New England Journal of Medicine</i> , 2008, 358, 888-899.	27.0	345
5	Genome-wide and fine-resolution association analysis of malaria in West Africa. <i>Nature Genetics</i> , 2009, 41, 657-665.	21.4	345
6	Genome-wide association analyses identifies a susceptibility locus for tuberculosis on chromosome 18q11.2. <i>Nature Genetics</i> , 2010, 42, 739-741.	21.4	332
7	Evolution and expansion of multidrug-resistant malaria in southeast Asia: a genomic epidemiology study. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 943-951.	9.1	219
8	A novel locus of resistance to severe malaria in a region of ancient balancing selection. <i>Nature</i> , 2015, 526, 253-257.	27.8	182
9	Common variation in the ABO glycosyltransferase is associated with susceptibility to severe <i>Plasmodium falciparum</i> malaria. <i>Human Molecular Genetics</i> , 2008, 17, 567-576.	2.9	148
10	Resistance to malaria through structural variation of red blood cell invasion receptors. <i>Science</i> , 2017, 356, .	12.6	135
11	Whole genome sequencing of <i>Plasmodium falciparum</i> from dried blood spots using selective whole genome amplification. <i>Malaria Journal</i> , 2016, 15, 597.	2.3	129
12	Admixture into and within sub-Saharan Africa. <i>ELife</i> , 2016, 5, .	6.0	120
13	Allelic heterogeneity of G6PD deficiency in West Africa and severe malaria susceptibility. <i>European Journal of Human Genetics</i> , 2009, 17, 1080-1085.	2.8	109
14	Characterization of Within-Host <i>Plasmodium falciparum</i> Diversity Using Next-Generation Sequence Data. <i>PLoS ONE</i> , 2012, 7, e32891.	2.5	102
15	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
16	Imputation-Based Meta-Analysis of Severe Malaria in Three African Populations. <i>PLoS Genetics</i> , 2013, 9, e1003509.	3.5	95
17	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
18	Human candidate gene polymorphisms and risk of severe malaria in children in Kilifi, Kenya: a case-control association study. <i>Lancet Haematology</i> , the, 2018, 5, e333-e345.	4.6	90

#	ARTICLE	IF	CITATIONS
19	Glucose-6-phosphate dehydrogenase deficiency and the risk of malaria and other diseases in children in Kenya: a case-control and a cohort study. <i>Lancet Haematology</i> , 2015, 2, e437-e444.	4.6	74
20	Red blood cell tension protects against severe malaria in the Dantu blood group. <i>Nature</i> , 2020, 585, 579-583.	27.8	69
21	An Effective Method to Purify Plasmodium falciparum DNA Directly from Clinical Blood Samples for Whole Genome High-Throughput Sequencing. <i>PLoS ONE</i> , 2011, 6, e22213.	2.5	68
22	Characterisation of the opposing effects of G6PD deficiency on cerebral malaria and severe malarial anaemia. <i>ELife</i> , 2017, 6, .	6.0	64
23	Population Genetic Analysis of Plasmodium falciparum Parasites Using a Customized Illumina GoldenGate Genotyping Assay. <i>PLoS ONE</i> , 2011, 6, e20251.	2.5	63
24	Seasonal Childhood Anaemia in West Africa Is Associated with the Haptoglobin 2-2 Genotype. <i>PLoS Medicine</i> , 2006, 3, e172.	8.4	60
25	Genetic surveillance in the Greater Mekong subregion and South Asia to support malaria control and elimination. <i>ELife</i> , 2021, 10, .	6.0	53
26	An open dataset of Plasmodium falciparum genome variation in 7,000 worldwide samples. <i>Wellcome Open Research</i> , 2021, 6, 42.	1.8	51
27	Drug-Resistant Genotypes and Multi-Clonality in Plasmodium falciparum Analysed by Direct Genome Sequencing from Peripheral Blood of Malaria Patients. <i>PLoS ONE</i> , 2011, 6, e23204.	2.5	41
28	Candidate Polymorphisms and Severe Malaria in a Malian Population. <i>PLoS ONE</i> , 2012, 7, e43987.	2.5	41
29	A high throughput multi-locus insecticide resistance marker panel for tracking resistance emergence and spread in Anopheles gambiae. <i>Scientific Reports</i> , 2019, 9, 13335.	3.3	41
30	Polymorphism in a lincRNA Associates with a Doubled Risk of Pneumococcal Bacteremia in Kenyan Children. <i>American Journal of Human Genetics</i> , 2016, 98, 1092-1100.	6.2	39
31	Tumor necrosis factor SNP haplotypes are associated with iron deficiency anemia in West African children. <i>Blood</i> , 2008, 112, 4276-4283.	1.4	38
32	The genetic risk of acute seizures in African children with falciparum malaria. <i>Epilepsia</i> , 2013, 54, 990-1001.	5.1	36
33	Malaria protection due to sickle haemoglobin depends on parasite genotype. <i>Nature</i> , 2022, 602, 106-111.	27.8	36
34	Malaria is a cause of iron deficiency in African children. <i>Nature Medicine</i> , 2021, 27, 653-658.	30.7	35
35	Candidate malaria susceptibility/protective SNPs in hospital and population-based studies: the effect of sub-structuring. <i>Malaria Journal</i> , 2010, 9, 119.	2.3	28
36	Micro-epidemiological structuring of Plasmodium falciparum parasite populations in regions with varying transmission intensities in Africa. <i>Wellcome Open Research</i> , 2017, 2, 10.	1.8	27

#	ARTICLE	IF	CITATIONS
37	A Genome Wide Association Study of Plasmodium falciparum Susceptibility to 22 Antimalarial Drugs in Kenya. PLoS ONE, 2014, 9, e96486.	2.5	27
38	Genetic determinants of anti-malarial acquired immunity in a large multi-centre study. Malaria Journal, 2015, 14, 333.	2.3	26
39	Novel Insights Into the Protective Role of Hemoglobin S and C Against Plasmodium falciparum Parasitemia. Journal of Infectious Diseases, 2015, 212, 626-634.	4.0	26
40	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.	2.3	25
41	Two complement receptor one alleles have opposing associations with cerebral malaria and interact with $\beta\text{-thalassaemia}$. ELife, 2018, 7, .	6.0	25
42	Tumour necrosis factor alpha promoter polymorphism, TNF-238 is associated with severe clinical outcome of falciparum malaria in Ibadan southwest Nigeria. Acta Tropica, 2016, 161, 62-67.	2.0	24
43	Epistasis between the haptoglobin common variant and $\beta\text{-thalassaemia}$ influences risk of severe malaria in Kenyan children. Blood, 2014, 123, 2008-2016.	1.4	23
44	Improving statistical power in severe malaria genetic association studies by augmenting phenotypic precision. ELife, 2021, 10, .	6.0	22
45	Environmental Correlation Analysis for Genes Associated with Protection against Malaria. Molecular Biology and Evolution, 2016, 33, 1188-1204.	8.9	21
46	The ferroportin Q248H mutation protects from anemia, but not malaria or bacteremia. Science Advances, 2019, 5, eaaw0109.	10.3	20
47	Severe anemia in Malawian children. Malawi Medical Journal, 2016, 28, 99-107.	0.6	19
48	Evaluating the Performance of Malaria Genetics for Inferring Changes in Transmission Intensity Using Transmission Modeling. Molecular Biology and Evolution, 2021, 38, 274-289.	8.9	17
49	Geographic-genetic analysis of Plasmodium falciparum parasite populations from surveys of primary school children in Western Kenya. Wellcome Open Research, 2017, 2, 29.	1.8	14
50	Malaria Host Candidate Genes Validated by Association With Current, Recent, and Historical Measures of Transmission Intensity. Journal of Infectious Diseases, 2017, 216, 45-54.	4.0	13
51	Conjunctival fibrosis and the innate barriers to Chlamydia trachomatis intracellular infection: a genome wide association study. Scientific Reports, 2015, 5, 17447.	3.3	11
52	Implications of inter-population linkage disequilibrium patterns on the approach to a disease association study in the human MHC class III. Immunogenetics, 2006, 58, 465-470.	2.4	10
53	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
54	G6PD gene variants and its association with malaria in a Sri Lankan population. Malaria Journal, 2015, 14, 93.	2.3	9

#	ARTICLE	IF	CITATIONS
55	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.	4.8	7
56	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.	1.8	7
57	Temporal evolution of sulfadoxine-pyrimethamine resistance genotypes and genetic diversity in response to a decade of increased interventions against <i>Plasmodium falciparum</i> in northern Ghana. <i>Malaria Journal</i> , 2021, 20, 152.	2.3	6
58	High-throughput genotyping of <i>Anopheles</i> mosquitoes using intact legs by <i>PLEX</i> . <i>Molecular Ecology Resources</i> , 2016, 16, 480-486.	4.8	5
59	Risk of pneumococcal bacteremia in Kenyan children with glucose-6-phosphate dehydrogenase deficiency. <i>BMC Medicine</i> , 2020, 18, 148.	5.5	4
60	Haplotype heterogeneity and low linkage disequilibrium reduce reliable prediction of genotypes for the $\beta^{\pm 3.71}$ form of β^{\pm} -thalassaemia using genome-wide microarray data. <i>Wellcome Open Research</i> , 2020, 5, 287.	1.8	4
61	Interferon-gamma polymorphisms and risk of iron deficiency and anaemia in Gambian children. <i>Wellcome Open Research</i> , 2020, 5, 40.	1.8	4
62	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
63	Haplotype heterogeneity and low linkage disequilibrium reduce reliable prediction of genotypes for the $\beta^{\pm 3.71}$ form of β^{\pm} -thalassaemia using genome-wide microarray data. <i>Wellcome Open Research</i> , 2020, 5, 287.	1.8	3
64	Interferon-gamma polymorphisms and risk of iron deficiency and anaemia in Gambian children. <i>Wellcome Open Research</i> , 2020, 5, 40.	1.8	3
65	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.	3.3	2
66	High-throughput genotyping assays for identification of glycoophorin B deletion variants in population studies. <i>Experimental Biology and Medicine</i> , 2021, 246, 916-928.	2.4	2
67	A haptoglobin gene promoter polymorphism (A \rightarrow G1C) protects from anaemia in pregnant Zanzibari women. <i>FASEB Journal</i> , 2007, 21, A1119.	0.5	0
68	A \rightarrow G1 haptoglobin gene promoter polymorphism and protection from malaria in Gambian children.. <i>FASEB Journal</i> , 2007, 21, A164.	0.5	0