

# Sarah Auburn

## List of Publications by Year in descending order

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Version: 2024-02-01

73  
papers

4,332  
citations

159525

30  
h-index

118793

62  
g-index

76  
all docs

76  
docs citations

76  
times ranked

4915  
citing authors

#	ARTICLE	IF	CITATIONS
1	Analysis of <i>Plasmodium falciparum</i> diversity in natural infections by deep sequencing. <i>Nature</i> , 2012, 487, 375-379.	13.7	450
2	Multiple populations of artemisinin-resistant <i>Plasmodium falciparum</i> in Cambodia. <i>Nature Genetics</i> , 2013, 45, 648-655.	9.4	424
3	Genome-wide and fine-resolution association analysis of malaria in West Africa. <i>Nature Genetics</i> , 2009, 41, 657-665.	9.4	345
4	Genetic loci associated with delayed clearance of <i>Plasmodium falciparum</i> following artemisinin treatment in Southeast Asia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 240-245.	3.3	242
5	A Prospective Comparative Study of Knowlesi, <i>Falciparum</i> , and <i>Vivax</i> Malaria in Sabah, Malaysia: High Proportion With Severe Disease From <i>Plasmodium Knowlesi</i> and <i>Plasmodium Vivax</i> But No Mortality With Early Referral and Artesunate Therapy. <i>Clinical Infectious Diseases</i> , 2013, 56, 383-397.	2.9	207
6	Genomic analysis of local variation and recent evolution in <i>Plasmodium vivax</i> . <i>Nature Genetics</i> , 2016, 48, 959-964.	9.4	169
7	<i>Plasmodium malariae</i> and <i>P. ovale</i> genomes provide insights into malaria parasite evolution. <i>Nature</i> , 2017, 542, 101-104.	13.7	150
8	A global network for investigating the genomic epidemiology of malaria. <i>Nature</i> , 2008, 456, 732-737.	13.7	148
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.	1.4	148
10	Review of key knowledge gaps in glucose-6-phosphate dehydrogenase deficiency detection with regard to the safe clinical deployment of 8-aminoquinoline treatment regimens: a workshop report. <i>Malaria Journal</i> , 2013, 12, 112.	0.8	112
11	Allelic heterogeneity of G6PD deficiency in West Africa and severe malaria susceptibility. <i>European Journal of Human Genetics</i> , 2009, 17, 1080-1085.	1.4	109
12	Short-course primaquine for the radical cure of <i>Plasmodium vivax</i> malaria: a multicentre, randomised, placebo-controlled non-inferiority trial. <i>Lancet</i> , The, 2019, 394, 929-938.	6.3	106
13	Characterization of Within-Host <i>Plasmodium falciparum</i> Diversity Using Next-Generation Sequence Data. <i>PLoS ONE</i> , 2012, 7, e32891.	1.1	102
14	Emergence of artemisinin-resistant <i>Plasmodium falciparum</i> with kelch13 C580Y mutations on the island of New Guinea. <i>PLoS Pathogens</i> , 2020, 16, e1009133.	2.1	81
15	Using CF11 cellulose columns to inexpensively and effectively remove human DNA from <i>Plasmodium falciparum</i> -infected whole blood samples. <i>Malaria Journal</i> , 2012, 11, 41.	0.8	79
16	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.	1.6	75
17	Phenotypic and genotypic characterisation of drug-resistant <i>Plasmodium vivax</i> . <i>Trends in Parasitology</i> , 2012, 28, 522-529.	1.5	70
18	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.	1.1	68

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19	Comparison of artemether-lumefantrine and chloroquine with and without primaquine for the treatment of <i>Plasmodium vivax</i> infection in Ethiopia: A randomized controlled trial. <i>PLoS Medicine</i> , 2017, 14, e1002299.	3.9	64
20	Positive selection of a CD36 nonsense variant in sub-Saharan Africa, but no association with severe malaria phenotypes. <i>Human Molecular Genetics</i> , 2009, 18, 2683-2692.	1.4	63
21	Contrasting Transmission Dynamics of Co-endemic <i>Plasmodium vivax</i> and <i>P. falciparum</i> : Implications for Malaria Control and Elimination. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003739.	1.3	63
22	Population Genetic Analysis of <i>Plasmodium falciparum</i> Parasites Using a Customized Illumina GoldenGate Genotyping Assay. <i>PLoS ONE</i> , 2011, 6, e20251.	1.1	63
23	Genomic analysis of a pre-elimination Malaysian <i>Plasmodium vivax</i> population reveals selective pressures and changing transmission dynamics. <i>Nature Communications</i> , 2018, 9, 2585.	5.8	59
24	Dissecting malaria biology and epidemiology using population genetics and genomics. <i>International Journal for Parasitology</i> , 2017, 47, 77-85.	1.3	56
25	Tumor Necrosis Factor and Lymphotoxin- $\alpha$ Polymorphisms and Severe Malaria in African Populations. <i>Journal of Infectious Diseases</i> , 2009, 199, 569-575.	1.9	52
26	Submicroscopic and Asymptomatic <i>Plasmodium</i> Parasitaemia Associated with Significant Risk of Anaemia in Papua, Indonesia. <i>PLoS ONE</i> , 2016, 11, e0165340.	1.1	48
27	<i>Plasmodium vivax</i> Population Structure and Transmission Dynamics in Sabah Malaysia. <i>PLoS ONE</i> , 2013, 8, e82553.	1.1	45
28	Efficacy of Artesunate-mefloquine for Chloroquine-resistant <i>Plasmodium vivax</i> Malaria in Malaysia: An Open-label, Randomized, Controlled Trial. <i>Clinical Infectious Diseases</i> , 2016, 62, 1403-1411.	2.9	44
29	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.	1.1	41
30	Variation in the ICAM1 gene is not associated with severe malaria phenotypes. <i>Genes and Immunity</i> , 2008, 9, 462-469.	2.2	38
31	Genomic Characterization of Recrudescence <i>Plasmodium malariae</i> after Treatment with Artemether/Lumefantrine. <i>Emerging Infectious Diseases</i> , 2017, 23, 1300-1307.	2.0	36
32	Variation in Complexity of Infection and Transmission Stability between Neighbouring Populations of <i>Plasmodium vivax</i> in Southern Ethiopia. <i>PLoS ONE</i> , 2015, 10, e0140780.	1.1	33
33	Implementing parasite genotyping into national surveillance frameworks: feedback from control programmes and researchers in the Asia-Pacific region. <i>Malaria Journal</i> , 2020, 19, 271.	0.8	31
34	TLR9 polymorphisms in African populations: no association with severe malaria, but evidence of cis-variants acting on gene expression. <i>Malaria Journal</i> , 2009, 8, 44.	0.8	30
35	The changing epidemiology of <i>Plasmodium vivax</i> : Insights from conventional and novel surveillance tools. <i>PLoS Medicine</i> , 2021, 18, e1003560.	3.9	28
36	G6PD Deficiency and Antimalarial Efficacy for Uncomplicated Malaria in Bangladesh: A Prospective Observational Study. <i>PLoS ONE</i> , 2016, 11, e0154015.	1.1	28

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37	A genetic association study in the Gambia using tagging polymorphisms in the major histocompatibility complex class III region implicates a HLA-B associated transcript 2 polymorphism in severe malaria susceptibility. <i>Human Genetics</i> , 2009, 125, 105-109.	1.8	27
38	Effective Preparation of <i>Plasmodium vivax</i> Field Isolates for High-Throughput Whole Genome Sequencing. <i>PLoS ONE</i> , 2013, 8, e53160.	1.1	26
39	Genetic determinants of anti-malarial acquired immunity in a large multi-centre study. <i>Malaria Journal</i> , 2015, 14, 333.	0.8	26
40	Chloroquine efficacy for <i>Plasmodium vivax</i> malaria treatment in southern Ethiopia. <i>Malaria Journal</i> , 2015, 14, 525.	0.8	26
41	Expression of <i>Plasmodium vivax</i> <i>cr1</i> Is Related to Parasite Stage but Not <i>Ex Vivo</i> Chloroquine Susceptibility. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 361-367.	1.4	25
42	Whole genome sequencing of <i>Plasmodium vivax</i> isolates reveals frequent sequence and structural polymorphisms in erythrocyte binding genes. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008234.	1.3	25
43	Chloroquine efficacy for <i>Plasmodium vivax</i> in Myanmar in populations with high genetic diversity and moderate parasite gene flow. <i>Malaria Journal</i> , 2017, 16, 281.	0.8	24
44	Validating Discovered Cis-Acting Regulatory Genetic Variants: Application of an Allele Specific Expression Approach to HapMap Populations. <i>PLoS ONE</i> , 2008, 3, e4105.	1.1	22
45	Where chloroquine still works: the genetic make-up and susceptibility of <i>Plasmodium vivax</i> to chloroquine plus primaquine in Bhutan. <i>Malaria Journal</i> , 2016, 15, 277.	0.8	21
46	Dihydrofolate-Reductase Mutations in <i>Plasmodium knowlesi</i> Appear Unrelated to Selective Drug Pressure from Putative Human-To-Human Transmission in Sabah, Malaysia. <i>PLoS ONE</i> , 2016, 11, e0149519.	1.1	17
47	Molecular Epidemiology of <i>P. vivax</i> in Iran: High Diversity and Complex Sub-Structure Using Neutral Markers, but No Evidence of Y976F Mutation at <i>pvmdr1</i> . <i>PLoS ONE</i> , 2016, 11, e0166124.	1.1	17
48	Genetic micro-epidemiology of malaria in Papua Indonesia: Extensive <i>P. vivax</i> diversity and a distinct subpopulation of asymptomatic <i>P. falciparum</i> infections. <i>PLoS ONE</i> , 2017, 12, e0177445.	1.1	16
49	Passively versus Actively Detected Malaria: Similar Genetic Diversity but Different Complexity of Infection. <i>American Journal of Tropical Medicine and Hygiene</i> , 2017, 97, 1788-1796.	0.6	16
50	Further Evidence Supporting a Role for Gs Signal Transduction in Severe Malaria Pathogenesis. <i>PLoS ONE</i> , 2010, 5, e10017.	1.1	14
51	VivaxGEN: An open access platform for comparative analysis of short tandem repeat genotyping data in <i>Plasmodium vivax</i> populations. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005465.	1.3	13
52	Further Evidence of Increasing Diversity of <i>Plasmodium vivax</i> in the Republic of Korea in Recent Years. <i>PLoS ONE</i> , 2016, 11, e0151514.	1.1	13
53	Association of the GNAS locus with severe malaria. <i>Human Genetics</i> , 2008, 124, 499-506.	1.8	12
54	Lack of Association of Interferon Regulatory Factor 1 with Severe Malaria in Affected Child-Parental Trio Studies across Three African Populations. <i>PLoS ONE</i> , 2009, 4, e4206.	1.1	11

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55	Glucose-6-phosphate dehydrogenase activity in individuals with and without malaria: Analysis of clinical trial, cross-sectional and case-control data from Bangladesh. PLoS Medicine, 2021, 18, e1003576.	3.9	10
56	SnoopCGH: software for visualizing comparative genomic hybridization data. Bioinformatics, 2009, 25, 2732-2733.	1.8	9
57	Molecular surveillance over 14 years confirms reduction of Plasmodium vivax and falciparum transmission after implementation of Artemisinin-based combination therapy in Papua, Indonesia. PLoS Neglected Tropical Diseases, 2020, 14, e0008295.	1.3	9
58	VarB: a variation browsing and analysis tool for variants derived from next-generation sequencing data. Bioinformatics, 2012, 28, 2983-2985.	1.8	8
59	Wide range of G6PD activities found among ethnic groups of the Chittagong Hill Tracts, Bangladesh. PLoS Neglected Tropical Diseases, 2020, 14, e0008697.	1.3	8
60	Multi-locus genotyping reveals established endemicity of a geographically distinct Plasmodium vivax population in Mauritania, West Africa. PLoS Neglected Tropical Diseases, 2020, 14, e0008945.	1.3	7
61	A Bayesian approach using covariance of single nucleotide polymorphism data to detect differences in linkage disequilibrium patterns between groups of individuals. Bioinformatics, 2010, 26, 1999-2003.	1.8	5
62	Genetic diversity and neutral selection in Plasmodium vivax erythrocyte binding protein correlates with patient antigenicity. PLoS Neglected Tropical Diseases, 2020, 14, e0008202.	1.3	5
63	Longitudinal ex vivo and molecular trends of chloroquine and piperaquine activity against Plasmodium falciparum and P. vivax before and after introduction of artemisinin-based combination therapy in Papua, Indonesia. International Journal for Parasitology: Drugs and Drug Resistance, 2021, 17, 46-56.	1.4	4
64	Geographical distribution and genetic diversity of Plasmodium vivax reticulocyte binding protein 1a correlates with patient antigenicity. PLoS Neglected Tropical Diseases, 2022, 16, e0010492.	1.3	2
65	Title is missing!. , 2020, 14, e0008295.		0
66	Title is missing!. , 2020, 14, e0008295.		0
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73	Title is missing!. , 2020, 14, e0008945.		0