

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	Geographical distribution and genetic diversity of <i>Plasmodium vivax</i> reticulocyte binding protein 1a correlates with patient antigenicity. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010492.	1.3	2
2	Glucose-6-phosphate dehydrogenase activity in individuals with and without malaria: Analysis of clinical trial, cross-sectional and case-control data from Bangladesh. <i>PLoS Medicine</i> , 2021, 18, e1003576.	3.9	10
3	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
4	Longitudinal ex vivo and molecular trends of chloroquine and piperazine activity against <i>Plasmodium falciparum</i> and <i>P. vivax</i> before and after introduction of artemisinin-based combination therapy in Papua, Indonesia. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2021, 17, 46-56.	1.4	4
5	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
6	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
7	Wide range of G6PD activities found among ethnic groups of the Chittagong Hill Tracts, Bangladesh. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008697.	1.3	8
8	Molecular surveillance over 14 years confirms reduction of <i>Plasmodium vivax</i> and <i>falciparum</i> transmission after implementation of Artemisinin-based combination therapy in Papua, Indonesia. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008295.	1.3	9
9	Genetic diversity and neutral selection in <i>Plasmodium vivax</i> erythrocyte binding protein correlates with patient antigenicity. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008202.	1.3	5
10	Multi-locus genotyping reveals established endemicity of a geographically distinct <i>Plasmodium vivax</i> population in Mauritania, West Africa. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008945.	1.3	7
11	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
12	Title is missing!. , 2020, 14, e0008295.		0
13	Title is missing!. , 2020, 14, e0008295.		0
14	Title is missing!. , 2020, 14, e0008295.		0
15	Title is missing!. , 2020, 14, e0008295.		0
16	Title is missing!. , 2020, 14, e0008295.		0
17	Title is missing!. , 2020, 14, e0008945.		0
18	Title is missing!. , 2020, 14, e0008945.		0

#	ARTICLE	IF	CITATIONS
19	Title is missing!. , 2020, 14, e0008945.		0
20	Title is missing!. , 2020, 14, e0008945.		0
21	Short-course primaquine for the radical cure of Plasmodium vivax malaria: a multicentre, randomised, placebo-controlled non-inferiority trial. Lancet, The, 2019, 394, 929-938.	6.3	106
22	Genomic analysis of a pre-elimination Malaysian Plasmodium vivax population reveals selective pressures and changing transmission dynamics. Nature Communications, 2018, 9, 2585.	5.8	59
23	Plasmodium malariae and P. ovale genomes provide insights into malaria parasite evolution. Nature, 2017, 542, 101-104.	13.7	150
24	Dissecting malaria biology and epidemiology using population genetics and genomics. International Journal for Parasitology, 2017, 47, 77-85.	1.3	56
25	Chloroquine efficacy for Plasmodium vivax in Myanmar in populations with high genetic diversity and moderate parasite gene flow. Malaria Journal, 2017, 16, 281.	0.8	24
26	Genomic Characterization of Recrudescence of Plasmodium malariae after Treatment with Artemether/Lumefantrine. Emerging Infectious Diseases, 2017, 23, 1300-1307.	2.0	36
27	Comparison of artemether-lumefantrine and chloroquine with and without primaquine for the treatment of Plasmodium vivax infection in Ethiopia: A randomized controlled trial. PLoS Medicine, 2017, 14, e1002299.	3.9	64
28	VivaxGEN: An open access platform for comparative analysis of short tandem repeat genotyping data in Plasmodium vivax populations. PLoS Neglected Tropical Diseases, 2017, 11, e0005465.	1.3	13
29	Genetic micro-epidemiology of malaria in Papua Indonesia: Extensive P. vivax diversity and a distinct subpopulation of asymptomatic P. falciparum infections. PLoS ONE, 2017, 12, e0177445.	1.1	16
30	Passively versus Actively Detected Malaria: Similar Genetic Diversity but Different Complexity of Infection. American Journal of Tropical Medicine and Hygiene, 2017, 97, 1788-1796.	0.6	16
31	Where chloroquine still works: the genetic make-up and susceptibility of Plasmodium vivax to chloroquine plus primaquine in Bhutan. Malaria Journal, 2016, 15, 277.	0.8	21
32	Efficacy of Artesunate-mefloquine for Chloroquine-resistant Plasmodium vivax Malaria in Malaysia: An Open-label, Randomized, Controlled Trial. Clinical Infectious Diseases, 2016, 62, 1403-1411.	2.9	44
33	Genomic analysis of local variation and recent evolution in Plasmodium vivax. Nature Genetics, 2016, 48, 959-964.	9.4	169
34	Expression of Plasmodium vivax crt-o Is Related to Parasite Stage but Not Ex Vivo Chloroquine Susceptibility. Antimicrobial Agents and Chemotherapy, 2016, 60, 361-367.	1.4	25
35	Dihydrofolate-Reductase Mutations in Plasmodium knowlesi Appear Unrelated to Selective Drug Pressure from Putative Human-To-Human Transmission in Sabah, Malaysia. PLoS ONE, 2016, 11, e0149519.	1.1	17
36	Further Evidence of Increasing Diversity of Plasmodium vivax in the Republic of Korea in Recent Years. PLoS ONE, 2016, 11, e0151514.	1.1	13

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37	G6PD Deficiency and Antimalarial Efficacy for Uncomplicated Malaria in Bangladesh: A Prospective Observational Study. <i>PLoS ONE</i> , 2016, 11, e0154015.	1.1	28
38	Submicroscopic and Asymptomatic Plasmodium Parasitaemia Associated with Significant Risk of Anaemia in Papua, Indonesia. <i>PLoS ONE</i> , 2016, 11, e0165340.	1.1	48
39	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
40	Genetic determinants of anti-malarial acquired immunity in a large multi-centre study. <i>Malaria Journal</i> , 2015, 14, 333.	0.8	26
41	Chloroquine efficacy for <i>Plasmodium vivax</i> malaria treatment in southern Ethiopia. <i>Malaria Journal</i> , 2015, 14, 525.	0.8	26
42	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
43	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
44	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
45	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
46	Multiple populations of artemisinin-resistant <i>Plasmodium falciparum</i> in Cambodia. <i>Nature Genetics</i> , 2013, 45, 648-655.	9.4	424
47	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
48	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
49	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
50	<i>Plasmodium vivax</i> Population Structure and Transmission Dynamics in Sabah Malaysia. <i>PLoS ONE</i> , 2013, 8, e82553.	1.1	45
51	VarB: a variation browsing and analysis tool for variants derived from next-generation sequencing data. <i>Bioinformatics</i> , 2012, 28, 2983-2985.	1.8	8
52	Phenotypic and genotypic characterisation of drug-resistant <i>Plasmodium vivax</i> . <i>Trends in Parasitology</i> , 2012, 28, 522-529.	1.5	70
53	Characterization of Within-Host <i>Plasmodium falciparum</i> Diversity Using Next-Generation Sequence Data. <i>PLoS ONE</i> , 2012, 7, e32891.	1.1	102
54	Analysis of <i>Plasmodium falciparum</i> diversity in natural infections by deep sequencing. <i>Nature</i> , 2012, 487, 375-379.	13.7	450

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55	Using CF11 cellulose columns to inexpensively and effectively remove human DNA from Plasmodium falciparum-infected whole blood samples. <i>Malaria Journal</i> , 2012, 11, 41.	0.8	79
56	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.	1.1	68
57	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.	1.1	41
58	Population Genetic Analysis of Plasmodium falciparum Parasites Using a Customized Illumina GoldenGate Genotyping Assay. <i>PLoS ONE</i> , 2011, 6, e20251.	1.1	63
59	A Bayesian approach using covariance of single nucleotide polymorphism data to detect differences in linkage disequilibrium patterns between groups of individuals. <i>Bioinformatics</i> , 2010, 26, 1999-2003.	1.8	5
60	Further Evidence Supporting a Role for Gs Signal Transduction in Severe Malaria Pathogenesis. <i>PLoS ONE</i> , 2010, 5, e10017.	1.1	14
61	Tumor Necrosis Factor and Lymphotoxin α Polymorphisms and Severe Malaria in African Populations. <i>Journal of Infectious Diseases</i> , 2009, 199, 569-575.	1.9	52
62	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
63	SnoopCGH: software for visualizing comparative genomic hybridization data. <i>Bioinformatics</i> , 2009, 25, 2732-2733.	1.8	9
64	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
65	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
66	Genome-wide and fine-resolution association analysis of malaria in West Africa. <i>Nature Genetics</i> , 2009, 41, 657-665.	9.4	345
67	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
68	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
69	Association of the GNAS locus with severe malaria. <i>Human Genetics</i> , 2008, 124, 499-506.	1.8	12
70	Variation in the ICAM1 gene is not associated with severe malaria phenotypes. <i>Genes and Immunity</i> , 2008, 9, 462-469.	2.2	38
71	A global network for investigating the genomic epidemiology of malaria. <i>Nature</i> , 2008, 456, 732-737.	13.7	148
72	Common variation in the ABO glycosyltransferase is associated with susceptibility to severe Plasmodium falciparum malaria. <i>Human Molecular Genetics</i> , 2008, 17, 567-576.	1.4	148

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73	Validating Discovered Cis-Acting Regulatory Genetic Variants: Application of an Allele Specific Expression Approach to HapMap Populations. PLoS ONE, 2008, 3, e4105.	1.1	22