

Sarah K Volkman

List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

2,414
citations

279798

23
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233421

45
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56
all docs

56
docs citations

56
times ranked

2436
citing authors

#	ARTICLE	IF	CITATIONS
1	Plasmodium falciparum genomic surveillance reveals spatial and temporal trends, association of genetic and physical distance, and household clustering. Scientific Reports, 2022, 12, 938.	3.3	13
2	Allelic diversity of MSP1 and MSP2 repeat loci correlate with levels of malaria endemicity in Senegal and Nigerian populations. Malaria Journal, 2021, 20, 38.	2.3	5
3	Polymorphisms in Plasmodium falciparum chloroquine resistance transporter (Pfcrt) and multidrug-resistant gene 1 (Pfmdr-1) in Nigerian children 10 years post-adoption of artemisinin-based combination treatments. International Journal for Parasitology, 2021, 51, 301-310.	3.1	7
4	Genetic surveillance for monitoring the impact of drug use on Plasmodium falciparum populations. International Journal for Parasitology: Drugs and Drug Resistance, 2021, 17, 12-22.	3.4	15
5	Genetic evidence for imported malaria and local transmission in Richard Toll, Senegal. Malaria Journal, 2020, 19, 276.	2.3	12
6	Genetic analysis reveals unique characteristics of Plasmodium falciparum parasite populations in Haiti. Malaria Journal, 2020, 19, 379.	2.3	3
7	Genetic background and PfKelch13 affect artemisinin susceptibility of PfCoronin mutants in Plasmodium falciparum. PLoS Genetics, 2020, 16, e1009266.	3.5	17
8	Population genomics of Plasmodium vivax in Panama to assess the risk of case importation on malaria elimination. PLoS Neglected Tropical Diseases, 2020, 14, e0008962.	3.0	18
9	Title is missing!. , 2020, 14, e0008962.		0
10	Title is missing!. , 2020, 14, e0008962.		0
11	Title is missing!. , 2020, 14, e0008962.		0
12	Title is missing!. , 2020, 14, e0008962.		0
13	Long-distance transmission patterns modelled from SNP barcodes of Plasmodium falciparum infections in The Gambia. Scientific Reports, 2019, 9, 13515.	3.3	5
14	Cohort Description of the Madagascar Health and Environmental Research (Antongil) (MAHERY (Antongil) Study in Madagascar. Frontiers in Nutrition, 2019, 6, 109.	3.7	12
15	Dramatic Changes in Malaria Population Genetic Complexity in Dielmo and Ndiop, Senegal, Revealed Using Genomic Surveillance. Journal of Infectious Diseases, 2018, 217, 622-627.	4.0	31
16	Plasmepsin II copy number accounts for bimodal piperaquine resistance among Cambodian Plasmodium falciparum. Nature Communications, 2018, 9, 1769.	12.8	85
17	Mutations in Plasmodium falciparum actin-binding protein coronin confer reduced artemisinin susceptibility. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 12799-12804.	7.1	114
18	Transmission of molecularly undetectable circulating parasite clones leads to high infection complexity in mosquitoes post feeding. International Journal for Parasitology, 2018, 48, 671-677.	3.1	25

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19	Long read assemblies of geographically dispersed <i>Plasmodium falciparum</i> isolates reveal highly structured subtelomeres. Wellcome Open Research, 2018, 3, 52.	1.8	114
20	Artemisinin resistance without pfcy5 mutations in <i>Plasmodium falciparum</i> isolates from Cambodia. Malaria Journal, 2017, 16, 195.	2.3	99
21	Malaria Genomics in the Era of Eradication. Cold Spring Harbor Perspectives in Medicine, 2017, 7, a025544.	6.2	33
22	Case report of <i>Plasmodium ovale curtisi</i> malaria in Sri Lanka: relevance for the maintenance of elimination status. BMC Infectious Diseases, 2017, 17, 307.	2.9	3
23	Evidence of non- <i>Plasmodium falciparum</i> malaria infection in Kédougou, Sénégal. Malaria Journal, 2017, 16, 9.	2.3	38
24	Ex vivo susceptibility and genotyping of <i>Plasmodium falciparum</i> isolates from Pikine, Senegal. Malaria Journal, 2017, 16, 250.	2.3	9
25	Genetic relatedness analysis reveals the cotransmission of genetically related <i>Plasmodium falciparum</i> parasites in Thiès, Senegal. Genome Medicine, 2017, 9, 5.	8.2	47
26	Genome-Wide Association Studies of Drug-Resistance Determinants. Trends in Parasitology, 2017, 33, 214-230.	3.3	16
27	Malaria prevalence, prevention and treatment seeking practices among nomadic pastoralists in northern Senegal. Malaria Journal, 2017, 16, 413.	2.3	25
28	High <i>Plasmodium falciparum</i> longitudinal prevalence is associated with high multiclonality and reduced clinical malaria risk in a seasonal transmission area of Mali. PLoS ONE, 2017, 12, e0170948.	2.5	8
29	West Africa International Centers of Excellence for Malaria Research: Drug Resistance Patterns to Artemether-Lumefantrine in Senegal, Mali, and The Gambia. American Journal of Tropical Medicine and Hygiene, 2016, 95, 1054-1060.	1.4	19
30	Persistence of <i>Plasmodium falciparum</i> parasitemia after artemisinin combination therapy: evidence from a randomized trial in Uganda. Scientific Reports, 2016, 6, 26330.	3.3	34
31	Genetic evidence that the Makira region in northeastern Madagascar is a hotspot of malaria transmission. Malaria Journal, 2016, 15, 596.	2.3	16
32	Methods to Increase the Sensitivity of High Resolution Melting Single Nucleotide Polymorphism Genotyping in Malaria. Journal of Visualized Experiments, 2015, , e52839.	0.3	9
33	RDTs as a source of DNA to study <i>Plasmodium falciparum</i> drug resistance in isolates from Senegal and the Comoros Islands. Malaria Journal, 2015, 14, 373.	2.3	17
34	COIL: a methodology for evaluating malarial complexity of infection using likelihood from single nucleotide polymorphism data. Malaria Journal, 2015, 14, 4.	2.3	71
35	Immune Characterization of <i>Plasmodium falciparum</i> Parasites with a Shared Genetic Signature in a Region of Decreasing Transmission. Infection and Immunity, 2015, 83, 276-285.	2.2	11
36	Modeling malaria genomics reveals transmission decline and rebound in Senegal. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7067-7072.	7.1	163

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37	Development of a Single Nucleotide Polymorphism Barcode to Genotype <i>Plasmodium vivax</i> Infections. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003539.	3.0	90
38	Adaptive evolution of malaria parasites in French Guiana: Reversal of chloroquine resistance by acquisition of a mutation in <i>pfprt</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 11672-11677.	7.1	101
39	Malaria Molecular Epidemiology: Lessons from the International Centers of Excellence for Malaria Research Network. <i>American Journal of Tropical Medicine and Hygiene</i> , 2015, 93, 79-86.	1.4	80
40	Clonal Outbreak of <i>Plasmodium falciparum</i> Infection in Eastern Panama. <i>Journal of Infectious Diseases</i> , 2015, 211, 1087-1096.	4.0	71
41	Pre-amplification methods for tracking low-grade <i>Plasmodium falciparum</i> populations during scaled-up interventions in Southern Zambia. <i>Malaria Journal</i> , 2014, 13, 89.	2.3	29
42	An Adjustable Gas-Mixing Device to Increase Feasibility of In Vitro Culture of <i>Plasmodium falciparum</i> Parasites in the Field. <i>PLoS ONE</i> , 2014, 9, e90928.	2.5	6
43	Polymorphism in <i>dhfr/dhps</i> genes, parasite density and <i>ex vivo</i> response to pyrimethamine in <i>Plasmodium falciparum</i> malaria parasites in Thies, Senegal. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2013, 3, 135-142.	3.4	27
44	Malaria life cycle intensifies both natural selection and random genetic drift. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20129-20134.	7.1	67
45	Genetic Surveillance Detects Both Clonal and Epidemic Transmission of Malaria following Enhanced Intervention in Senegal. <i>PLoS ONE</i> , 2013, 8, e60780.	2.5	87
46	Application of genomics to field investigations of malaria by the international centers of excellence for malaria research. <i>Acta Tropica</i> , 2012, 121, 324-332.	2.0	33
47	Harnessing genomics and genome biology to understand malaria biology. <i>Nature Reviews Genetics</i> , 2012, 13, 315-328.	16.3	95
48	A general SNP-based molecular barcode for <i>Plasmodium falciparum</i> identification and tracking. <i>Malaria Journal</i> , 2008, 7, 223.	2.3	213
49	Genomic heterogeneity in the density of noncoding single-nucleotide and microsatellite polymorphisms in <i>Plasmodium falciparum</i> . <i>Gene</i> , 2007, 387, 1-6.	2.2	8
50	A genome-wide map of diversity in <i>Plasmodium falciparum</i> . <i>Nature Genetics</i> , 2007, 39, 113-119.	21.4	320
51	PARASITOLOGY: A Game of Cat and Mouth. <i>Science</i> , 2003, 299, 353-354.	12.6	11
52	Excess Polymorphisms in Genes for Membrane Proteins in <i>Plasmodium falciparum</i> . <i>Science</i> , 2002, 298, 216-218.	12.6	80