

Shannon Takala-Harrison

List of Publications by Year in descending order

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Version: 2024-02-01

57
papers

3,995
citations

257450

24
h-index

155660

55
g-index

63
all docs

63
docs citations

63
times ranked

3587
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic architecture of artemisinin-resistant <i>Plasmodium falciparum</i> . <i>Nature Genetics</i> , 2015, 47, 226-234.	21.4	515
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	Independent Emergence of Artemisinin Resistance Mutations Among <i>Plasmodium falciparum</i> in Southeast Asia. <i>Journal of Infectious Diseases</i> , 2015, 211, 670-679.	4.0	368
5	A Field Trial to Assess a Blood-Stage Malaria Vaccine. <i>New England Journal of Medicine</i> , 2011, 365, 1004-1013.	27.0	311
6	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.	7.1	242
7	Emerging Southeast Asian PfCRT mutations confer <i>Plasmodium falciparum</i> resistance to the first-line antimalarial piperazine. <i>Nature Communications</i> , 2018, 9, 3314.	12.8	183
8	Return of Chloroquine-Susceptible <i>Falciparum</i> Malaria in Malawi Was a Reexpansion of Diverse Susceptible Parasites. <i>Journal of Infectious Diseases</i> , 2010, 202, 801-808.	4.0	126
9	A Single Mutation in K13 Predominates in Southern China and Is Associated With Delayed Clearance of <i>Plasmodium falciparum</i> Following Artemisinin Treatment. <i>Journal of Infectious Diseases</i> , 2015, 212, 1629-1635.	4.0	125
10	Association of a Novel Mutation in the <i>Plasmodium falciparum</i> Chloroquine Resistance Transporter With Decreased Piperazine Sensitivity. <i>Journal of Infectious Diseases</i> , 2017, 216, 468-476.	4.0	102
11	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
12	Polymorphisms in the K13-Propeller Gene in Artemisinin-Susceptible <i>Plasmodium falciparum</i> Parasites from Bougoula-Hameau and Bandiagara, Mali. <i>American Journal of Tropical Medicine and Hygiene</i> , 2015, 92, 1202-1206.	1.4	89
13	Antimalarial drug resistance in Africa: key lessons for the future. <i>Annals of the New York Academy of Sciences</i> , 2015, 1342, 62-67.	3.8	83
14	Return of Widespread Chloroquine-Sensitive <i>Plasmodium falciparum</i> to Malawi. <i>Journal of Infectious Diseases</i> , 2014, 210, 1110-1114.	4.0	79
15	Molecular Basis of Allele-Specific Efficacy of a Blood-Stage Malaria Vaccine: Vaccine Development Implications. <i>Journal of Infectious Diseases</i> , 2013, 207, 511-519.	4.0	66
16	<i>Ex Vivo</i> Drug Susceptibility Testing and Molecular Profiling of Clinical <i>Plasmodium falciparum</i> Isolates from Cambodia from 2008 to 2013 Suggest Emerging Piperazine Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 4631-4643.	3.2	63
17	Lack of allele-specific efficacy of a bivalent AMA1 malaria vaccine. <i>Malaria Journal</i> , 2010, 9, 175.	2.3	61
18	Strains used in whole organism <i>Plasmodium falciparum</i> vaccine trials differ in genome structure, sequence, and immunogenic potential. <i>Genome Medicine</i> , 2020, 12, 6.	8.2	61

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19	An open dataset of Plasmodium falciparum genome variation in 7,000 worldwide samples. Wellcome Open Research, 2021, 6, 42.	1.8	51
20	Genomic structure and diversity of Plasmodium falciparum in Southeast Asia reveal recent parasite migration patterns. Nature Communications, 2019, 10, 2665.	12.8	46
21	Extended Safety, Immunogenicity and Efficacy of a Blood-Stage Malaria Vaccine in Malian Children: 24-Month Follow-Up of a Randomized, Double-Blinded Phase 2 Trial. PLoS ONE, 2013, 8, e79323.	2.5	38
22	Children with cerebral malaria or severe malarial anaemia lack immunity to distinct variant surface antigen subsets. Scientific Reports, 2018, 8, 6281.	3.3	31
23	Multidrug-resistant malaria and the impact of mass drug administration. Infection and Drug Resistance, 2018, Volume 11, 299-306.	2.7	31
24	Next Generation Sequencing to Detect Variation in the Plasmodium falciparum Circumsporozoite Protein. American Journal of Tropical Medicine and Hygiene, 2012, 86, 775-781.	1.4	30
25	Persistence of Sulfadoxine-Pyrimethamine Resistance Despite Reduction of Drug Pressure in Malawi. Journal of Infectious Diseases, 2015, 212, 694-701.	4.0	25
26	Microarray analyses reveal strain-specific antibody responses to Plasmodium falciparum apical membrane antigen 1 variants following natural infection and vaccination. Scientific Reports, 2020, 10, 3952.	3.3	24
27	Prevalence of Clinical and Subclinical Plasmodium falciparum and Plasmodium vivax Malaria in Two Remote Rural Communities on the Myanmarâ€“China Border. American Journal of Tropical Medicine and Hygiene, 2017, 97, 1524-1531.	1.4	24
28	Antibodies to Peptides in Semiconserved Domains of RIFINs and STEVORs Correlate with Malaria Exposure. MSphere, 2019, 4, .	2.9	23
29	Variation in the Circumsporozoite Protein of Plasmodium falciparum: Vaccine Development Implications. PLoS ONE, 2014, 9, e101783.	2.5	22
30	Seroreactivity to Plasmodium falciparum Erythrocyte Membrane Protein 1 Intracellular Domain in Malaria-Exposed Children and Adults. Journal of Infectious Diseases, 2013, 208, 1514-1519.	4.0	20
31	A microarray platform and novel SNP calling algorithm to evaluate Plasmodium falciparum field samples of low DNA quantity. BMC Genomics, 2014, 15, 719.	2.8	18
32	Plasmodium falciparum field isolates from areas of repeated emergence of drug resistant malaria show no evidence of hypermutator phenotype. Infection, Genetics and Evolution, 2015, 30, 318-322.	2.3	18
33	Prevalence of molecular markers of sulfadoxineâ€“pyrimethamine and artemisinin resistance in Plasmodium falciparum from Pakistan. Malaria Journal, 2018, 17, 471.	2.3	17
34	Hemoglobin C Trait Provides Protection From Clinical Falciparum Malaria in Malian Children. Journal of Infectious Diseases, 2015, 212, 1778-1786.	4.0	13
35	Optimal health and disease management using spatial uncertainty: a geographic characterization of emergent artemisinin-resistant Plasmodium falciparum distributions in Southeast Asia. International Journal of Health Geographics, 2016, 15, 37.	2.5	13
36	Differential Recognition of Terminal Extracellular Plasmodium falciparum VAR2CSA Domains by Sera from Multigravid, Malaria-Exposed Malian Women. American Journal of Tropical Medicine and Hygiene, 2015, 92, 1190-1194.	1.4	11

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37	Integration of population and functional genomics to understand mechanisms of artemisinin resistance in <i>Plasmodium falciparum</i> . <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2021, 16, 119-128.	3.4	11
38	Extent and Dynamics of Polymorphism in the Malaria Vaccine Candidate <i>Plasmodium falciparum</i> Reticulocyte-binding Protein Homologue-5 in Kalifabougou, Mali. <i>American Journal of Tropical Medicine and Hygiene</i> , 2018, 99, 43-50.	1.4	10
39	Distribution and Temporal Dynamics of <i>Plasmodium falciparum</i> Chloroquine Resistance Transporter Mutations Associated With Piperaquine Resistance in Northern Cambodia. <i>Journal of Infectious Diseases</i> , 2021, 224, 1077-1085.	4.0	8
40	Optimization of parasite DNA enrichment approaches to generate whole genome sequencing data for <i>Plasmodium falciparum</i> from low parasitaemia samples. <i>Malaria Journal</i> , 2020, 19, 135.	2.3	7
41	Host and Parasite Transcriptomic Changes upon Successive <i>Plasmodium falciparum</i> Infections in Early Childhood. <i>MSystems</i> , 2020, 5, .	3.8	7
42	Serologic responses to the PfEMP1 DBL-CIDR head structure may be a better indicator of malaria exposure than those to the DBL-1 tag. <i>Malaria Journal</i> , 2019, 18, 273.	2.3	6
43	The effect of local variation in malaria transmission on the prevalence of sulfadoxine-pyrimethamine resistant haplotypes and selective sweep characteristics in Malawi. <i>Malaria Journal</i> , 2015, 14, 387.	2.3	5
44	Epitope-based sieve analysis of <i>Plasmodium falciparum</i> sequences from a FMP2.1/AS02A vaccine trial is consistent with differential vaccine efficacy against immunologically relevant AMA1 variants. <i>Vaccine</i> , 2020, 38, 5700-5706.	3.8	5
45	No evidence of amplified <i>Plasmodium falciparum</i> plasmepsin II gene copy number in an area with artemisinin-resistant malaria along the China-Myanmar border. <i>Malaria Journal</i> , 2020, 19, 334.	2.3	5
46	Whole-genome analysis of Malawian <i>Plasmodium falciparum</i> isolates identifies possible targets of allele-specific immunity to clinical malaria. <i>PLoS Genetics</i> , 2021, 17, e1009576.	3.5	4
47	Successful Profiling of <i>Plasmodium falciparum</i> Gene Expression in Clinical Samples via a Custom Capture Array. <i>MSystems</i> , 2021, 6, e0022621.	3.8	4
48	Gametocyte Carriage, Antimalarial Use, and Drug Resistance in Cambodia, 2008-2014. <i>American Journal of Tropical Medicine and Hygiene</i> , 2018, 99, 1145-1149.	1.4	3
49	Epitope-Specific Antibody Responses to a <i>Plasmodium falciparum</i> Subunit Vaccine Target in a Malaria-Endemic Population. <i>Journal of Infectious Diseases</i> , 2021, 223, 1943-1947.	4.0	3
50	Detecting geospatial patterns of <i>Plasmodium falciparum</i> parasite migration in Cambodia using optimized estimated effective migration surfaces. <i>International Journal of Health Geographics</i> , 2020, 19, 13.	2.5	2
51	Malian adults maintain serologic responses to virulent PfEMP1s amid seasonal patterns of fluctuation. <i>Scientific Reports</i> , 2021, 11, 14401.	3.3	2
52	Immunoprofiles associated with controlled human malaria infection and naturally acquired immunity identify a shared IgA pre-erythrocytic immunoproteome. <i>Npj Vaccines</i> , 2021, 6, 115.	6.0	2
53	Differential Incidence of Malaria in Neighboring Villages in a High-Transmission Setting of Southern Mali. <i>American Journal of Tropical Medicine and Hygiene</i> , 2022, 106, 1209-1214.	1.4	2
54	An In Silico Analysis of Malaria Pre-Erythrocytic-Stage Antigens Interpreting Worldwide Genetic Data to Suggest Vaccine Candidate Variants and Epitopes. <i>Microorganisms</i> , 2022, 10, 1090.	3.6	2

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55	STRIDE: a command-line HMM-based identifier and sub-classifier of <i>Plasmodium falciparum</i> RIFIN and STEVOR variant surface antigen families. <i>BMC Bioinformatics</i> , 2022, 23, 15.	2.6	1
56	Genomic Epidemiology of Antimalarial Drug Resistance in <i>Plasmodium falciparum</i> in Southern China. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 610985.	3.9	0
57	#63: Antibodies to Peptides Representing <i>Plasmodium falciparum</i> Circumsporozoite Protein Reflect Acquisition of Naturally Acquired Immunity in Malian Adults and Children. <i>Journal of the Pediatric Infectious Diseases Society</i> , 2021, 10, S10-S12.	1.3	0