

Rachel F Daniels

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

1,828
citations

304743

22
h-index

302126

39
g-index

57
all docs

57
docs citations

57
times ranked

2059
citing authors

#	ARTICLE	IF	CITATIONS
1	A general SNP-based molecular barcode for Plasmodium falciparum identification and tracking. Malaria Journal, 2008, 7, 223.	2.3	213
2	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
3	Genome-wide SNP genotyping highlights the role of natural selection in Plasmodium falciparum population divergence. Genome Biology, 2008, 9, R171.	8.8	119
4	Artemisinin resistance without pfcy8r mutations in Plasmodium falciparum isolates from Cambodia. Malaria Journal, 2017, 16, 195.	2.3	99
5	Hybrid selection for sequencing pathogen genomes from clinical samples. Genome Biology, 2011, 12, R73.	9.6	97
6	Development of a Single Nucleotide Polymorphism Barcode to Genotype Plasmodium vivax Infections. PLoS Neglected Tropical Diseases, 2015, 9, e0003539.	3.0	90
7	Genetic Surveillance Detects Both Clonal and Epidemic Transmission of Malaria following Enhanced Intervention in Senegal. PLoS ONE, 2013, 8, e60780.	2.5	87
8	Identification and Functional Validation of the Novel Antimalarial Resistance Locus PF10_0355 in Plasmodium falciparum. PLoS Genetics, 2011, 7, e1001383.	3.5	85
9	COIL: a methodology for evaluating malarial complexity of infection using likelihood from single nucleotide polymorphism data. Malaria Journal, 2015, 14, 4.	2.3	71
10	Clonal Outbreak of Plasmodium falciparum Infection in Eastern Panama. Journal of Infectious Diseases, 2015, 211, 1087-1096.	4.0	71
11	Rapid, Field-Deployable Method for Genotyping and Discovery of Single-Nucleotide Polymorphisms Associated with Drug Resistance in Plasmodium falciparum. Antimicrobial Agents and Chemotherapy, 2012, 56, 2976-2986.	3.2	63
12	Genetic relatedness analysis reveals the cotransmission of genetically related Plasmodium falciparum parasites in Thiès, Senegal. Genome Medicine, 2017, 9, 5.	8.2	47
13	Natural Products from isnA-Containing Biosynthetic Gene Clusters Recovered from the Genomes of Cultured and Uncultured Bacteria. Journal of the American Chemical Society, 2007, 129, 12102-12103.	13.7	46
14	Detection of low-density Plasmodium falciparum infections using amplicon deep sequencing. Malaria Journal, 2019, 18, 219.	2.3	40
15	Evidence of non-Plasmodium falciparum malaria infection in Kédougou, Senegal. Malaria Journal, 2017, 16, 9.	2.3	38
16	Molecular Epidemiology of Plasmodium falciparum kelch13 Mutations in Senegal Determined by Using Targeted Amplicon Deep Sequencing. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	35
17	Persistence of Plasmodium falciparum parasitemia after artemisinin combination therapy: evidence from a randomized trial in Uganda. Scientific Reports, 2016, 6, 26330.	3.3	34
18	Application of genomics to field investigations of malaria by the international centers of excellence for malaria research. Acta Tropica, 2012, 121, 324-332.	2.0	33

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19	Dramatic Changes in Malaria Population Genetic Complexity in Dielmo and Ndiop, Senegal, Revealed Using Genomic Surveillance. <i>Journal of Infectious Diseases</i> , 2018, 217, 622-627.	4.0	31
20	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
21	Polymorphism in dhfr/dhps genes, parasite density and ex vivo 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
22	Malaria prevalence, prevention and treatment seeking practices among nomadic pastoralists in northern Senegal. <i>Malaria Journal</i> , 2017, 16, 413.	2.3	25
23	Transmission of molecularly undetectable circulating parasite clones leads to high infection complexity in mosquitoes post feeding. <i>International Journal for Parasitology</i> , 2018, 48, 671-677.	3.1	25
24	Human cerebral malaria and <i>Plasmodium falciparum</i> genotypes in Malawi. <i>Malaria Journal</i> , 2012, 11, 35.	2.3	24
25	Changes in drug sensitivity and anti-malarial drug resistance mutations over time among <i>Plasmodium falciparum</i> parasites in Senegal. <i>Malaria Journal</i> , 2013, 12, 441.	2.3	23
26	West Africa International Centers of Excellence for Malaria Research: Drug Resistance Patterns to Artemetherâ€“Lumefantrine in Senegal, Mali, and The Gambia. <i>American Journal of Tropical Medicine and Hygiene</i> , 2016, 95, 1054-1060.	1.4	19
27	RDTs as a source of DNA to study <i>Plasmodium falciparum</i> drug resistance in isolates from Senegal and the Comoros Islands. <i>Malaria Journal</i> , 2015, 14, 373.	2.3	17
28	Genetic surveillance for monitoring the impact of drug use on <i>Plasmodium falciparum</i> populations. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2021, 17, 12-22.	3.4	15
29	<i>Plasmodium falciparum</i> genomic surveillance reveals spatial and temporal trends, association of genetic and physical distance, and household clustering. <i>Scientific Reports</i> , 2022, 12, 938.	3.3	13
30	Improving malaria control in West Africa: Interruption of transmission as a paradigm shift. <i>Acta Tropica</i> , 2012, 121, 175-183.	2.0	12
31	Characterization of <i>Plasmodium falciparum</i> structure in Nigeria with malaria SNPs barcode. <i>Malaria Journal</i> , 2018, 17, 472.	2.3	12
32	Genetic evidence for imported malaria and local transmission in Richard Toll, Senegal. <i>Malaria Journal</i> , 2020, 19, 276.	2.3	12
33	Immune Characterization of <i>Plasmodium falciparum</i> Parasites with a Shared Genetic Signature in a Region of Decreasing Transmission. <i>Infection and Immunity</i> , 2015, 83, 276-285.	2.2	11
34	<i>Plasmodium falciparum</i> K76Tpfcr Gene Mutations and Parasite Population Structure, Haiti, 2006â€“2009. <i>Emerging Infectious Diseases</i> , 2016, 22, 786-793.	4.3	11
35	The utility of genomic data for <i>Plasmodium vivax</i> population surveillance. <i>Pathogens and Global Health</i> , 2015, 109, 153-161.	2.3	10
36	Adherence to Mass Drug Administration with Dihydroartemisininâ€“Piperazine and <i>Plasmodium falciparum</i> Clearance in Southern Province, Zambia. <i>American Journal of Tropical Medicine and Hygiene</i> , 2020, 103, 37-45.	1.4	10

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37	Methods to Increase the Sensitivity of High Resolution Melting Single Nucleotide Polymorphism Genotyping in Malaria. <i>Journal of Visualized Experiments</i> , 2015, , e52839.	0.3	9
38	High resolution melting: a useful field-deployable method to measure dhfr and dhps drug resistance in both highly and lowly endemic Plasmodium populations. <i>Malaria Journal</i> , 2017, 16, 153.	2.3	9
39	Relevance of Higher-Order Epistasis in Drug Resistance. <i>Molecular Biology and Evolution</i> , 2021, 38, 142-151.	8.9	9
40	High Plasmodium falciparum longitudinal prevalence is associated with high multiclonality and reduced clinical malaria risk in a seasonal transmission area of Mali. <i>PLoS ONE</i> , 2017, 12, e0170948.	2.5	8
41	Evidence for Reduced Malaria Parasite Population after Application of Population-Level Antimalarial Drug Strategies in Southern Province, Zambia. <i>American Journal of Tropical Medicine and Hygiene</i> , 2020, 103, 66-73.	1.4	8
42	Use of a Plasmodium vivax genetic barcode for genomic surveillance and parasite tracking in Sri Lanka. <i>Malaria Journal</i> , 2020, 19, 342.	2.3	6
43	Surveillance of molecular markers for antimalarial resistance in Zambia: Polymorphism of Pfk13, Pfmdr1 and Pfdhfr/Pfdhps genes. <i>Acta Tropica</i> , 2020, 212, 105704.	2.0	4
44	Case report of Plasmodium ovale curtisi malaria in Sri Lanka: relevance for the maintenance of elimination status. <i>BMC Infectious Diseases</i> , 2017, 17, 307.	2.9	3
45	Genetic analysis reveals unique characteristics of Plasmodium falciparum parasite populations in Haiti. <i>Malaria Journal</i> , 2020, 19, 379.	2.3	3
46	Altered drug susceptibility during host adaptation of a Plasmodium falciparum strain in a non-human primate model. <i>Scientific Reports</i> , 2016, 6, 21216.	3.3	1
47	Temporal changes in Plasmodium falciparum reticulocyte binding protein homolog 2b (PfRh2b) in Senegal and The Gambia. <i>Malaria Journal</i> , 2019, 18, 239.	2.3	1
48	Data on selected antimalarial drug resistance markers in Zambia. <i>Data in Brief</i> , 2021, 34, 106650.	1.0	1