

# Rachel F Daniels

## List of Publications by Year in descending order

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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	Plasmodium falciparum 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
2	Relevance of Higher-Order Epistasis in Drug Resistance. <i>Molecular Biology and Evolution</i> , 2021, 38, 142-151.	8.9	9
3	Data on selected antimalarial drug resistance markers in Zambia. <i>Data in Brief</i> , 2021, 34, 106650.	1.0	1
4	Genetic surveillance for monitoring the impact of drug use on Plasmodium falciparum populations. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2021, 17, 12-22.	3.4	15
5	Surveillance of molecular markers for antimalarial resistance in Zambia: Polymorphism of Pfkclch 13, Pfmdr1 and Pfdhfr/Pfdhps genes. <i>Acta Tropica</i> , 2020, 212, 105704.	2.0	4
6	Genetic evidence for imported malaria and local transmission in Richard Toll, Senegal. <i>Malaria Journal</i> , 2020, 19, 276.	2.3	12
7	Genetic analysis reveals unique characteristics of Plasmodium falciparum parasite populations in Haiti. <i>Malaria Journal</i> , 2020, 19, 379.	2.3	3
8	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
9	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
10	Adherence to Mass Drug Administration with Dihydroartemisininâ€“Piperaquine and Plasmodium falciparum Clearance in Southern Province, Zambia. <i>American Journal of Tropical Medicine and Hygiene</i> , 2020, 103, 37-45.	1.4	10
11	Detection of low-density Plasmodium falciparum infections using amplicon deep sequencing. <i>Malaria Journal</i> , 2019, 18, 219.	2.3	40
12	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
13	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
14	Characterization of Plasmodium falciparum structure in Nigeria with malaria SNPs barcode. <i>Malaria Journal</i> , 2018, 17, 472.	2.3	12
15	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
16	Molecular Epidemiology of Plasmodium falciparum kelch13 Mutations in Senegal Determined by Using Targeted Amplicon Deep Sequencing. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	35
17	Artemisinin resistance without pfkelch13 mutations in Plasmodium falciparum isolates from Cambodia. <i>Malaria Journal</i> , 2017, 16, 195.	2.3	99
18	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

#	ARTICLE	IF	CITATIONS
19	Evidence of non-Plasmodium falciparum malaria infection in KÃ©dougou, SÃ©nÃ©gal. Malaria Journal, 2017, 16, 9.	2.3	38
20	High resolution melting: a useful field-deployable method to measure dhfr and dhps drug resistance in both highly and lowly endemic Plasmodium populations. Malaria Journal, 2017, 16, 153.	2.3	9
21	Genetic relatedness analysis reveals the cotransmission of genetically related Plasmodium falciparum parasites in ThiÃ©s, Senegal. Genome Medicine, 2017, 9, 5.	8.2	47
22	Malaria prevalence, prevention and treatment seeking practices among nomadic pastoralists in northern Senegal. Malaria Journal, 2017, 16, 413.	2.3	25
23	High Plasmodium falciparum 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
24	Plasmodium falciparum K76Tpfcr Gene Mutations and Parasite Population Structure, Haiti, 2006â€“2009. Emerging Infectious Diseases, 2016, 22, 786-793.	4.3	11
25	West Africa International Centers of Excellence for Malaria Research: Drug Resistance Patterns to Artemetherâ€“Lumefantrine in Senegal, Mali, and The Gambia. American Journal of Tropical Medicine and Hygiene, 2016, 95, 1054-1060.	1.4	19
26	Persistence of Plasmodium falciparum parasitemia after artemisinin combination therapy: evidence from a randomized trial in Uganda. Scientific Reports, 2016, 6, 26330.	3.3	34
27	Altered drug susceptibility during host adaptation of a Plasmodium falciparum strain in a non-human primate model. Scientific Reports, 2016, 6, 21216.	3.3	1
28	Methods to Increase the Sensitivity of High Resolution Melting Single Nucleotide Polymorphism Genotyping in Malaria. Journal of Visualized Experiments, 2015, , e52839.	0.3	9
29	RDTs as a source of DNA to study Plasmodium falciparum drug resistance in isolates from Senegal and the Comoros Islands. Malaria Journal, 2015, 14, 373.	2.3	17
30	COIL: a methodology for evaluating malarial complexity of infection using likelihood from single nucleotide polymorphism data. Malaria Journal, 2015, 14, 4.	2.3	71
31	The utility of genomic data for Plasmodium vivax population surveillance. Pathogens and Global Health, 2015, 109, 153-161.	2.3	10
32	Immune Characterization of Plasmodium falciparum Parasites with a Shared Genetic Signature in a Region of Decreasing Transmission. Infection and Immunity, 2015, 83, 276-285.	2.2	11
33	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
34	Development of a Single Nucleotide Polymorphism Barcode to Genotype Plasmodium vivax Infections. PLoS Neglected Tropical Diseases, 2015, 9, e0003539.	3.0	90
35	Clonal Outbreak of Plasmodium falciparum Infection in Eastern Panama. Journal of Infectious Diseases, 2015, 211, 1087-1096.	4.0	71
36	Pre-amplification methods for tracking low-grade Plasmodium falciparum populations during scaled-up interventions in Southern Zambia. Malaria Journal, 2014, 13, 89.	2.3	29

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37	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
38	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
39	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
40	Rapid, Field-Deployable Method for Genotyping and Discovery of Single-Nucleotide Polymorphisms Associated with Drug Resistance in <i>Plasmodium falciparum</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 2976-2986.	3.2	63
41	Improving malaria control in West Africa: Interruption of transmission as a paradigm shift. <i>Acta Tropica</i> , 2012, 121, 175-183.	2.0	12
42	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
43	Human cerebral malaria and <i>Plasmodium falciparum</i> genotypes in Malawi. <i>Malaria Journal</i> , 2012, 11, 35.	2.3	24
44	Hybrid selection for sequencing pathogen genomes from clinical samples. <i>Genome Biology</i> , 2011, 12, R73.	9.6	97
45	Identification and Functional Validation of the Novel Antimalarial Resistance Locus PF10_0355 in <i>Plasmodium falciparum</i> . <i>PLoS Genetics</i> , 2011, 7, e1001383.	3.5	85
46	Genome-wide SNP genotyping highlights the role of natural selection in <i>Plasmodium falciparum</i> population divergence. <i>Genome Biology</i> , 2008, 9, R171.	8.8	119
47	A general SNP-based molecular barcode for <i>Plasmodium falciparum</i> identification and tracking. <i>Malaria Journal</i> , 2008, 7, 223.	2.3	213
48	Natural Products from <i>isnA</i> -Containing Biosynthetic Gene Clusters Recovered from the Genomes of Cultured and Uncultured Bacteria. <i>Journal of the American Chemical Society</i> , 2007, 129, 12102-12103.	13.7	46