

# Daniel E Neafsey

## List of Publications by Year in descending order

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Version: 2024-02-01

75  
papers

5,937  
citations

109137

35  
h-index

91712

69  
g-index

91  
all docs

91  
docs citations

91  
times ranked

6790  
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptional correlates of malaria in RTS,S/AS01-vaccinated African children: a matched case-control study. <i>ELife</i> , 2022, 11, .	2.8	4
2	A novel CSP C-terminal epitope targeted by an antibody with protective activity against <i>Plasmodium falciparum</i> . <i>PLoS Pathogens</i> , 2022, 18, e1010409.	2.1	14
3	Design and implementation of multiplexed amplicon sequencing panels to serve genomic epidemiology of infectious disease: A malaria case study. <i>Molecular Ecology Resources</i> , 2022, 22, 2285-2303.	2.2	18
4	A population genomic unveiling of a new cryptic mosquito taxon within the malaria-transmitting <i>Anopheles gambiae</i> complex. <i>Molecular Ecology</i> , 2021, 30, 775-790.	2.0	16
5	Breadth of humoral immune responses to the C-terminus of the circumsporozoite protein is associated with protective efficacy induced by the RTS,S malaria vaccine. <i>Vaccine</i> , 2021, 39, 968-975.	1.7	21
6	<i>Plasmodium simium</i> : Population Genomics Reveals the Origin of a Reverse Zoonosis. <i>Journal of Infectious Diseases</i> , 2021, 224, 1950-1961.	1.9	19
7	Advances and opportunities in malaria population genomics. <i>Nature Reviews Genetics</i> , 2021, 22, 502-517.	7.7	61
8	Molecular surveillance of malaria scales up. <i>Trends in Parasitology</i> , 2021, 37, 1020-1021.	1.5	2
9	Use of a <i>Plasmodium vivax</i> genetic barcode for genomic surveillance and parasite tracking in Sri Lanka. <i>Malaria Journal</i> , 2020, 19, 342.	0.8	6
10	The <i>Anopheles coluzzii</i> microbiome and its interaction with the intracellular parasite <i>Wolbachia</i> . <i>Scientific Reports</i> , 2020, 10, 13847.	1.6	21
11	Linked-read sequencing identifies abundant microinversions and introgression in the arboviral vector <i>Aedes aegypti</i> . <i>BMC Biology</i> , 2020, 18, 26.	1.7	16
12	Radiation with reticulation marks the origin of a major malaria vector. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 31583-31590.	3.3	29
13	Identity-by-descent with uncertainty characterises connectivity of <i>Plasmodium falciparum</i> populations on the Colombian-Pacific coast. <i>PLoS Genetics</i> , 2020, 16, e1009101.	1.5	19
14	Population genomics reveals the expansion of highly inbred <i>Plasmodium vivax</i> lineages in the main malaria hotspot of Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008808.	1.3	18
15	Population genomics of <i>Plasmodium vivax</i> in Panama to assess the risk of case importation on malaria elimination. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008962.	1.3	18
16	Local emergence in Amazonia of <i>Plasmodium falciparum</i> k13 C580Y mutants associated with in vitro artemisinin resistance. <i>ELife</i> , 2020, 9, .	2.8	102
17	Title is missing!. , 2020, 16, e1009101.		0
18	Title is missing!. , 2020, 16, e1009101.		0

#	ARTICLE	IF	CITATIONS
19	Title is missing!. , 2020, 16, e1009101.		0
20	Title is missing!. , 2020, 16, e1009101.		0
21	Title is missing!. , 2020, 14, e0008962.		0
22	Title is missing!. , 2020, 14, e0008962.		0
23	Title is missing!. , 2020, 14, e0008962.		0
24	Title is missing!. , 2020, 14, e0008962.		0
25	Detection of low-density Plasmodium falciparum infections using amplicon deep sequencing. Malaria Journal, 2019, 18, 219.	0.8	40
26	Genomic architecture and introgression shape a butterfly radiation. Science, 2019, 366, 594-599.	6.0	365
27	Estimating Relatedness Between Malaria Parasites. Genetics, 2019, 212, 1337-1351.	1.2	47
28	Resolving the cause of recurrent Plasmodium vivax malaria probabilistically. Nature Communications, 2019, 10, 5595.	5.8	70
29	Host-mediated selection impacts the diversity of Plasmodium falciparum antigens within infections. Nature Communications, 2018, 9, 1381.	5.8	27
30	Candidate-gene based GWAS identifies reproducible DNA markers for metabolic pyrethroid resistance from standing genetic variation in East African Anopheles gambiae. Scientific Reports, 2018, 8, 2920.	1.6	51
31	Mutations in <i>Plasmodium falciparum</i> 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.	3.3	114
32	Mapping malaria by combining parasite genomic and epidemiologic data. BMC Medicine, 2018, 16, 190.	2.3	68
33	hmmIBD: software to infer pairwise identity by descent between haploid genotypes. Malaria Journal, 2018, 17, 196.	0.8	103
34	De Novo Mutations Resolve Disease Transmission Pathways in Clonal Malaria. Molecular Biology and Evolution, 2018, 35, 1678-1689.	3.5	14
35	Probing Plasmodium falciparum sexual commitment at the single-cell level. Wellcome Open Research, 2018, 3, 70.	0.9	25
36	Longitudinal genomic surveillance of Plasmodium falciparum malaria parasites reveals complex genomic architecture of emerging artemisinin resistance. Genome Biology, 2017, 18, 78.	3.8	120

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37	Malaria Genomics in the Era of Eradication. Cold Spring Harbor Perspectives in Medicine, 2017, 7, a025544.	2.9	33
38	Genetic relatedness analysis reveals the cotransmission of genetically related Plasmodium falciparum parasites in ThiÁ's, Senegal. Genome Medicine, 2017, 9, 5.	3.6	47
39	THE REAL McCOIL: A method for the concurrent estimation of the complexity of infection and SNP allele frequency for malaria parasites. PLoS Computational Biology, 2017, 13, e1005348.	1.5	93
40	Quantifying connectivity between local Plasmodium falciparum malaria parasite populations using identity by descent. PLoS Genetics, 2017, 13, e1007065.	1.5	98
41	Mosquito Vectors and the Globalization of Plasmodium falciparum Malaria. Annual Review of Genetics, 2016, 50, 447-465.	3.2	51
42	Population genomics studies identify signatures of global dispersal and drug resistance in Plasmodium vivax. Nature Genetics, 2016, 48, 953-958.	9.4	194
43	Evaluation of DISCOVAR de novo using a mosquito sample for cost-effective short-read genome assembly. BMC Genomics, 2016, 17, 187.	1.2	60
44	Chromerid genomes reveal the evolutionary path from photosynthetic algae to obligate intracellular parasites. ELife, 2015, 4, e06974.	2.8	198
45	COIL: a methodology for evaluating malarial complexity of infection using likelihood from single nucleotide polymorphism data. Malaria Journal, 2015, 14, 4.	0.8	71
46	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.	3.3	163
47	Development of a Single Nucleotide Polymorphism Barcode to Genotype Plasmodium vivax Infections. PLoS Neglected Tropical Diseases, 2015, 9, e0003539.	1.3	90
48	Genetic Diversity and Protective Efficacy of the RTS,S/AS01 Malaria Vaccine. New England Journal of Medicine, 2015, 373, 2025-2037.	13.9	332
49	Adaptive evolution of malaria parasites in French Guiana: Reversal of chloroquine resistance by acquisition of a mutation in <i>pfcr</i> . Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11672-11677.	3.3	101
50	Extensive introgression in a malaria vector species complex revealed by phylogenomics. Science, 2015, 347, 1258524.	6.0	527
51	Highly evolvable malaria vectors: The genomes of 16 <i>Anopheles</i> mosquitoes. Science, 2015, 347, 1258522.	6.0	492
52	Genome-Level Determination of Plasmodium falciparum Blood-Stage Targets of Malarial Clinical Immunity in the Peruvian Amazon. Journal of Infectious Diseases, 2015, 211, 1342-1351.	1.9	25
53	“Big data” from shrinking pathogen populations. Molecular Ecology, 2013, 22, 271-272.	2.0	2
54	Genome sequencing sheds light on emerging drug resistance in malaria parasites. Nature Genetics, 2013, 45, 589-590.	9.4	8

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55	Malaria life cycle intensifies both natural selection and random genetic drift. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20129-20134.	3.3	67
56	Genetic Surveillance Detects Both Clonal and Epidemic Transmission of Malaria following Enhanced Intervention in Senegal. PLoS ONE, 2013, 8, e60780.	1.1	87
57	VAR2CSA Signatures of High Plasmodium falciparum Parasitemia in the Placenta. PLoS ONE, 2013, 8, e69753.	1.1	11
58	SNP Genotyping Identifies New Signatures of Selection in a Deep Sample of West African Plasmodium falciparum Malaria Parasites. Molecular Biology and Evolution, 2012, 29, 3249-3253.	3.5	41
59	Sequence-based association and selection scans identify drug resistance loci in the <i>Plasmodium falciparum</i> malaria parasite. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13052-13057.	3.3	99
60	Genomic Sequencing of Plasmodium falciparum Malaria Parasites from Senegal Reveals the Demographic History of the Population. Molecular Biology and Evolution, 2012, 29, 3427-3439.	3.5	58
61	Harnessing genomics and genome biology to understand malaria biology. Nature Reviews Genetics, 2012, 13, 315-328.	7.7	95
62	The malaria parasite Plasmodium vivax exhibits greater genetic diversity than Plasmodium falciparum. Nature Genetics, 2012, 44, 1046-1050.	9.4	256
63	Hybrid selection for sequencing pathogen genomes from clinical samples. Genome Biology, 2011, 12, R73.	13.9	97
64	Identification and Functional Validation of the Novel Antimalarial Resistance Locus PF10_0355 in Plasmodium falciparum. PLoS Genetics, 2011, 7, e1001383.	1.5	85
65	Population genetic analysis of large sequence polymorphisms in Plasmodium falciparum blood-stage antigens. Infection, Genetics and Evolution, 2010, 10, 200-206.	1.0	20
66	Comparative evolutionary genomics of human malaria parasites. Trends in Parasitology, 2008, 24, 545-550.	1.5	57
67	Genome-wide SNP genotyping highlights the role of natural selection in Plasmodium falciparum population divergence. Genome Biology, 2008, 9, R171.	3.8	119
68	A general SNP-based molecular barcode for Plasmodium falciparum identification and tracking. Malaria Journal, 2008, 7, 223.	0.8	213
69	Dual Modes of Natural Selection on Upstream Open Reading Frames. Molecular Biology and Evolution, 2007, 24, 1744-1751.	3.5	46
70	A genome-wide map of diversity in Plasmodium falciparum. Nature Genetics, 2007, 39, 113-119.	9.4	320
71	Positive selection for unpreferred codon usage in eukaryotic genomes. BMC Evolutionary Biology, 2007, 7, 119.	3.2	22
72	Evolution of Noncoding and Silent Coding Sites in the Plasmodium falciparum and Plasmodium reichenowi Genomes. Molecular Biology and Evolution, 2005, 22, 1621-1626.	3.5	19

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73	Convergent loss of an anciently duplicated, functionally divergent RH2 opsin gene in the fugu and Tetraodon pufferfish lineages. <i>Gene</i> , 2005, 350, 161-171.	1.0	30
74	Different Regulatory Mechanisms Underlie Similar Transposable Element Profiles in Pufferfish and Fruitflies. <i>Molecular Biology and Evolution</i> , 2004, 21, 2310-2318.	3.5	30
75	Genome Size Evolution in Pufferfish: A Comparative Analysis of Diodontid and Tetraodontid Pufferfish Genomes. <i>Genome Research</i> , 2003, 13, 821-830.	2.4	98