

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	Extensive introgression in a malaria vector species complex revealed by phylogenomics. <i>Science</i> , 2015, 347, 1258524.	6.0	527
2	Highly evolvable malaria vectors: The genomes of 16 <i>Anopheles</i> mosquitoes. <i>Science</i> , 2015, 347, 1258522.	6.0	492
3	Genomic architecture and introgression shape a butterfly radiation. <i>Science</i> , 2019, 366, 594-599.	6.0	365
4	Genetic Diversity and Protective Efficacy of the RTS,S/AS01 Malaria Vaccine. <i>New England Journal of Medicine</i> , 2015, 373, 2025-2037.	13.9	332
5	A genome-wide map of diversity in <i>Plasmodium falciparum</i> . <i>Nature Genetics</i> , 2007, 39, 113-119.	9.4	320
6	The malaria parasite <i>Plasmodium vivax</i> exhibits greater genetic diversity than <i>Plasmodium falciparum</i> . <i>Nature Genetics</i> , 2012, 44, 1046-1050.	9.4	256
7	A general SNP-based molecular barcode for <i>Plasmodium falciparum</i> identification and tracking. <i>Malaria Journal</i> , 2008, 7, 223.	0.8	213
8	Chromerid genomes reveal the evolutionary path from photosynthetic algae to obligate intracellular parasites. <i>ELife</i> , 2015, 4, e06974.	2.8	198
9	Population genomics studies identify signatures of global dispersal and drug resistance in <i>Plasmodium vivax</i> . <i>Nature Genetics</i> , 2016, 48, 953-958.	9.4	194
10	Modeling malaria genomics reveals transmission decline and rebound in Senegal. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 7067-7072.	3.3	163
11	Longitudinal genomic surveillance of <i>Plasmodium falciparum</i> malaria parasites reveals complex genomic architecture of emerging artemisinin resistance. <i>Genome Biology</i> , 2017, 18, 78.	3.8	120
12	Genome-wide SNP genotyping highlights the role of natural selection in <i>Plasmodium falciparum</i> population divergence. <i>Genome Biology</i> , 2008, 9, R171.	3.8	119
13	Mutations in <i>Plasmodium falciparum</i> actin-binding protein coronin confer reduced artemisinin susceptibility. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12799-12804.	3.3	114
14	hmmIBD: software to infer pairwise identity by descent between haploid genotypes. <i>Malaria Journal</i> , 2018, 17, 196.	0.8	103
15	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
16	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.	3.3	101
17	Sequence-based association and selection scans identify drug resistance loci in the <i>Plasmodium falciparum</i> malaria parasite. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13052-13057.	3.3	99
18	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

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19	Quantifying connectivity between local <i>Plasmodium falciparum</i> malaria parasite populations using identity by descent. <i>PLoS Genetics</i> , 2017, 13, e1007065.	1.5	98
20	Hybrid selection for sequencing pathogen genomes from clinical samples. <i>Genome Biology</i> , 2011, 12, R73.	13.9	97
21	Harnessing genomics and genome biology to understand malaria biology. <i>Nature Reviews Genetics</i> , 2012, 13, 315-328.	7.7	95
22	THE REAL McCOIL: A method for the concurrent estimation of the complexity of infection and SNP allele frequency for malaria parasites. <i>PLoS Computational Biology</i> , 2017, 13, e1005348.	1.5	93
23	Development of a Single Nucleotide Polymorphism Barcode to Genotype <i>Plasmodium vivax</i> Infections. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003539.	1.3	90
24	Genetic Surveillance Detects Both Clonal and Epidemic Transmission of Malaria following Enhanced Intervention in Senegal. <i>PLoS ONE</i> , 2013, 8, e60780.	1.1	87
25	Identification and Functional Validation of the Novel Antimalarial Resistance Locus PF10_0355 in <i>Plasmodium falciparum</i> . <i>PLoS Genetics</i> , 2011, 7, e1001383.	1.5	85
26	COIL: a methodology for evaluating malarial complexity of infection using likelihood from single nucleotide polymorphism data. <i>Malaria Journal</i> , 2015, 14, 4.	0.8	71
27	Resolving the cause of recurrent <i>Plasmodium vivax</i> malaria probabilistically. <i>Nature Communications</i> , 2019, 10, 5595.	5.8	70
28	Mapping malaria by combining parasite genomic and epidemiologic data. <i>BMC Medicine</i> , 2018, 16, 190.	2.3	68
29	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.	3.3	67
30	Advances and opportunities in malaria population genomics. <i>Nature Reviews Genetics</i> , 2021, 22, 502-517.	7.7	61
31	Evaluation of DISCOVAR de novo using a mosquito sample for cost-effective short-read genome assembly. <i>BMC Genomics</i> , 2016, 17, 187.	1.2	60
32	Genomic Sequencing of <i>Plasmodium falciparum</i> Malaria Parasites from Senegal Reveals the Demographic History of the Population. <i>Molecular Biology and Evolution</i> , 2012, 29, 3427-3439.	3.5	58
33	Comparative evolutionary genomics of human malaria parasites. <i>Trends in Parasitology</i> , 2008, 24, 545-550.	1.5	57
34	Mosquito Vectors and the Globalization of <i>Plasmodium falciparum</i> Malaria. <i>Annual Review of Genetics</i> , 2016, 50, 447-465.	3.2	51
35	Candidate-gene based GWAS identifies reproducible DNA markers for metabolic pyrethroid resistance from standing genetic variation in East African <i>Anopheles gambiae</i> . <i>Scientific Reports</i> , 2018, 8, 2920.	1.6	51
36	Genetic relatedness analysis reveals the cotransmission of genetically related <i>Plasmodium falciparum</i> parasites in Thiès, Senegal. <i>Genome Medicine</i> , 2017, 9, 5.	3.6	47

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37	Estimating Relatedness Between Malaria Parasites. <i>Genetics</i> , 2019, 212, 1337-1351.	1.2	47
38	Dual Modes of Natural Selection on Upstream Open Reading Frames. <i>Molecular Biology and Evolution</i> , 2007, 24, 1744-1751.	3.5	46
39	SNP Genotyping Identifies New Signatures of Selection in a Deep Sample of West African <i>Plasmodium falciparum</i> Malaria Parasites. <i>Molecular Biology and Evolution</i> , 2012, 29, 3249-3253.	3.5	41
40	Detection of low-density <i>Plasmodium falciparum</i> infections using amplicon deep sequencing. <i>Malaria Journal</i> , 2019, 18, 219.	0.8	40
41	Malaria Genomics in the Era of Eradication. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2017, 7, a025544.	2.9	33
42	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
43	Convergent loss of an anciently duplicated, functionally divergent RH2 opsin gene in the fugu and <i>Tetraodon</i> pufferfish lineages. <i>Gene</i> , 2005, 350, 161-171.	1.0	30
44	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
45	Host-mediated selection impacts the diversity of <i>Plasmodium falciparum</i> antigens within infections. <i>Nature Communications</i> , 2018, 9, 1381.	5.8	27
46	Genome-Level Determination of <i>Plasmodium falciparum</i> Blood-Stage Targets of Malarial Clinical Immunity in the Peruvian Amazon. <i>Journal of Infectious Diseases</i> , 2015, 211, 1342-1351.	1.9	25
47	Probing <i>Plasmodium falciparum</i> sexual commitment at the single-cell level. <i>Wellcome Open Research</i> , 2018, 3, 70.	0.9	25
48	Positive selection for unpreferred codon usage in eukaryotic genomes. <i>BMC Evolutionary Biology</i> , 2007, 7, 119.	3.2	22
49	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
50	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
51	Population genetic analysis of large sequence polymorphisms in <i>Plasmodium falciparum</i> blood-stage antigens. <i>Infection, Genetics and Evolution</i> , 2010, 10, 200-206.	1.0	20
52	Evolution of Noncoding and Silent Coding Sites in the <i>Plasmodium falciparum</i> and <i>Plasmodium reichenowi</i> Genomes. <i>Molecular Biology and Evolution</i> , 2005, 22, 1621-1626.	3.5	19
53	<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
54	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

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55	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
56	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
57	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
58	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
59	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
60	De Novo Mutations Resolve Disease Transmission Pathways in Clonal Malaria. <i>Molecular Biology and Evolution</i> , 2018, 35, 1678-1689.	3.5	14
61	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
62	VAR2CSA Signatures of High <i>Plasmodium falciparum</i> Parasitemia in the Placenta. <i>PLoS ONE</i> , 2013, 8, e69753.	1.1	11
63	Genome sequencing sheds light on emerging drug resistance in malaria parasites. <i>Nature Genetics</i> , 2013, 45, 589-590.	9.4	8
64	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
65	Transcriptional correlates of malaria in RTS,S/AS01-vaccinated African children: a matched case-control study. <i>ELife</i> , 2022, 11, .	2.8	4
66	"Big data" from shrinking pathogen populations. <i>Molecular Ecology</i> , 2013, 22, 271-272.	2.0	2
67	Molecular surveillance of malaria scales up. <i>Trends in Parasitology</i> , 2021, 37, 1020-1021.	1.5	2
68	Title is missing!. , 2020, 16, e1009101.		0
69	Title is missing!. , 2020, 16, e1009101.		0
70	Title is missing!. , 2020, 16, e1009101.		0
71	Title is missing!. , 2020, 16, e1009101.		0
72	Title is missing!. , 2020, 14, e0008962.		0

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73	Title is missing!. , 2020, 14, e0008962.		0
74	Title is missing!. , 2020, 14, e0008962.		0
75	Title is missing!.. , 2020, 14, e0008962.		0