

# Alyssa E Barry

## List of Publications by Year in descending order

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83  
papers

3,944  
citations

94433

37  
h-index

144013

57  
g-index

95  
all docs

95  
docs citations

95  
times ranked

3662  
citing authors

#	ARTICLE	IF	CITATIONS
1	Population-level genome-wide STR discovery and validation for population structure and genetic diversity assessment of <i>Plasmodium</i> species. <i>PLoS Genetics</i> , 2022, 18, e1009604.	3.5	8
2	Global diversity and balancing selection of 23 leading <i>Plasmodium falciparum</i> candidate vaccine antigens. <i>PLoS Computational Biology</i> , 2022, 18, e1009801.	3.2	14
3	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
4	Community-based molecular and serological surveillance of subclinical malaria in Myanmar. <i>BMC Medicine</i> , 2021, 19, 121.	5.5	6
5	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
6	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	51
7	Surveillance of molecular markers of <i>Plasmodium falciparum</i> artemisinin resistance (kelch13) Tj ETQq1 1 0.784314 rgBT /Overlock 10 and Drug Resistance, 2021, 16, 188-193.	3.4	15
8	Complex infections in vivax malaria: the more you look, the more you find. <i>Trends in Parasitology</i> , 2021, 37, 1022-1023.	3.3	1
9	Monitoring <i>Plasmodium falciparum</i> and <i>Plasmodium vivax</i> using microsatellite markers indicates limited changes in population structure after substantial transmission decline in Papua New Guinea. <i>Molecular Ecology</i> , 2020, 29, 4525-4541.	3.9	15
10	Implementing parasite genotyping into national surveillance frameworks: feedback from control programmes and researchers in the Asia-Pacific region. <i>Malaria Journal</i> , 2020, 19, 271.	2.3	31
11	Population genomics identifies a distinct <i>Plasmodium vivax</i> population on the China-Myanmar border of Southeast Asia. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008506.	3.0	18
12	SNP barcodes provide higher resolution than microsatellite markers to measure <i>Plasmodium vivax</i> population genetics. <i>Malaria Journal</i> , 2020, 19, 375.	2.3	25
13	Evaluation of the effectiveness of topical repellent distributed by village health volunteer networks against <i>Plasmodium</i> spp. infection in Myanmar: A stepped-wedge cluster randomised trial. <i>PLoS Medicine</i> , 2020, 17, e1003177.	8.4	16
14	A Natural Peptide Antigen within the <i>Plasmodium</i> Ribosomal Protein RPL6 Confers Liver TRM Cell-Mediated Immunity against Malaria in Mice. <i>Cell Host and Microbe</i> , 2020, 27, 950-962.e7.	11.0	45
15	The epidemiology of <i>Plasmodium falciparum</i> and <i>Plasmodium vivax</i> in East Sepik Province, Papua New Guinea, pre- and post-implementation of national malaria control efforts. <i>Malaria Journal</i> , 2020, 19, 198.	2.3	12
16	Emergence of artemisinin-resistant <i>Plasmodium falciparum</i> with kelch13 C580Y mutations on the island of New Guinea. <i>PLoS Pathogens</i> , 2020, 16, e1009133.	4.7	81
17	Title is missing!. , 2020, 14, e0008506.		0
18	Title is missing!. , 2020, 14, e0008506.		0

#	ARTICLE	IF	CITATIONS
19	Title is missing!. , 2020, 14, e0008506.		0
20	Title is missing!. , 2020, 14, e0008506.		0
21	Title is missing!. , 2020, 14, e0008506.		0
22	Title is missing!. , 2020, 14, e0008506.		0
23	Title is missing!. , 2020, 16, e1009133.		0
24	Title is missing!. , 2020, 16, e1009133.		0
25	Title is missing!. , 2020, 16, e1009133.		0
26	Title is missing!. , 2020, 16, e1009133.		0
27	Protective Immunity against Severe Malaria in Children Is Associated with a Limited Repertoire of Antibodies to Conserved PfEMP1 Variants. <i>Cell Host and Microbe</i> , 2019, 26, 579-590.e5.	11.0	40
28	Molecular epidemiology of residual <i>Plasmodium vivax</i> transmission in a paediatric cohort in Solomon Islands. <i>Malaria Journal</i> , 2019, 18, 106.	2.3	9
29	Differential impact of malaria control interventions on <i>P. falciparum</i> and <i>P. vivax</i> infections in young Papua New Guinean children. <i>BMC Medicine</i> , 2019, 17, 220.	5.5	19
30	Re-emergence of yaws after single mass azithromycin treatment followed by targeted treatment: a longitudinal study. <i>Lancet</i> , The, 2018, 391, 1599-1607.	13.7	70
31	Nationwide genetic surveillance of <i>Plasmodium vivax</i> in Papua New Guinea reveals heterogeneous transmission dynamics and routes of migration amongst subdivided populations. <i>Infection, Genetics and Evolution</i> , 2018, 58, 83-95.	2.3	19
32	Identity-by-descent analyses for measuring population dynamics and selection in recombining pathogens. <i>PLoS Genetics</i> , 2018, 14, e1007279.	3.5	86
33	Antibodies to Intercellular Adhesion Molecule 1-Binding <i>Plasmodium falciparum</i> Erythrocyte Membrane Protein 1-DBL $\beta$ Are Biomarkers of Protective Immunity to Malaria in a Cohort of Young Children from Papua New Guinea. <i>Infection and Immunity</i> , 2018, 86, .	2.2	23
34	Increasingly inbred and fragmented populations of <i>Plasmodium vivax</i> associated with the eastward decline in malaria transmission across the Southwest Pacific. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006146.	3.0	27
35	Higher Complexity of Infection and Genetic Diversity of <i>Plasmodium vivax</i> Than <i>Plasmodium falciparum</i> across all Malaria Transmission Zones of Papua New Guinea. <i>American Journal of Tropical Medicine and Hygiene</i> , 2017, 96, 16-0716.	1.4	45
36	Editorial: Molecular Approaches to Malaria, 2016. <i>International Journal for Parasitology</i> , 2017, 47, 75.	3.1	0

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37	Challenges for achieving safe and effective radical cure of <i>Plasmodium vivax</i> : a round table discussion of the APMEN Vivax Working Group. <i>Malaria Journal</i> , 2017, 16, 141.	2.3	52
38	Dissecting malaria biology and epidemiology using population genetics and genomics. <i>International Journal for Parasitology</i> , 2017, 47, 77-85.	3.1	56
39	Sustained Malaria Control Over an 8-Year Period in Papua New Guinea: The Challenge of Low-Density Asymptomatic <i>Plasmodium</i> Infections. <i>Journal of Infectious Diseases</i> , 2017, 216, 1434-1443.	4.0	41
40	Development of a Multilocus Sequence Typing (MLST) scheme for <i>Treponema pallidum</i> subsp. <i>pertenue</i> : Application to yaws in Lihir Island, Papua New Guinea. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0006113.	3.0	23
41	Spatial Effects on the Multiplicity of <i>Plasmodium falciparum</i> Infections. <i>PLoS ONE</i> , 2016, 11, e0164054.	2.5	23
42	Naturally acquired immunity to malaria. <i>Parasitology</i> , 2016, 143, 125-128.	1.5	18
43	Implications of <i>Plasmodium vivax</i> Biology for Control, Elimination, and Research. <i>American Journal of Tropical Medicine and Hygiene</i> , 2016, 95, 4-14.	1.4	60
44	Population genomics studies identify signatures of global dispersal and drug resistance in <i>Plasmodium vivax</i> . <i>Nature Genetics</i> , 2016, 48, 953-958.	21.4	194
45	Genomic analysis of local variation and recent evolution in <i>Plasmodium vivax</i> . <i>Nature Genetics</i> , 2016, 48, 959-964.	21.4	169
46	Structurally conserved erythrocyte-binding domain in <i>Plasmodium</i> provides a versatile scaffold for alternate receptor engagement. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E191-200.	7.1	43
47	<i>Plasmodium vivax</i> Populations Are More Genetically Diverse and Less Structured than Sympatric <i>Plasmodium falciparum</i> Populations. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003634.	3.0	62
48	High Rates of Asymptomatic, Sub-microscopic <i>Plasmodium vivax</i> Infection and Disappearing <i>Plasmodium falciparum</i> Malaria in an Area of Low Transmission in Solomon Islands. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003758.	3.0	82
49	Uncovering the transmission dynamics of <i>Plasmodium vivax</i> using population genetics. <i>Pathogens and Global Health</i> , 2015, 109, 142-152.	2.3	52
50	Designing malaria vaccines to circumvent antigen variability. <i>Vaccine</i> , 2015, 33, 7506-7512.	3.8	54
51	Phylogeography of <i>var</i> gene repertoires reveals fine-scale geospatial clustering of <i>Plasmodium falciparum</i> populations in a highly endemic area. <i>Molecular Ecology</i> , 2015, 24, 484-497.	3.9	39
52	Malaria Molecular Epidemiology: Lessons from the International Centers of Excellence for Malaria Research Network. <i>American Journal of Tropical Medicine and Hygiene</i> , 2015, 93, 79-86.	1.4	80
53	Blood-Stage Parasitaemia and Age Determine <i>Plasmodium falciparum</i> and <i>P. vivax</i> Gametocytaemia in Papua New Guinea. <i>PLoS ONE</i> , 2015, 10, e0126747.	2.5	94
54	Limited antigenic diversity of <i>Plasmodium falciparum</i> apical membrane antigen 1 supports the development of effective multi-allele vaccines. <i>BMC Medicine</i> , 2014, 12, 183.	5.5	47

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55	Strategies for Designing and Monitoring Malaria Vaccines Targeting Diverse Antigens. <i>Frontiers in Immunology</i> , 2014, 5, 359.	4.8	101
56	Genetic diversity of VAR2CSA ID1-DBL2Xb in worldwide <i>Plasmodium falciparum</i> populations: Impact on vaccine design for placental malaria. <i>Infection, Genetics and Evolution</i> , 2014, 25, 81-92.	2.3	20
57	Distinct patterns of diversity, population structure and evolution in the AMA1 genes of sympatric <i>Plasmodium falciparum</i> and <i>Plasmodium vivax</i> populations of Papua New Guinea from an area of similarly high transmission. <i>Malaria Journal</i> , 2014, 13, 233.	2.3	35
58	Escaping the immune system: How the malaria parasite makes vaccine development a challenge. <i>Trends in Parasitology</i> , 2013, 29, 612-622.	3.3	54
59	Global Population Structure of the Genes Encoding the Malaria Vaccine Candidate, <i>Plasmodium vivax</i> Apical Membrane Antigen 1 (PvAMA1). <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2506.	3.0	47
60	High Genetic Diversity of <i>Plasmodium vivax</i> on the North Coast of Papua New Guinea. <i>American Journal of Tropical Medicine and Hygiene</i> , 2013, 89, 188-194.	1.4	23
61	High Levels of Genetic Diversity of <i>Plasmodium falciparum</i> Populations in Papua New Guinea despite Variable Infection Prevalence. <i>American Journal of Tropical Medicine and Hygiene</i> , 2013, 88, 718-725.	1.4	49
62	A Large <i>Plasmodium vivax</i> Reservoir and Little Population Structure in the South Pacific. <i>PLoS ONE</i> , 2013, 8, e66041.	2.5	48
63	The <i>Plasmodium falciparum</i> Erythrocyte Invasion Ligand Pfrh4 as a Target of Functional and Protective Human Antibodies against Malaria. <i>PLoS ONE</i> , 2012, 7, e45253.	2.5	51
64	Hepatitis C Virus Phylogenetic Clustering Is Associated with the Social-Injecting Network in a Cohort of People Who Inject Drugs. <i>PLoS ONE</i> , 2012, 7, e47335.	2.5	68
65	Understanding the population genetics of <i>Plasmodium vivax</i> is essential for malaria control and elimination. <i>Malaria Journal</i> , 2012, 11, 14.	2.3	98
66	A Molecular Epidemiological Study of var Gene Diversity to Characterize the Reservoir of <i>Plasmodium falciparum</i> in Humans in Africa. <i>PLoS ONE</i> , 2011, 6, e16629.	2.5	73
67	Population genetic analysis of the <i>Plasmodium falciparum</i> 6-cys protein Pf38 in Papua New Guinea reveals domain-specific balancing selection. <i>Malaria Journal</i> , 2011, 10, 126.	2.3	18
68	The Stability and Complexity of Antibody Responses to the Major Surface Antigen of <i>Plasmodium falciparum</i> Are Associated with Age in a Malaria Endemic Area. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.008326.	3.8	78
69	Evidence That the Erythrocyte Invasion Ligand PfRh2 is a Target of Protective Immunity against <i>Plasmodium falciparum</i> . <i>Malaria Journal of Immunology</i> , 2010, 185, 6157-6167.	0.8	84
70	Multilocus haplotypes reveal variable levels of diversity and population structure of <i>Plasmodium falciparum</i> in Papua New Guinea, a region of intense perennial transmission. <i>Malaria Journal</i> , 2010, 9, 336.	2.3	79
71	Contrasting Population Structures of the Genes Encoding Ten Leading Vaccine-Candidate Antigens of the Human Malaria Parasite, <i>Plasmodium falciparum</i> . <i>PLoS ONE</i> , 2009, 4, e8497.	2.5	100
72	Population Genomics of the Immune Evasion (var) Genes of <i>Plasmodium falciparum</i> . <i>PLoS Pathogens</i> , 2007, 3, e34.	4.7	150

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73	Genomic heterogeneity in the density of noncoding single-nucleotide and microsatellite polymorphisms in <i>Plasmodium falciparum</i> . <i>Gene</i> , 2007, 387, 1-6.	2.2	8
74	Variable SNP density in aspartyl-protease genes of the malaria parasite <i>Plasmodium falciparum</i> . <i>Gene</i> , 2006, 376, 163-173.	2.2	4
75	DNA sequence artifacts and the estimation of time to the most recent common ancestor (TMRCA) of <i>Plasmodium falciparum</i> . <i>Molecular and Biochemical Parasitology</i> , 2003, 130, 143-147.	1.1	8
76	The paradoxical population genetics of <i>Plasmodium falciparum</i> . <i>Trends in Parasitology</i> , 2002, 18, 266-272.	3.3	45
77	Recent Origin of <i>Plasmodium falciparum</i> from a Single Progenitor. <i>Science</i> , 2001, 293, 482-484.	12.6	197
78	The 10q25 Neocentromere and its Inactive Progenitor Have Identical Primary Nucleotide Sequence: Further Evidence for Epigenetic Modification. <i>Genome Research</i> , 2000, 10, 832-838.	5.5	39
79	Sequence analysis of an 80 kb human neocentromere. <i>Human Molecular Genetics</i> , 1999, 8, 217-227.	2.9	99
80	Direct Cloning of Human 10q25 Neocentromere DNA Using Transformation-Associated Recombination (TAR) in Yeast. <i>Genomics</i> , 1998, 47, 399-404.	2.9	37
81	A functional neo-centromere formed through activation of a latent human centromere and consisting of non-alpha-satellite DNA. <i>Nature Genetics</i> , 1997, 16, 144-153.	21.4	319
82	Protective Immunity Against Severe Malaria is Associated with a Repertoire of Antibodies to Conserved PfEMP1 Variants. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
83	An open dataset of <i>Plasmodium vivax</i> genome variation in 1,895 worldwide samples. <i>Wellcome Open Research</i> , 0, 7, 136.	1.8	16