

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	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
2	Recent Origin of <i>Plasmodium falciparum</i> from a Single Progenitor. <i>Science</i> , 2001, 293, 482-484.	12.6	197
3	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
4	Genomic analysis of local variation and recent evolution in <i>Plasmodium vivax</i> . <i>Nature Genetics</i> , 2016, 48, 959-964.	21.4	169
5	Population Genomics of the Immune Evasion (var) Genes of <i>Plasmodium falciparum</i> . <i>PLoS Pathogens</i> , 2007, 3, e34.	4.7	150
6	Strategies for Designing and Monitoring Malaria Vaccines Targeting Diverse Antigens. <i>Frontiers in Immunology</i> , 2014, 5, 359.	4.8	101
7	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
8	Sequence analysis of an 80 kb human neocentromere. <i>Human Molecular Genetics</i> , 1999, 8, 217-227.	2.9	99
9	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
10	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
11	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
12	Identity-by-descent analyses for measuring population dynamics and selection in recombining pathogens. <i>PLoS Genetics</i> , 2018, 14, e1007279.	3.5	86
13	Evidence That the Erythrocyte Invasion Ligand PfRh2 is a Target of Protective Immunity against <i>Plasmodium falciparum</i> Malaria. <i>Journal of Immunology</i> , 2010, 185, 6157-6167.	0.8	84
14	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
15	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
16	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
17	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
18	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

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19	A Molecular Epidemiological Study of var Gene Diversity to Characterize the Reservoir of Plasmodium falciparum in Humans in Africa. PLoS ONE, 2011, 6, e16629.	2.5	73
20	Re-emergence of yaws after single mass azithromycin treatment followed by targeted treatment: a longitudinal study. Lancet, The, 2018, 391, 1599-1607.	13.7	70
21	Hepatitis C Virus Phylogenetic Clustering Is Associated with the Social-Injecting Network in a Cohort of People Who Inject Drugs. PLoS ONE, 2012, 7, e47335.	2.5	68
22	Plasmodium vivax Populations Are More Genetically Diverse and Less Structured than Sympatric Plasmodium falciparum Populations. PLoS Neglected Tropical Diseases, 2015, 9, e0003634.	3.0	62
23	Implications of <i>Plasmodium vivax</i> Biology for Control, Elimination, and Research. American Journal of Tropical Medicine and Hygiene, 2016, 95, 4-14.	1.4	60
24	Dissecting malaria biology and epidemiology using population genetics and genomics. International Journal for Parasitology, 2017, 47, 77-85.	3.1	56
25	Escaping the immune system: How the malaria parasite makes vaccine development a challenge. Trends in Parasitology, 2013, 29, 612-622.	3.3	54
26	Designing malaria vaccines to circumvent antigen variability. Vaccine, 2015, 33, 7506-7512.	3.8	54
27	Uncovering the transmission dynamics of <i>Plasmodium vivax</i> using population genetics. Pathogens and Global Health, 2015, 109, 142-152.	2.3	52
28	Challenges for achieving safe and effective radical cure of Plasmodium vivax: a round table discussion of the APMEN Vivax Working Group. Malaria Journal, 2017, 16, 141.	2.3	52
29	The Plasmodium falciparum Erythrocyte Invasion Ligand Pfrh4 as a Target of Functional and Protective Human Antibodies against Malaria. PLoS ONE, 2012, 7, e45253.	2.5	51
30	An open dataset of Plasmodium falciparum genome variation in 7,000 worldwide samples. Wellcome Open Research, 2021, 6, 42.	1.8	51
31	High Levels of Genetic Diversity of Plasmodium falciparum Populations in Papua New Guinea despite Variable Infection Prevalence. American Journal of Tropical Medicine and Hygiene, 2013, 88, 718-725.	1.4	49
32	A Large Plasmodium vivax Reservoir and Little Population Structure in the South Pacific. PLoS ONE, 2013, 8, e66041.	2.5	48
33	Global Population Structure of the Genes Encoding the Malaria Vaccine Candidate, Plasmodium vivax Apical Membrane Antigen 1 (PvAMA1). PLoS Neglected Tropical Diseases, 2013, 7, e2506.	3.0	47
34	Limited antigenic diversity of Plasmodium falciparum apical membrane antigen 1 supports the development of effective multi-allele vaccines. BMC Medicine, 2014, 12, 183.	5.5	47
35	The paradoxical population genetics of Plasmodium falciparum. Trends in Parasitology, 2002, 18, 266-272.	3.3	45
36	Higher Complexity of Infection and Genetic Diversity of Plasmodium vivax Than Plasmodium falciparum across all Malaria Transmission Zones of Papua New Guinea. American Journal of Tropical Medicine and Hygiene, 2017, 96, 16-0716.	1.4	45

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37	A Natural Peptide Antigen within the Plasmodium 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
38	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
39	Sustained Malaria Control Over an 8-Year Period in Papua New Guinea: The Challenge of Low-Density Asymptomatic Plasmodium Infections. <i>Journal of Infectious Diseases</i> , 2017, 216, 1434-1443.	4.0	41
40	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
41	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
42	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
43	Direct Cloning of Human 10q25 Neocentromere DNA Using Transformation-Associated Recombination (TAR) in Yeast. <i>Genomics</i> , 1998, 47, 399-404.	2.9	37
44	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
45	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
46	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
47	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
48	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
49	Spatial Effects on the Multiplicity of <i>Plasmodium falciparum</i> Infections. <i>PLoS ONE</i> , 2016, 11, e0164054.	2.5	23
50	Antibodies to Intercellular Adhesion Molecule 1-Binding <i>Plasmodium falciparum</i> Erythrocyte Membrane Protein 1-DBL α 2 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
51	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
52	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
53	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
54	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

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55	Population genetic analysis of the Plasmodium falciparum 6-cys protein Pf38 in Papua New Guinea reveals domain-specific balancing selection. <i>Malaria Journal</i> , 2011, 10, 126.	2.3	18
56	Naturally acquired immunity to malaria. <i>Parasitology</i> , 2016, 143, 125-128.	1.5	18
57	Population genomics identifies a distinct Plasmodium vivax population on the China-Myanmar border of Southeast Asia. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008506.	3.0	18
58	Evaluation of the effectiveness of topical repellent distributed by village health volunteer networks against Plasmodium spp. infection in Myanmar: A stepped-wedge cluster randomised trial. <i>PLoS Medicine</i> , 2020, 17, e1003177.	8.4	16
59	An open dataset of Plasmodium vivax genome variation in 1,895 worldwide samples. <i>Wellcome Open Research</i> , 0, 7, 136.	1.8	16
60	Monitoring Plasmodium falciparum and Plasmodium vivax 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
61	Surveillance of molecular markers of Plasmodium falciparum artemisinin resistance (kelch13) Tj ETQq1 1 0.784314 rgBT /Overlock 10 and Drug Resistance, 2021, 16, 188-193.	3.4	15
62	Global diversity and balancing selection of 23 leading Plasmodium falciparum candidate vaccine antigens. <i>PLoS Computational Biology</i> , 2022, 18, e1009801.	3.2	14
63	The epidemiology of Plasmodium falciparum and Plasmodium vivax 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
64	Molecular epidemiology of residual Plasmodium vivax transmission in a paediatric cohort in Solomon Islands. <i>Malaria Journal</i> , 2019, 18, 106.	2.3	9
65	DNA sequence artifacts and the estimation of time to the most recent common ancestor (TMRCA) of Plasmodium falciparum. <i>Molecular and Biochemical Parasitology</i> , 2003, 130, 143-147.	1.1	8
66	Genomic heterogeneity in the density of noncoding single-nucleotide and microsatellite polymorphisms in Plasmodium falciparum. <i>Gene</i> , 2007, 387, 1-6.	2.2	8
67	Population-level genome-wide STR discovery and validation for population structure and genetic diversity assessment of Plasmodium species. <i>PLoS Genetics</i> , 2022, 18, e1009604.	3.5	8
68	Community-based molecular and serological surveillance of subclinical malaria in Myanmar. <i>BMC Medicine</i> , 2021, 19, 121.	5.5	6
69	Variable SNP density in aspartyl-protease genes of the malaria parasite Plasmodium falciparum. <i>Gene</i> , 2006, 376, 163-173.	2.2	4
70	Whole-genome analysis of Malawian Plasmodium falciparum isolates identifies possible targets of allele-specific immunity to clinical malaria. <i>PLoS Genetics</i> , 2021, 17, e1009576.	3.5	4
71	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
72	Editorial: Molecular Approaches to Malaria, 2016. <i>International Journal for Parasitology</i> , 2017, 47, 75.	3.1	0

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73	Protective Immunity Against Severe Malaria is Associated with a Repertoire of Antibodies to Conserved PfEMP1 Variants. SSRN Electronic Journal, 0, , .	0.4	0
74	Title is missing!. , 2020, 14, e0008506.		0
75	Title is missing!. , 2020, 14, e0008506.		0
76	Title is missing!. , 2020, 14, e0008506.		0
77	Title is missing!. , 2020, 14, e0008506.		0
78	Title is missing!. , 2020, 14, e0008506.		0
79	Title is missing!. , 2020, 14, e0008506.		0
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83	Title is missing!. , 2020, 16, e1009133.		0