

# Dyann F Wirth

## List of Publications by Citations

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150  
papers

6,950  
citations

49  
h-index

79  
g-index

163  
ext. papers

8,227  
ext. citations

9.1  
avg, IF

5.29  
L-index

#	Paper	IF	Citations
150	A genome-wide map of diversity in <i>Plasmodium falciparum</i> . <i>Nature Genetics</i> , <b>2007</b> , 39, 113-9	36.3	265
149	Amplification of pfmdr 1 associated with mefloquine and halofantrine resistance in <i>Plasmodium falciparum</i> from Thailand. <i>Molecular and Biochemical Parasitology</i> , <b>1993</b> , 57, 151-60	1.9	241
148	Halofuginone and other febrifugine derivatives inhibit prolyl-tRNA synthetase. <i>Nature Chemical Biology</i> , <b>2012</b> , 8, 311-7	11.7	229
147	Diversity-oriented synthesis yields novel multistage antimalarial inhibitors. <i>Nature</i> , <b>2016</b> , 538, 344-349	50.4	172
146	A systematic map of genetic variation in <i>Plasmodium falciparum</i> . <i>PLoS Pathogens</i> , <b>2006</b> , 2, e57	7.6	159
145	Lysophosphatidylcholine Regulates Sexual Stage Differentiation in the Human Malaria Parasite <i>Plasmodium falciparum</i> . <i>Cell</i> , <b>2017</b> , 171, 1532-1544.e15	56.2	157
144	Stable expression of the bacterial neor gene in <i>Leishmania enriettii</i> . <i>Nature</i> , <b>1990</b> , 343, 572-4	50.4	155
143	A general SNP-based molecular barcode for <i>Plasmodium falciparum</i> identification and tracking. <i>Malaria Journal</i> , <b>2008</b> , 7, 223	3.6	154
142	Recent origin of <i>Plasmodium falciparum</i> from a single progenitor. <i>Science</i> , <b>2001</b> , 293, 482-4	33.3	152
141	malERA: An updated research agenda for malaria elimination and eradication. <i>PLoS Medicine</i> , <b>2017</b> , 14, e1002456	11.6	148
140	High-throughput <i>Plasmodium falciparum</i> growth assay for malaria drug discovery. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2007</b> , 51, 716-23	5.9	133
139	Serial analysis of gene expression in <i>Plasmodium falciparum</i> reveals the global expression profile of erythrocytic stages and the presence of anti-sense transcripts in the malarial parasite. <i>Molecular Biology of the Cell</i> , <b>2001</b> , 12, 3114-25	3.5	125
138	Mapping the malaria parasite druggable genome by using in vitro evolution and chemogenomics. <i>Science</i> , <b>2018</b> , 359, 191-199	33.3	124
137	Examining the human infectious reservoir for <i>Plasmodium falciparum</i> malaria in areas of differing transmission intensity. <i>Nature Communications</i> , <b>2017</b> , 8, 1133	17.4	117
136	Population structure and transmission dynamics of <i>Plasmodium vivax</i> in rural Amazonia. <i>Journal of Infectious Diseases</i> , <b>2007</b> , 195, 1218-26	7	116
135	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> , <b>2015</b> , 112, 7067-72	11.5	114
134	Novel inhibitors of <i>Plasmodium falciparum</i> dihydroorotate dehydrogenase with anti-malarial activity in the mouse model. <i>Journal of Biological Chemistry</i> , <b>2010</b> , 285, 33054-33064	5.4	105

133	Drugs for neglected diseases: a failure of the market and a public health failure?. <i>Tropical Medicine and International Health</i> , <b>2001</b> , 6, 945-51	2.3	105
132	Strand-specific RNA sequencing in Plasmodium falciparum malaria identifies developmentally regulated long non-coding RNA and circular RNA. <i>BMC Genomics</i> , <b>2015</b> , 16, 454	4.5	104
131	A global transcriptional analysis of Plasmodium falciparum malaria reveals a novel family of telomere-associated lncRNAs. <i>Genome Biology</i> , <b>2011</b> , 12, R56	18.3	99
130	Extensive microsatellite diversity in the human malaria parasite Plasmodium vivax. <i>Gene</i> , <b>2008</b> , 410, 105-18	3.8	96
129	Widespread distribution of antisense transcripts in the Plasmodium falciparum genome. <i>Molecular and Biochemical Parasitology</i> , <b>2004</b> , 136, 35-42	1.9	95
128	Bone Marrow Is a Major Parasite Reservoir in Plasmodium vivax Infection. <i>MBio</i> , <b>2018</b> , 9,	7.8	93
127	A high-throughput screen targeting malaria transmission stages opens new avenues for drug development. <i>Journal of Infectious Diseases</i> , <b>2011</b> , 203, 1445-53	7	90
126	Sequence of the immunodominant epitope for the surface protein on sporozoites of Plasmodium vivax. <i>Science</i> , <b>1985</b> , 230, 1381-3	33.3	87
125	Sequence-based association and selection scans identify drug resistance loci in the Plasmodium falciparum malaria parasite. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 13052-7	11.5	85
124	In vivo transcriptome of Plasmodium falciparum reveals overexpression of transcripts that encode surface proteins. <i>Journal of Infectious Diseases</i> , <b>2005</b> , 191, 1196-203	7	83
123	Isolation and functional characterization of two distinct sexual-stage-specific promoters of the human malaria parasite Plasmodium falciparum. <i>Molecular and Cellular Biology</i> , <b>1999</b> , 19, 967-78	4.8	83
122	Geographic structure of Plasmodium vivax: microsatellite analysis of parasite populations from Sri Lanka, Myanmar, and Ethiopia. <i>American Journal of Tropical Medicine and Hygiene</i> , <b>2010</b> , 82, 235-42	3.2	81
121	Identification of regulatory elements in the Plasmodium falciparum genome. <i>Molecular and Biochemical Parasitology</i> , <b>2004</b> , 134, 75-88	1.9	79
120	Excess polymorphisms in genes for membrane proteins in Plasmodium falciparum. <i>Science</i> , <b>2002</b> , 298, 216-8	33.3	73
119	Adaptive evolution of malaria parasites in French Guiana: Reversal of chloroquine resistance by acquisition of a mutation in pfcrt. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, 11672-7	11.5	72
118	Mutations in actin-binding protein coronin confer reduced artemisinin susceptibility. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, 12799-12804	11.5	72
117	Artemisinin resistance without pfkclch13 mutations in Plasmodium falciparum isolates from Cambodia. <i>Malaria Journal</i> , <b>2017</b> , 16, 195	3.6	71
116	Genetic surveillance detects both clonal and epidemic transmission of malaria following enhanced intervention in Senegal. <i>PLoS ONE</i> , <b>2013</b> , 8, e60780	3.7	71

115	A broad analysis of resistance development in the malaria parasite. <i>Nature Communications</i> , <b>2016</b> , 7, 11901	17.4	70
114	Harnessing genomics and genome biology to understand malaria biology. <i>Nature Reviews Genetics</i> , <b>2012</b> , 13, 315-28	30.1	70
113	Identification and characterization of small molecule inhibitors of Plasmodium falciparum dihydroorotate dehydrogenase. <i>Journal of Biological Chemistry</i> , <b>2008</b> , 283, 35078-85	5.4	70
112	Development of a single nucleotide polymorphism barcode to genotype Plasmodium vivax infections. <i>PLoS Neglected Tropical Diseases</i> , <b>2015</b> , 9, e0003539	4.8	62
111	Open-source discovery of chemical leads for next-generation chemoprotective antimalarials. <i>Science</i> , <b>2018</b> , 362,	33.3	60
110	Torins are potent antimalarials that block replenishment of Plasmodium liver stage parasitophorous vacuole membrane proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, E2838-47	11.5	59
109	Plasmepsin II-III copy number accounts for bimodal piperazine resistance among Cambodian Plasmodium falciparum. <i>Nature Communications</i> , <b>2018</b> , 9, 1769	17.4	58
108	Clonal outbreak of Plasmodium falciparum infection in eastern Panama. <i>Journal of Infectious Diseases</i> , <b>2015</b> , 211, 1087-96	7	56
107	In vitro chloroquine susceptibility and PCR analysis of pfcrt and pfmdr1 polymorphisms in Plasmodium falciparum isolates from Senegal. <i>American Journal of Tropical Medicine and Hygiene</i> , <b>2002</b> , 66, 474-80	3.2	56
106	The cytoplasmic prolyl-tRNA synthetase of the malaria parasite is a dual-stage target of febrifugine and its analogs. <i>Science Translational Medicine</i> , <b>2015</b> , 7, 288ra77	17.5	55
105	Genetic diversity and selection at the Plasmodium vivax apical membrane antigen-1 (PVAMA-1) locus in a Sri Lankan population. <i>Molecular Biology and Evolution</i> , <b>2007</b> , 24, 939-47	8.3	55
104	COIL: a methodology for evaluating malarial complexity of infection using likelihood from single nucleotide polymorphism data. <i>Malaria Journal</i> , <b>2015</b> , 14, 4	3.6	50
103	Rapid, field-deployable method for genotyping and discovery of single-nucleotide polymorphisms associated with drug resistance in Plasmodium falciparum. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2012</b> , 56, 2976-86	5.9	50
102	RNA polymerase II synthesizes antisense RNA in Plasmodium falciparum. <i>Rna</i> , <b>2005</b> , 11, 365-70	5.8	49
101	Gene conversion as a source of nucleotide diversity in Plasmodium falciparum. <i>Molecular Biology and Evolution</i> , <b>2003</b> , 20, 726-34	8.3	47
100	The Sri Lankan paradox: high genetic diversity in Plasmodium vivax populations despite decreasing levels of malaria transmission. <i>Parasitology</i> , <b>2014</b> , 141, 880-90	2.7	46
99	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> , <b>2013</b> , 110, 20129-34	11.5	46
98	Genomic sequencing of Plasmodium falciparum malaria parasites from Senegal reveals the demographic history of the population. <i>Molecular Biology and Evolution</i> , <b>2012</b> , 29, 3427-39	8.3	46

97	Plasmodium falciparum: genome wide perturbations in transcript profiles among mixed stage cultures after chloroquine treatment. <i>Experimental Parasitology</i> , <b>2007</b> , 117, 87-92	2.1	46
96	In vivo transcriptional profiling of Plasmodium falciparum. <i>Malaria Journal</i> , <b>2004</b> , 3, 30	3.6	46
95	Control of tubulin gene expression in the parasitic protozoan Leishmania enriettii. <i>Nature</i> , <b>1984</b> , 309, 716-7	50.4	46
94	Harnessing evolutionary fitness in Plasmodium falciparum for drug discovery and suppressing resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 799-804	11.5	45
93	In vitro resistance selections for Plasmodium falciparum dihydroorotate dehydrogenase inhibitors give mutants with multiple point mutations in the drug-binding site and altered growth. <i>Journal of Biological Chemistry</i> , <b>2014</b> , 289, 17980-95	5.4	45
92	hmmIBD: software to infer pairwise identity by descent between haploid genotypes. <i>Malaria Journal</i> , <b>2018</b> , 17, 196	3.6	44
91	Serial analysis of gene expression (SAGE) in Plasmodium falciparum: application of the technique to A-T rich genomes. <i>Molecular and Biochemical Parasitology</i> , <b>2001</b> , 113, 23-34	1.9	44
90	On the road to eliminate malaria in Sri Lanka: lessons from history, challenges, gaps in knowledge and research needs. <i>Malaria Journal</i> , <b>2014</b> , 13, 59	3.6	43
89	Type II NADH dehydrogenase of the respiratory chain of Plasmodium falciparum and its inhibitors. <i>Bioorganic and Medicinal Chemistry Letters</i> , <b>2009</b> , 19, 972-5	2.9	43
88	Drug-induced alterations in gene expression of the asexual blood forms of Plasmodium falciparum. <i>Molecular Microbiology</i> , <b>2003</b> , 50, 1229-39	4.1	43
87	Single-nucleotide polymorphism, linkage disequilibrium and geographic structure in the malaria parasite Plasmodium vivax: prospects for genome-wide association studies. <i>BMC Genetics</i> , <b>2010</b> , 11, 65	2.6	42
86	Triaminopyrimidine is a fast-killing and long-acting antimalarial clinical candidate. <i>Nature Communications</i> , <b>2015</b> , 6, 6715	17.4	41
85	Dietary restriction protects against experimental cerebral malaria via leptin modulation and T-cell mTORC1 suppression. <i>Nature Communications</i> , <b>2015</b> , 6, 6050	17.4	41
84	Patterns of gene-specific and total transcriptional activity during the Plasmodium falciparum intraerythrocytic developmental cycle. <i>Eukaryotic Cell</i> , <b>2009</b> , 8, 327-38		41
83	Inferring developmental stage composition from gene expression in human malaria. <i>PLoS Computational Biology</i> , <b>2013</b> , 9, e1003392	5	40
82	Identification and validation of tetracyclic benzothiazepines as Plasmodium falciparum cytochrome bc1 inhibitors. <i>Chemistry and Biology</i> , <b>2011</b> , 18, 1602-10		40
81	Duplication, gene conversion, and genetic diversity in the species-specific acyl-CoA synthetase gene family of Plasmodium falciparum. <i>Molecular and Biochemical Parasitology</i> , <b>2006</b> , 150, 10-24	1.9	40
80	Stage-specific transcripts of the Plasmodium falciparum pfmdr 1 gene. <i>Molecular and Biochemical Parasitology</i> , <b>1993</b> , 57, 203-11	1.9	37

79	Comparison of thick films, in vitro culture and DNA hybridization probes for detecting Plasmodium falciparum malaria. <i>American Journal of Tropical Medicine and Hygiene</i> , <b>1989</b> , 40, 3-6	3.2	31
78	Mapping of the Plasmodium falciparum multidrug resistance gene 5'upstream region, and evidence of induction of transcript levels by antimalarial drugs in chloroquine sensitive parasites. <i>Molecular Microbiology</i> , <b>2003</b> , 49, 671-83	4.1	30
77	Genetic relatedness analysis reveals the cotransmission of genetically related Plasmodium falciparum parasites in Thiès, Senegal. <i>Genome Medicine</i> , <b>2017</b> , 9, 5	14.4	29
76	Regulatory motifs uncovered among gene expression clusters in Plasmodium falciparum. <i>Molecular and Biochemical Parasitology</i> , <b>2007</b> , 153, 19-30	1.9	29
75	Responses to Bacteria, Virus, and Malaria Distinguish the Etiology of Pediatric Clinical Pneumonia. <i>American Journal of Respiratory and Critical Care Medicine</i> , <b>2016</b> , 193, 448-59	10.2	27
74	A new reporter gene for transient transfection of Plasmodium falciparum. <i>Parasitology Research</i> , <b>2003</b> , 89, 154-7	2.4	27
73	Plasmodium falciparum Cyclic Amine Resistance Locus (PFCARL), a Resistance Mechanism for Two Distinct Compound Classes. <i>ACS Infectious Diseases</i> , <b>2016</b> , 2, 816-826	5.5	26
72	Evidence of non-Plasmodium falciparum malaria infection in Kédougou, Senegal. <i>Malaria Journal</i> , <b>2017</b> , 16, 9	3.6	25
71	A non-radioactive DAPI-based high-throughput in vitro assay to assess Plasmodium falciparum responsiveness to antimalarials--increased sensitivity of P. falciparum to chloroquine in Senegal. <i>American Journal of Tropical Medicine and Hygiene</i> , <b>2010</b> , 82, 228-30	3.2	25
70	3TUTR elements enhance expression of Pgs28, an ookinete protein of Plasmodium gallinaceum. <i>Molecular and Biochemical Parasitology</i> , <b>2000</b> , 105, 61-70	1.9	25
69	Naturally acquired immunity against immature gametocytes. <i>Science Translational Medicine</i> , <b>2019</b> , 11,	17.5	24
68	Application of genomics to field investigations of malaria by the international centers of excellence for malaria research. <i>Acta Tropica</i> , <b>2012</b> , 121, 324-32	3.2	24
67	Aminoazabenzimidazoles, a novel class of orally active antimalarial agents. <i>Journal of Medicinal Chemistry</i> , <b>2014</b> , 57, 5702-13	8.3	23
66	Persistence of Plasmodium falciparum parasitemia after artemisinin combination therapy: evidence from a randomized trial in Uganda. <i>Scientific Reports</i> , <b>2016</b> , 6, 26330	4.9	22
65	Detection of low-density Plasmodium falciparum infections using amplicon deep sequencing. <i>Malaria Journal</i> , <b>2019</b> , 18, 219	3.6	22
64	Polymorphism in dhfr/dhps genes, parasite density and ex vivo response to pyrimethamine in Plasmodium falciparum malaria parasites in Thiès, Senegal. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , <b>2013</b> , 3, 135-42	4	22
63	Inactivation of Plasmepsins 2 and 3 Sensitizes Plasmodium falciparum to the Antimalarial Drug Piperaquine. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2018</b> , 62,	5.9	21
62	Changes in drug sensitivity and anti-malarial drug resistance mutations over time among Plasmodium falciparum parasites in Senegal. <i>Malaria Journal</i> , <b>2013</b> , 12, 441	3.6	21

61	Diversity-oriented synthesis probe targets <i>Plasmodium falciparum</i> cytochrome b ubiquinone reduction site and synergizes with oxidation site inhibitors. <i>Journal of Infectious Diseases</i> , <b>2015</b> , 211, 1097-103	7	21
60	New paradigms for understanding and step changes in treating active and chronic, persistent apicomplexan infections. <i>Scientific Reports</i> , <b>2016</b> , 6, 29179	4.9	20
59	Exploring the 3-piperidin-4-yl-1H-indole scaffold as a novel antimalarial chemotype. <i>European Journal of Medicinal Chemistry</i> , <b>2015</b> , 102, 320-33	6.8	19
58	Dramatic Changes in Malaria Population Genetic Complexity in Dielmo and Ndiop, Senegal, Revealed Using Genomic Surveillance. <i>Journal of Infectious Diseases</i> , <b>2018</b> , 217, 622-627	7	19
57	Identification of <i>Brugia malayi</i> in vectors with a species-specific DNA probe. <i>American Journal of Tropical Medicine and Hygiene</i> , <b>1986</b> , 35, 559-64	3.2	19
56	Evolution of the pfcr1 T76 and pfmdr1 Y86 markers and chloroquine susceptibility 8 years after cessation of chloroquine use in Pikine, Senegal. <i>Parasitology Research</i> , <b>2012</b> , 111, 1541-6	2.4	18
55	The role of DNA mismatch repair in generating genetic diversity and drug resistance in malaria parasites. <i>Molecular and Biochemical Parasitology</i> , <b>2007</b> , 155, 18-25	1.9	18
54	Linker scanning mutagenesis of the <i>Plasmodium gallinaceum</i> sexual stage specific gene pgs28 reveals a novel downstream cis-control element. <i>Molecular and Biochemical Parasitology</i> , <b>2003</b> , 129, 199-208	1.8	18
53	MalDA, Accelerating Malaria Drug Discovery. <i>Trends in Parasitology</i> , <b>2021</b> , 37, 493-507	6.4	18
52	Quantitative Proteomic Profiling Reveals Novel Surface Antigens and Possible Vaccine Candidates. <i>Molecular and Cellular Proteomics</i> , <b>2018</b> , 17, 43-60	7.6	18
51	West Africa International Centers of Excellence for Malaria Research: Drug Resistance Patterns to Artemether-Lumefantrine in Senegal, Mali, and The Gambia. <i>American Journal of Tropical Medicine and Hygiene</i> , <b>2016</b> , 95, 1054-1060	3.2	17
50	Host-mediated selection impacts the diversity of <i>Plasmodium falciparum</i> antigens within infections. <i>Nature Communications</i> , <b>2018</b> , 9, 1381	17.4	15
49	RDTs as a source of DNA to study <i>Plasmodium falciparum</i> drug resistance in isolates from Senegal and the Comoros Islands. <i>Malaria Journal</i> , <b>2015</b> , 14, 373	3.6	15
48	Modeling the genetic relatedness of <i>Plasmodium falciparum</i> parasites following meiotic recombination and cotransmission. <i>PLoS Computational Biology</i> , <b>2018</b> , 14, e1005923	5	15
47	In vitro selection predicts malaria parasite resistance to dihydroorotate dehydrogenase inhibitors in a mouse infection model. <i>Science Translational Medicine</i> , <b>2019</b> , 11,	17.5	15
46	A Novel Methodology for Bioenergetic Analysis of <i>Plasmodium falciparum</i> Reveals a Glucose-Regulated Metabolic Shift and Enables Mode of Action Analyses of Mitochondrial Inhibitors. <i>ACS Infectious Diseases</i> , <b>2016</b> , 2, 903-916	5.5	14
45	A framework for microbiome science in public health. <i>Nature Medicine</i> , <b>2021</b> , 27, 766-774	50.5	14
44	Transmission of molecularly undetectable circulating parasite clones leads to high infection complexity in mosquitoes post feeding. <i>International Journal for Parasitology</i> , <b>2018</b> , 48, 671-677	4.3	13

43	In vivo and in vitro analysis of chloroquine resistance in Plasmodium falciparum isolates from Senegal. <i>Parasitology Research</i> , <b>2005</b> , 97, 136-40	2.4	13
42	Deletion analysis of the 5Tflanking sequence of the Plasmodium gallinaceum sexual stage specific gene pgs28 suggests a bipartite arrangement of cis-control elements. <i>Molecular and Biochemical Parasitology</i> , <b>2001</b> , 113, 183-7	1.9	12
41	A cloned DNA fragment for identification of Mycobacterium tuberculosis. <i>Clinical Infectious Diseases</i> , <b>1989</b> , 11 Suppl 2, S411-9	11.6	12
40	Plasmodium falciparum Gametocyte Density and Infectivity in Peripheral Blood and Skin Tissue of Naturally Infected Parasite Carriers in Burkina Faso. <i>Journal of Infectious Diseases</i> , <b>2021</b> , 223, 1822-1830	7	12
39	De Novo Mutations Resolve Disease Transmission Pathways in Clonal Malaria. <i>Molecular Biology and Evolution</i> , <b>2018</b> , 35, 1678-1689	8.3	11
38	Chemogenomics identifies acetyl-coenzyme A synthetase as a target for malaria treatment and prevention. <i>Cell Chemical Biology</i> , <b>2021</b> ,	8.2	11
37	Identification of Collateral Sensitivity to Dihydroorotate Dehydrogenase Inhibitors in Plasmodium falciparum. <i>ACS Infectious Diseases</i> , <b>2018</b> , 4, 508-515	5.5	9
36	Global action for training in malaria elimination. <i>Malaria Journal</i> , <b>2018</b> , 17, 51	3.6	9
35	Mutations in PFCRT K76T do not correlate with sulfadoxine-pyrimethamine-amodiaquine failure in Pikine, Senegal. <i>Parasitology Research</i> , <b>2008</b> , 103, 765-9	2.4	8
34	Methods to Increase the Sensitivity of High Resolution Melting Single Nucleotide Polymorphism Genotyping in Malaria. <i>Journal of Visualized Experiments</i> , <b>2015</b> , e52839	1.6	7
33	Immune characterization of Plasmodium falciparum parasites with a shared genetic signature in a region of decreasing transmission. <i>Infection and Immunity</i> , <b>2015</b> , 83, 276-85	3.7	7
32	Genomic heterogeneity in the density of noncoding single-nucleotide and microsatellite polymorphisms in Plasmodium falciparum. <i>Gene</i> , <b>2007</b> , 387, 1-6	3.8	7
31	Genetic background and PfKelch13 affect artemisinin susceptibility of PfCoronin mutants in Plasmodium falciparum. <i>PLoS Genetics</i> , <b>2020</b> , 16, e1009266	6	7
30	Characterization of Plasmodium falciparum structure in Nigeria with malaria SNPs barcode. <i>Malaria Journal</i> , <b>2018</b> , 17, 472	3.6	7
29	High resolution melting: a useful field-deployable method to measure dhfr and dhps drug resistance in both highly and lowly endemic Plasmodium populations. <i>Malaria Journal</i> , <b>2017</b> , 16, 153	3.6	6
28	Plasmodium falciparum gene expression measured directly from tissue during human infection. <i>Genome Medicine</i> , <b>2014</b> , 6, 110	14.4	6
27	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> , <b>2020</b> , 103, 66-73	3.2	6
26	Quantitative imaging of intraerythrocytic hemozoin by transient absorption microscopy. <i>Journal of Biomedical Optics</i> , <b>2019</b> , 25, 1-11	3.5	5



25	hmmIBD: software to infer pairwise identity by descent between haploid genotypes		5
24	An adjustable gas-mixing device to increase feasibility of in vitro culture of Plasmodium falciparum parasites in the field. <i>PLoS ONE</i> , <b>2014</b> , 9, e90928	3.7	4
23	Polymorphisms in Plasmodium falciparum chloroquine resistance transporter (Pfcr1) and multidrug-resistant gene 1 (Pfmdr-1) in Nigerian children 10 years post-adoption of artemisinin-based combination treatments. <i>International Journal for Parasitology</i> , <b>2021</b> , 51, 301-310	4.3	4
22	Reply to Velavan et al.: Polymorphisms of in natural populations: Implications for functional significance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2019</b> , 116, 12613-12614	11.5	3
21	Transcriptional Categorization of the Etiology of Pneumonia Syndrome in Pediatric Patients in Malaria-Endemic Areas. <i>Journal of Infectious Diseases</i> , <b>2017</b> , 215, 312-320	7	3
20	The Plasmodium falciparum ABC transporter ABCI3 confers parasite strain-dependent pleiotropic antimalarial drug resistance. <i>Cell Chemical Biology</i> , <b>2021</b> ,	8.2	3
19	Biomarkers to Distinguish Bacterial From Viral Pediatric Clinical Pneumonia in a Malaria-Endemic Setting. <i>Clinical Infectious Diseases</i> , <b>2021</b> , 73, e3939-e3948	11.6	3
18	Prioritization of Molecular Targets for Antimalarial Drug Discovery. <i>ACS Infectious Diseases</i> , <b>2021</b> , 7, 2764-2776	5.3	3
17	Case report of Plasmodium ovale curtisi malaria in Sri Lanka: relevance for the maintenance of elimination status. <i>BMC Infectious Diseases</i> , <b>2017</b> , 17, 307	4	2
16	The signal sequence and C-terminal hydrophobic domain are required for localization of the sexual stage antigen pgs28 to the surface of P. gallinaceum ookinetes. <i>Molecular and Biochemical Parasitology</i> , <b>2000</b> , 111, 425-35	1.9	2
15	Host cell proteins bind specifically to the capsid-cleaved 5Tend of Leishmanivirus RNA. <i>Journal of Biochemistry</i> , <b>1999</b> , 126, 538-44	3.1	2
14	Plasmodium falciparum population genetic complexity influences transcriptional profile and immune recognition of highly related genotypic clusters		2
13	Genetic evidence for imported malaria and local transmission in Richard Toll, Senegal. <i>Malaria Journal</i> , <b>2020</b> , 19, 276	3.6	2
12	Use of a Plasmodium vivax genetic barcode for genomic surveillance and parasite tracking in Sri Lanka. <i>Malaria Journal</i> , <b>2020</b> , 19, 342	3.6	2
11	Characterization of the filarial genome. <i>Novartis Foundation Symposium</i> , <b>1987</b> , 127, 107-24		2
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8	The Adaptive Proline Response in P. falciparum Is Independent of Pfk1 and eIF2 $\beta$ Signaling. <i>ACS Infectious Diseases</i> , <b>2019</b> , 5, 515-520	5.5	1

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6	Genetic surveillance for monitoring the impact of drug use on Plasmodium falciparum populations. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , <b>2021</b> , 17, 12-22	4	1
5	Plasmodium falciparum genomic surveillance reveals spatial and temporal trends, association of genetic and physical distance, and household clustering.. <i>Scientific Reports</i> , <b>2022</b> , 12, 938	4.9	0
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