

# Dyann F Wirth

## List of Publications by Year in descending order

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148  
papers

9,123  
citations

34105

52  
h-index

51608

86  
g-index

163  
all docs

163  
docs citations

163  
times ranked

7958  
citing authors

#	ARTICLE	IF	CITATIONS
1	A genome-wide map of diversity in <i>Plasmodium falciparum</i> . <i>Nature Genetics</i> , 2007, 39, 113-119.	21.4	320
2	Halofuginone and other febrifugine derivatives inhibit prolyl-tRNA synthetase. <i>Nature Chemical Biology</i> , 2012, 8, 311-317.	8.0	301
3	Amplification of <i>pfmdr1</i> associated with mefloquine and halofantrine resistance in <i>Plasmodium falciparum</i> from Thailand. <i>Molecular and Biochemical Parasitology</i> , 1993, 57, 151-160.	1.1	263
4	Lysophosphatidylcholine Regulates Sexual Stage Differentiation in the Human Malaria Parasite <i>Plasmodium falciparum</i> . <i>Cell</i> , 2017, 171, 1532-1544.e15.	28.9	259
5	malERA: An updated research agenda for malaria elimination and eradication. <i>PLoS Medicine</i> , 2017, 14, e1002456.	8.4	221
6	Diversity-oriented synthesis yields novel multistage antimalarial inhibitors. <i>Nature</i> , 2016, 538, 344-349.	27.8	214
7	A general SNP-based molecular barcode for <i>Plasmodium falciparum</i> identification and tracking. <i>Malaria Journal</i> , 2008, 7, 223.	2.3	213
8	Recent Origin of <i>Plasmodium falciparum</i> from a Single Progenitor. <i>Science</i> , 2001, 293, 482-484.	12.6	197
9	Mapping the malaria parasite druggable genome by using in vitro evolution and chemogenomics. <i>Science</i> , 2018, 359, 191-199.	12.6	194
10	A Systematic Map of Genetic Variation in <i>Plasmodium falciparum</i> . <i>PLoS Pathogens</i> , 2006, 2, e57.	4.7	176
11	Examining the human infectious reservoir for <i>Plasmodium falciparum</i> malaria in areas of differing transmission intensity. <i>Nature Communications</i> , 2017, 8, 1133.	12.8	174
12	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.	7.1	163
13	Strand-specific RNA sequencing in <i>Plasmodium falciparum</i> malaria identifies developmentally regulated long non-coding RNA and circular RNA. <i>BMC Genomics</i> , 2015, 16, 454.	2.8	160
14	Stable expression of the bacterial <i>neor</i> gene in <i>Leishmania enriettii</i> . <i>Nature</i> , 1990, 343, 572-574.	27.8	158
15	High-Throughput <i>Plasmodium falciparum</i> Growth Assay for Malaria Drug Discovery. <i>Antimicrobial Agents and Chemotherapy</i> , 2007, 51, 716-723.	3.2	150
16	Bone Marrow Is a Major Parasite Reservoir in <i>Plasmodium vivax</i> Infection. <i>MBio</i> , 2018, 9, .	4.1	141
17	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> , 2001, 12, 3114-3125.	2.1	139
18	Drugs for neglected diseases: a failure of the market and a public health failure?. <i>Tropical Medicine and International Health</i> , 2001, 6, 945-951.	2.3	131

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19	Population Structure and Transmission Dynamics of <i>Plasmodium vivax</i> in Rural Amazonia. <i>Journal of Infectious Diseases</i> , 2007, 195, 1218-1226.	4.0	129
20	A global transcriptional analysis of <i>Plasmodium falciparum</i> malaria reveals a novel family of telomere-associated lncRNAs. <i>Genome Biology</i> , 2011, 12, R56.	9.6	124
21	Novel Inhibitors of <i>Plasmodium falciparum</i> Dihydroorotate Dehydrogenase with Anti-malarial Activity in the Mouse Model*. <i>Journal of Biological Chemistry</i> , 2010, 285, 33054-33064.	3.4	121
22	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.	7.1	114
23	A High-Throughput Screen Targeting Malaria Transmission Stages Opens New Avenues for Drug Development. <i>Journal of Infectious Diseases</i> , 2011, 203, 1445-1453.	4.0	105
24	Widespread distribution of antisense transcripts in the <i>Plasmodium falciparum</i> genome. <i>Molecular and Biochemical Parasitology</i> , 2004, 136, 35-42.	1.1	104
25	Extensive microsatellite diversity in the human malaria parasite <i>Plasmodium vivax</i> . <i>Gene</i> , 2008, 410, 105-112.	2.2	103
26	hmmIBD: software to infer pairwise identity by descent between haploid genotypes. <i>Malaria Journal</i> , 2018, 17, 196.	2.3	103
27	Sequence of the immunodominant epitope for the surface protein on sporozoites of <i>Plasmodium vivax</i> . <i>Science</i> , 1985, 230, 1381-1383.	12.6	101
28	Adaptive evolution of malaria parasites in French Guiana: Reversal of chloroquine resistance by acquisition of a mutation in <i>pfcr1</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 11672-11677.	7.1	101
29	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.	7.1	99
30	Artemisinin resistance without <i>pfkelch13</i> mutations in <i>Plasmodium falciparum</i> isolates from Cambodia. <i>Malaria Journal</i> , 2017, 16, 195.	2.3	99
31	Open-source discovery of chemical leads for next-generation chemoprotective antimalarials. <i>Science</i> , 2018, 362, .	12.6	99
32	Harnessing genomics and genome biology to understand malaria biology. <i>Nature Reviews Genetics</i> , 2012, 13, 315-328.	16.3	95
33	A broad analysis of resistance development in the malaria parasite. <i>Nature Communications</i> , 2016, 7, 11901.	12.8	94
34	In Vivo Transcriptome of <i>Plasmodium falciparum</i> Reveals Overexpression of Transcripts That Encode Surface Proteins. <i>Journal of Infectious Diseases</i> , 2005, 191, 1196-1203.	4.0	92
35	Development of a Single Nucleotide Polymorphism Barcode to Genotype <i>Plasmodium vivax</i> Infections. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003539.	3.0	90
36	Isolation and Functional Characterization of Two Distinct Sexual-Stage-Specific Promoters of the Human Malaria Parasite <i>Plasmodium falciparum</i> . <i>Molecular and Cellular Biology</i> , 1999, 19, 967-978.	2.3	89

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37	Geographic Structure of <i>Plasmodium vivax</i> : Microsatellite Analysis of Parasite Populations from Sri Lanka, Myanmar, and Ethiopia. <i>American Journal of Tropical Medicine and Hygiene</i> , 2010, 82, 235-242.	1.4	88
38	Genetic Surveillance Detects Both Clonal and Epidemic Transmission of Malaria following Enhanced Intervention in Senegal. <i>PLoS ONE</i> , 2013, 8, e60780.	2.5	87
39	Identification of regulatory elements in the <i>Plasmodium falciparum</i> genome. <i>Molecular and Biochemical Parasitology</i> , 2004, 134, 75-88.	1.1	85
40	Plasmepsin II copy number accounts for bimodal piperazine resistance among Cambodian <i>Plasmodium falciparum</i> . <i>Nature Communications</i> , 2018, 9, 1769.	12.8	85
41	The cytoplasmic prolyl-tRNA synthetase of the malaria parasite is a dual-stage target of febrifugine and its analogs. <i>Science Translational Medicine</i> , 2015, 7, 288ra77.	12.4	82
42	Excess Polymorphisms in Genes for Membrane Proteins in <i>Plasmodium falciparum</i> . <i>Science</i> , 2002, 298, 216-218.	12.6	80
43	Identification and Characterization of Small Molecule Inhibitors of <i>Plasmodium falciparum</i> Dihydroorotate Dehydrogenase. <i>Journal of Biological Chemistry</i> , 2008, 283, 35078-35085.	3.4	78
44	Torins are potent antimalarials that block replenishment of <i>Plasmodium</i> liver stage parasitophorous vacuole membrane proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2838-47.	7.1	73
45	COIL: a methodology for evaluating malarial complexity of infection using likelihood from single nucleotide polymorphism data. <i>Malaria Journal</i> , 2015, 14, 4.	2.3	71
46	Clonal Outbreak of <i>Plasmodium falciparum</i> Infection in Eastern Panama. <i>Journal of Infectious Diseases</i> , 2015, 211, 1087-1096.	4.0	71
47	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.	7.1	67
48	In vitro chloroquine susceptibility and PCR analysis of <i>pfcr</i> and <i>pfmdr1</i> polymorphisms in <i>Plasmodium falciparum</i> isolates from Senegal. <i>American Journal of Tropical Medicine and Hygiene</i> , 2002, 66, 474-480.	1.4	67
49	Genetic Diversity and Selection at the <i>Plasmodium vivax</i> Apical Membrane Antigen-1 (PvAMA-1) Locus in a Sri Lankan Population. <i>Molecular Biology and Evolution</i> , 2007, 24, 939-947.	8.9	66
50	Rapid, Field-Deployable Method for Genotyping and Discovery of Single-Nucleotide Polymorphisms Associated with Drug Resistance in <i>Plasmodium falciparum</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 2976-2986.	3.2	63
51	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.	8.9	58
52	Dietary restriction protects against experimental cerebral malaria via leptin modulation and T-cell mTORC1 suppression. <i>Nature Communications</i> , 2015, 6, 6050.	12.8	58
53	RNA polymerase II synthesizes antisense RNA in <i>Plasmodium falciparum</i> . <i>Rna</i> , 2005, 11, 365-370.	3.5	56
54	Patterns of Gene-Specific and Total Transcriptional Activity during the <i>Plasmodium falciparum</i> Intraerythrocytic Developmental Cycle. <i>Eukaryotic Cell</i> , 2009, 8, 327-338.	3.4	55

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55	The Sri Lankan paradox: high genetic diversity in <i>Plasmodium vivax</i> populations despite decreasing levels of malaria transmission. <i>Parasitology</i> , 2014, 141, 880-890.	1.5	55
56	On the road to eliminate malaria in Sri Lanka: lessons from history, challenges, gaps in knowledge and research needs. <i>Malaria Journal</i> , 2014, 13, 59.	2.3	55
57	Triaminopyrimidine is a fast-killing and long-acting antimalarial clinical candidate. <i>Nature Communications</i> , 2015, 6, 6715.	12.8	55
58	In Vitro Resistance Selections for <i>Plasmodium falciparum</i> Dihydroorotate Dehydrogenase Inhibitors Give Mutants with Multiple Point Mutations in the Drug-binding Site and Altered Growth. <i>Journal of Biological Chemistry</i> , 2014, 289, 17980-17995.	3.4	54
59	Harnessing evolutionary fitness in <i>Plasmodium falciparum</i> for drug discovery and suppressing resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 799-804.	7.1	54
60	In vivo transcriptional profiling of <i>Plasmodium falciparum</i> . <i>Malaria Journal</i> , 2004, 3, 30.	2.3	52
61	Gene Conversion as a Source of Nucleotide Diversity in <i>Plasmodium falciparum</i> . <i>Molecular Biology and Evolution</i> , 2003, 20, 726-734.	8.9	51
62	MalDA, Accelerating Malaria Drug Discovery. <i>Trends in Parasitology</i> , 2021, 37, 493-507.	3.3	51
63	Identification and Validation of Tetracyclic Benzothiazepines as <i>Plasmodium falciparum</i> Cytochrome bc1 Inhibitors. <i>Chemistry and Biology</i> , 2011, 18, 1602-1610.	6.0	50
64	Control of tubulin gene expression in the parasitic protozoan <i>Leishmania enriettii</i> . <i>Nature</i> , 1984, 309, 716-717.	27.8	49
65	<i>Plasmodium falciparum</i> : Genome wide perturbations in transcript profiles among mixed stage cultures after chloroquine treatment. <i>Experimental Parasitology</i> , 2007, 117, 87-92.	1.2	49
66	Drug-induced alterations in gene expression of the asexual blood forms of <i>Plasmodium falciparum</i> . <i>Molecular Microbiology</i> , 2003, 50, 1229-1239.	2.5	48
67	Duplication, gene conversion, and genetic diversity in the species-specific acyl-CoA synthetase gene family of <i>Plasmodium falciparum</i> . <i>Molecular and Biochemical Parasitology</i> , 2006, 150, 10-24.	1.1	47
68	Type II NADH dehydrogenase of the respiratory chain of <i>Plasmodium falciparum</i> and its inhibitors. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2009, 19, 972-975.	2.2	47
69	Genetic relatedness analysis reveals the cotransmission of genetically related <i>Plasmodium falciparum</i> parasites in Thiès, Senegal. <i>Genome Medicine</i> , 2017, 9, 5.	8.2	47
70	A framework for microbiome science in public health. <i>Nature Medicine</i> , 2021, 27, 766-774.	30.7	47
71	Single-nucleotide polymorphism, linkage disequilibrium and geographic structure in the malaria parasite <i>Plasmodium vivax</i> : prospects for genome-wide association studies. <i>BMC Genetics</i> , 2010, 11, 65.	2.7	46
72	Serial analysis of gene expression (SAGE) in <i>Plasmodium falciparum</i> : application of the technique to AT rich genomes. <i>Molecular and Biochemical Parasitology</i> , 2001, 113, 23-34.	1.1	45

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73	Inferring Developmental Stage Composition from Gene Expression in Human Malaria. PLoS Computational Biology, 2013, 9, e1003392.	3.2	45
74	Responses to Bacteria, Virus, and Malaria Distinguish the Etiology of Pediatric Clinical Pneumonia. American Journal of Respiratory and Critical Care Medicine, 2016, 193, 448-459.	5.6	42
75	New paradigms for understanding and step changes in treating active and chronic, persistent apicomplexan infections. Scientific Reports, 2016, 6, 29179.	3.3	40
76	Detection of low-density Plasmodium falciparum infections using amplicon deep sequencing. Malaria Journal, 2019, 18, 219.	2.3	40
77	Stage-specific transcripts of the Plasmodium falciparum pfm-dr1 gene. Molecular and Biochemical Parasitology, 1993, 57, 203-211.	1.1	39
78	Chemogenomics identifies acetyl-coenzyme A synthetase as a target for malaria treatment and prevention. Cell Chemical Biology, 2022, 29, 191-201.e8.	5.2	39
79	Modeling the genetic relatedness of Plasmodium falciparum parasites following meiotic recombination and cotransmission. PLoS Computational Biology, 2018, 14, e1005923.	3.2	39
80	Evidence of non-Plasmodium falciparum malaria infection in KÃ©dougou, SÃ©nÃ©gal. Malaria Journal, 2017, 16, 9.	2.3	38
81	Comparison of Thick Films, in Vitro Culture and DNA Hybridization Probes for Detecting Plasmodium falciparum Malaria. American Journal of Tropical Medicine and Hygiene, 1989, 40, 3-6.	1.4	38
82	Mapping of the Plasmodium falciparum multidrug resistance gene 5â€™-upstream region, and evidence of induction of transcript levels by antimalarial drugs in chloroquine sensitive parasites. Molecular Microbiology, 2004, 49, 671-683.	2.5	35
83	Prioritization of Molecular Targets for Antimalarial Drug Discovery. ACS Infectious Diseases, 2021, 7, 2764-2776.	3.8	35
84	Plasmodium falciparum Cyclic Amine Resistance Locus (PFCARL), a Resistance Mechanism for Two Distinct Compound Classes. ACS Infectious Diseases, 2016, 2, 816-826.	3.8	34
85	Persistence of Plasmodium falciparum parasitemia after artemisinin combination therapy: evidence from a randomized trial in Uganda. Scientific Reports, 2016, 6, 26330.	3.3	34
86	Application of genomics to field investigations of malaria by the international centers of excellence for malaria research. Acta Tropica, 2012, 121, 324-332.	2.0	33
87	Regulatory motifs uncovered among gene expression clusters in Plasmodium falciparum. Molecular and Biochemical Parasitology, 2007, 153, 19-30.	1.1	31
88	Exploring the 3-piperidin-4-yl-1H-indole scaffold as a novel antimalarial chemotype. European Journal of Medicinal Chemistry, 2015, 102, 320-333.	5.5	31
89	Dramatic Changes in Malaria Population Genetic Complexity in Dielmo and Ndiop, Senegal, Revealed Using Genomic Surveillance. Journal of Infectious Diseases, 2018, 217, 622-627.	4.0	31
90	Naturally acquired immunity against immature Plasmodium falciparum gametocytes. Science Translational Medicine, 2019, 11, .	12.4	31

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91	In vitro selection predicts malaria parasite resistance to dihydroorotate dehydrogenase inhibitors in a mouse infection model. <i>Science Translational Medicine</i> , 2019, 11, .	12.4	30
92	A new reporter gene for transient transfection of <i>Plasmodium falciparum</i> . <i>Parasitology Research</i> , 2003, 89, 154-157.	1.6	29
93	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> , 2015, 211, 1097-1103.	4.0	29
94	Quantitative Proteomic Profiling Reveals Novel <i>Plasmodium falciparum</i> Surface Antigens and Possible Vaccine Candidates. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 43-60.	3.8	29
95	3' UTR elements enhance expression of Pgs28, an ookinete protein of <i>Plasmodium gallinaceum</i> . <i>Molecular and Biochemical Parasitology</i> , 2000, 105, 61-70.	1.1	28
96	A Non-Radioactive DAPI-based High-Throughput In Vitro Assay to Assess <i>Plasmodium falciparum</i> Responsiveness to Antimalarials—Increased Sensitivity of <i>P. falciparum</i> to Chloroquine in Senegal. <i>American Journal of Tropical Medicine and Hygiene</i> , 2010, 82, 228-230.	1.4	27
97	Polymorphism in dhfr/dhps genes, parasite density and ex vivo response to pyrimethamine in <i>Plasmodium falciparum</i> malaria parasites in Thies, Senegal. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2013, 3, 135-142.	3.4	27
98	Host-mediated selection impacts the diversity of <i>Plasmodium falciparum</i> antigens within infections. <i>Nature Communications</i> , 2018, 9, 1381.	12.8	27
99	Inactivation of Plasmepsins 2 and 3 Sensitizes <i>Plasmodium falciparum</i> to the Antimalarial Drug Piperazine. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	27
100	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> , 2016, 2, 903-916.	3.8	26
101	Transmission of molecularly undetectable circulating parasite clones leads to high infection complexity in mosquitoes post feeding. <i>International Journal for Parasitology</i> , 2018, 48, 671-677.	3.1	25
102	Aminoazabenzimidazoles, a Novel Class of Orally Active Antimalarial Agents. <i>Journal of Medicinal Chemistry</i> , 2014, 57, 5702-5713.	6.4	24
103	The role of DNA mismatch repair in generating genetic diversity and drug resistance in malaria parasites. <i>Molecular and Biochemical Parasitology</i> , 2007, 155, 18-25.	1.1	23
104	Changes in drug sensitivity and anti-malarial drug resistance mutations over time among <i>Plasmodium falciparum</i> parasites in Senegal. <i>Malaria Journal</i> , 2013, 12, 441.	2.3	23
105	Identification of <i>Brugia Malayi</i> in Vectors with a Species-Specific DNA Probe. <i>American Journal of Tropical Medicine and Hygiene</i> , 1986, 35, 559-564.	1.4	23
106	Evolution of the pfcrt T76 and pfmdr1 Y86 markers and chloroquine susceptibility 8 years after cessation of chloroquine use in Pikine, Senegal. <i>Parasitology Research</i> , 2012, 111, 1541-1546.	1.6	20
107	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> , 2003, 129, 199-208.	1.1	19
108	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> , 2016, 95, 1054-1060.	1.4	19

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109	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> , 2015, 14, 373.	2.3	17
110	<i>Plasmodium falciparum</i> Gametocyte Density and Infectivity in Peripheral Blood and Skin Tissue of Naturally Infected Parasite Carriers in Burkina Faso. <i>Journal of Infectious Diseases</i> , 2021, 223, 1822-1830.	4.0	17
111	Genetic background and PfKelch13 affect artemisinin susceptibility of PfCoronin mutants in <i>Plasmodium falciparum</i> . <i>PLoS Genetics</i> , 2020, 16, e1009266.	3.5	17
112	Global action for training in malaria elimination. <i>Malaria Journal</i> , 2018, 17, 51.	2.3	16
113	A Cloned DNA Fragment for Identification of <i>Mycobacterium tuberculosis</i> . <i>Clinical Infectious Diseases</i> , 1989, 11, S411-S419.	5.8	15
114	Identification of Collateral Sensitivity to Dihydroorotate Dehydrogenase Inhibitors in <i>Plasmodium falciparum</i> . <i>ACS Infectious Diseases</i> , 2018, 4, 508-515.	3.8	15
115	Genetic surveillance for monitoring the impact of drug use on <i>Plasmodium falciparum</i> populations. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2021, 17, 12-22.	3.4	15
116	In vivo and in vitro analysis of chloroquine resistance in <i>Plasmodium falciparum</i> isolates from Senegal. <i>Parasitology Research</i> , 2005, 97, 136-140.	1.6	14
117	De Novo Mutations Resolve Disease Transmission Pathways in Clonal Malaria. <i>Molecular Biology and Evolution</i> , 2018, 35, 1678-1689.	8.9	14
118	The <i>Plasmodium falciparum</i> ABC transporter ABCI3 confers parasite strain-dependent pleiotropic antimalarial drug resistance. <i>Cell Chemical Biology</i> , 2022, 29, 824-839.e6.	5.2	14
119	Deletion analysis of the 5' flanking sequence of the <i>Plasmodium gallinaceum</i> sexual stage specific gene <i>pgs28</i> suggests a bipartite arrangement of cis-control elements. <i>Molecular and Biochemical Parasitology</i> , 2001, 113, 183-187.	1.1	13
120	<i>Plasmodium falciparum</i> genomic surveillance reveals spatial and temporal trends, association of genetic and physical distance, and household clustering. <i>Scientific Reports</i> , 2022, 12, 938.	3.3	13
121	Malaria: A 21st century solution for an ancient disease. <i>Nature Medicine</i> , 1998, 4, 1360-1362.	30.7	12
122	Characterization of <i>Plasmodium falciparum</i> structure in Nigeria with malaria SNPs barcode. <i>Malaria Journal</i> , 2018, 17, 472.	2.3	12
123	Genetic evidence for imported malaria and local transmission in Richard Toll, Senegal. <i>Malaria Journal</i> , 2020, 19, 276.	2.3	12
124	<i>Plasmodium falciparum</i> gene expression measured directly from tissue during human infection. <i>Genome Medicine</i> , 2014, 6, 110.	8.2	11
125	Immune Characterization of <i>Plasmodium falciparum</i> Parasites with a Shared Genetic Signature in a Region of Decreasing Transmission. <i>Infection and Immunity</i> , 2015, 83, 276-285.	2.2	11
126	Methods to Increase the Sensitivity of High Resolution Melting Single Nucleotide Polymorphism Genotyping in Malaria. <i>Journal of Visualized Experiments</i> , 2015, , e52839.	0.3	9



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127	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> , 2017, 16, 153.	2.3	9
128	Polymorphisms in Plasmodium falciparum dihydropteroate synthetase and dihydrofolate reductase genes in Nigerian children with uncomplicated malaria using high-resolution melting technique. <i>Scientific Reports</i> , 2021, 11, 471.	3.3	9
129	Quantitative imaging of intraerythrocytic hemozoin by transient absorption microscopy. <i>Journal of Biomedical Optics</i> , 2019, 25, 1.	2.6	9
130	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
131	Mutations in PFCRT K76T do not correlate with sulfadoxine-pyrimethamine-amodiaquine failure in Pikine, Senegal. <i>Parasitology Research</i> , 2008, 103, 765-769.	1.6	8
132	Transcriptional categorization of the etiology of pneumonia syndrome in pediatric patients in malaria endemic areas. <i>Journal of Infectious Diseases</i> , 2017, 215, jiw531.	4.0	8
133	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> , 2020, 103, 66-73.	1.4	8
134	Adaptive laboratory evolution in <i>S. cerevisiae</i> highlights role of transcription factors in fungal xenobiotic resistance. <i>Communications Biology</i> , 2022, 5, 128.	4.4	8
135	Polymorphisms in Plasmodium falciparum chloroquine resistance transporter (Pfcrt) 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> , 2021, 51, 301-310.	3.1	7
136	Use of a Plasmodium vivax genetic barcode for genomic surveillance and parasite tracking in Sri Lanka. <i>Malaria Journal</i> , 2020, 19, 342.	2.3	6
137	Biomarkers to Distinguish Bacterial From Viral Pediatric Clinical Pneumonia in a Malaria-Endemic Setting. <i>Clinical Infectious Diseases</i> , 2021, 73, e3939-e3948.	5.8	6
138	An Adjustable Gas-Mixing Device to Increase Feasibility of In Vitro Culture of Plasmodium falciparum Parasites in the Field. <i>PLoS ONE</i> , 2014, 9, e90928.	2.5	6
139	Reply to Velavan et al.: Polymorphisms of pfcoronin natural populations: Implications for functional significance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 12613-12614.	7.1	5
140	The Adaptive Proline Response in <i>P. falciparum</i> Is Independent of <i>Pf</i> eIK1 and eIF2 $\pm$ Signaling. <i>ACS Infectious Diseases</i> , 2019, 5, 515-520.	3.8	5
141	Genomic investigation of atypical malaria cases in Kanel, northern Senegal. <i>Malaria Journal</i> , 2021, 20, 103.	2.3	4
142	Host Cell Proteins Bind Specifically to the Capsid-Cleaved 5' End of Leishmanivirus RNA. <i>Journal of Biochemistry</i> , 1999, 126, 538-544.	1.7	3
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