

Dyann F Wirth

List of Publications by Year in descending order

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148
papers

9,123
citations

39113

52
h-index

58552

86
g-index

163
all docs

163
docs citations

163
times ranked

8717
citing authors

#	ARTICLE	IF	CITATIONS
1	The Plasmodium falciparum ABC transporter ABCI3 confers parasite strain-dependent pleiotropic antimalarial drug resistance. <i>Cell Chemical Biology</i> , 2022, 29, 824-839.e6.	2.5	14
2	Chemogenomics identifies acetyl-coenzyme A synthetase as a target for malaria treatment and prevention. <i>Cell Chemical Biology</i> , 2022, 29, 191-201.e8.	2.5	39
3	Plasmodium falciparum genomic surveillance reveals spatial and temporal trends, association of genetic and physical distance, and household clustering. <i>Scientific Reports</i> , 2022, 12, 938.	1.6	13
4	Adaptive laboratory evolution in <i>S. cerevisiae</i> highlights role of transcription factors in fungal xenobiotic resistance. <i>Communications Biology</i> , 2022, 5, 128.	2.0	8
5	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> , 2021, 223, 1822-1830.	1.9	17
6	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.	1.6	9
7	Biomarkers to Distinguish Bacterial From Viral Pediatric Clinical Pneumonia in a Malaria-Endemic Setting. <i>Clinical Infectious Diseases</i> , 2021, 73, e3939-e3948.	2.9	6
8	Genomic investigation of atypical malaria cases in Kanel, northern Senegal. <i>Malaria Journal</i> , 2021, 20, 103.	0.8	4
9	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.	1.3	7
10	A framework for microbiome science in public health. <i>Nature Medicine</i> , 2021, 27, 766-774.	15.2	47
11	MalDA, Accelerating Malaria Drug Discovery. <i>Trends in Parasitology</i> , 2021, 37, 493-507.	1.5	51
12	Prioritization of Molecular Targets for Antimalarial Drug Discovery. <i>ACS Infectious Diseases</i> , 2021, 7, 2764-2776.	1.8	35
13	Genetic surveillance for monitoring the impact of drug use on Plasmodium falciparum populations. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2021, 17, 12-22.	1.4	15
14	Genetic evidence for imported malaria and local transmission in Richard Toll, Senegal. <i>Malaria Journal</i> , 2020, 19, 276.	0.8	12
15	Genetic analysis reveals unique characteristics of Plasmodium falciparum parasite populations in Haiti. <i>Malaria Journal</i> , 2020, 19, 379.	0.8	3
16	Use of a Plasmodium vivax genetic barcode for genomic surveillance and parasite tracking in Sri Lanka. <i>Malaria Journal</i> , 2020, 19, 342.	0.8	6
17	Genetic background and PfKelch13 affect artemisinin susceptibility of PfCoronin mutants in Plasmodium falciparum. <i>PLoS Genetics</i> , 2020, 16, e1009266.	1.5	17
18	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.	0.6	8

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19	Detection of low-density <i>Plasmodium falciparum</i> infections using amplicon deep sequencing. <i>Malaria Journal</i> , 2019, 18, 219.	0.8	40
20	Temporal changes in <i>Plasmodium falciparum</i> reticulocyte binding protein homolog 2b (PfRh2b) in Senegal and The Gambia. <i>Malaria Journal</i> , 2019, 18, 239.	0.8	1
21	Reply to Velavan et al.: Polymorphisms of <i>pf</i> coronin 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.	3.3	5
22	Naturally acquired immunity against immature <i>Plasmodium falciparum</i> gametocytes. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	31
23	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.	1.8	5
24	In vitro selection predicts malaria parasite resistance to dihydroorotate dehydrogenase inhibitors in a mouse infection model. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	30
25	Quantitative imaging of intraerythrocytic hemozoin by transient absorption microscopy. <i>Journal of Biomedical Optics</i> , 2019, 25, 1.	1.4	9
26	Host-mediated selection impacts the diversity of <i>Plasmodium falciparum</i> antigens within infections. <i>Nature Communications</i> , 2018, 9, 1381.	5.8	27
27	Inactivation of Plasmepsins 2 and 3 Sensitizes <i>Plasmodium falciparum</i> to the Antimalarial Drug Piperazine. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	27
28	Identification of Collateral Sensitivity to Dihydroorotate Dehydrogenase Inhibitors in <i>Plasmodium falciparum</i> . <i>ACS Infectious Diseases</i> , 2018, 4, 508-515.	1.8	15
29	Dramatic Changes in Malaria Population Genetic Complexity in Dielmo and Ndiop, Senegal, Revealed Using Genomic Surveillance. <i>Journal of Infectious Diseases</i> , 2018, 217, 622-627.	1.9	31
30	Mapping the malaria parasite druggable genome by using in vitro evolution and chemogenomics. <i>Science</i> , 2018, 359, 191-199.	6.0	194
31	Plasmepsin III copy number accounts for bimodal piperazine resistance among Cambodian <i>Plasmodium falciparum</i> . <i>Nature Communications</i> , 2018, 9, 1769.	5.8	85
32	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.	2.5	29
33	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
34	Characterization of <i>Plasmodium falciparum</i> structure in Nigeria with malaria SNPs barcode. <i>Malaria Journal</i> , 2018, 17, 472.	0.8	12
35	Open-source discovery of chemical leads for next-generation chemoprotective antimalarials. <i>Science</i> , 2018, 362, .	6.0	99
36	hmmIBD: software to infer pairwise identity by descent between haploid genotypes. <i>Malaria Journal</i> , 2018, 17, 196.	0.8	103

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37	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.	1.3	25
38	Global action for training in malaria elimination. <i>Malaria Journal</i> , 2018, 17, 51.	0.8	16
39	Bone Marrow Is a Major Parasite Reservoir in <i>Plasmodium vivax</i> Infection. <i>MBio</i> , 2018, 9, .	1.8	141
40	De Novo Mutations Resolve Disease Transmission Pathways in Clonal Malaria. <i>Molecular Biology and Evolution</i> , 2018, 35, 1678-1689.	3.5	14
41	Modeling the genetic relatedness of <i>Plasmodium falciparum</i> parasites following meiotic recombination and cotransmission. <i>PLoS Computational Biology</i> , 2018, 14, e1005923.	1.5	39
42	Transcriptional categorization of the etiology of pneumonia syndrome in pediatric patients in malaria endemic areas. <i>Journal of Infectious Diseases</i> , 2017, 215, jiw531.	1.9	8
43	Artemisinin resistance without pfcfch13 mutations in <i>Plasmodium falciparum</i> isolates from Cambodia. <i>Malaria Journal</i> , 2017, 16, 195.	0.8	99
44	Examining the human infectious reservoir for <i>Plasmodium falciparum</i> malaria in areas of differing transmission intensity. <i>Nature Communications</i> , 2017, 8, 1133.	5.8	174
45	Lysophosphatidylcholine Regulates Sexual Stage Differentiation in the Human Malaria Parasite <i>Plasmodium falciparum</i> . <i>Cell</i> , 2017, 171, 1532-1544.e15.	13.5	259
46	Case report of <i>Plasmodium ovale curtisi</i> malaria in Sri Lanka: relevance for the maintenance of elimination status. <i>BMC Infectious Diseases</i> , 2017, 17, 307.	1.3	3
47	Evidence of non- <i>Plasmodium falciparum</i> malaria infection in KÃ©doukou, SÃ©nÃ©gal. <i>Malaria Journal</i> , 2017, 16, 9.	0.8	38
48	High resolution melting: a useful field-deployable method to measure dhfr and dhps drug resistance in both highly and lowly endemic <i>Plasmodium</i> populations. <i>Malaria Journal</i> , 2017, 16, 153.	0.8	9
49	Genetic relatedness analysis reveals the cotransmission of genetically related <i>Plasmodium falciparum</i> parasites in ThiÃ©s, Senegal. <i>Genome Medicine</i> , 2017, 9, 5.	3.6	47
50	malERA: An updated research agenda for malaria elimination and eradication. <i>PLoS Medicine</i> , 2017, 14, e1002456.	3.9	221
51	New paradigms for understanding and step changes in treating active and chronic, persistent apicomplexan infections. <i>Scientific Reports</i> , 2016, 6, 29179.	1.6	40
52	<i>Plasmodium falciparum</i> Cyclic Amine Resistance Locus (PfCARL), a Resistance Mechanism for Two Distinct Compound Classes. <i>ACS Infectious Diseases</i> , 2016, 2, 816-826.	1.8	34
53	Diversity-oriented synthesis yields novel multistage antimalarial inhibitors. <i>Nature</i> , 2016, 538, 344-349.	13.7	214
54	West Africa International Centers of Excellence for Malaria Research: Drug Resistance Patterns to ArtemetherÃ©lumefantrine in Senegal, Mali, and The Gambia. <i>American Journal of Tropical Medicine and Hygiene</i> , 2016, 95, 1054-1060.	0.6	19

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55	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.	1.8	26
56	Persistence of <i>Plasmodium falciparum</i> parasitemia after artemisinin combination therapy: evidence from a randomized trial in Uganda. <i>Scientific Reports</i> , 2016, 6, 26330.	1.6	34
57	A broad analysis of resistance development in the malaria parasite. <i>Nature Communications</i> , 2016, 7, 11901.	5.8	94
58	Responses to Bacteria, Virus, and Malaria Distinguish the Etiology of Pediatric Clinical Pneumonia. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2016, 193, 448-459.	2.5	42
59	Methods to Increase the Sensitivity of High Resolution Melting Single Nucleotide Polymorphism Genotyping in Malaria. <i>Journal of Visualized Experiments</i> , 2015, , e52839.	0.2	9
60	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.	0.8	17
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> , 2015, 211, 1097-1103.	1.9	29
62	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
63	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.	5.8	82
64	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.	1.0	11
65	Dietary restriction protects against experimental cerebral malaria via leptin modulation and T-cell mTORC1 suppression. <i>Nature Communications</i> , 2015, 6, 6050.	5.8	58
66	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.	1.2	160
67	Exploring the 3-piperidin-4-yl-1H-indole scaffold as a novel antimalarial chemotype. <i>European Journal of Medicinal Chemistry</i> , 2015, 102, 320-333.	2.6	31
68	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
69	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
70	Triaminopyrimidine is a fast-killing and long-acting antimalarial clinical candidate. <i>Nature Communications</i> , 2015, 6, 6715.	5.8	55
71	Adaptive evolution of malaria parasites in French Guiana: Reversal of chloroquine resistance by acquisition of a mutation in <i>pfcr</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 11672-11677.	3.3	101
72	Clonal Outbreak of <i>Plasmodium falciparum</i> Infection in Eastern Panama. <i>Journal of Infectious Diseases</i> , 2015, 211, 1087-1096.	1.9	71

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73	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> , 2014, 289, 17980-17995.	1.6	54
74	The Sri Lankan paradox: high genetic diversity in Plasmodium vivax populations despite decreasing levels of malaria transmission. <i>Parasitology</i> , 2014, 141, 880-890.	0.7	55
75	Plasmodium falciparum gene expression measured directly from tissue during human infection. <i>Genome Medicine</i> , 2014, 6, 110.	3.6	11
76	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> , 2014, 111, 799-804.	3.3	54
77	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.	0.8	55
78	Aminoazabenzimidazoles, a Novel Class of Orally Active Antimalarial Agents. <i>Journal of Medicinal Chemistry</i> , 2014, 57, 5702-5713.	2.9	24
79	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.	1.1	6
80	Changes in drug sensitivity and anti-malarial drug resistance mutations over time among Plasmodium falciparum parasites in Senegal. <i>Malaria Journal</i> , 2013, 12, 441.	0.8	23
81	Polymorphism in dhfr/dhps genes, parasite density and ex vivo response to pyrimethamine in Plasmodium falciparum malaria parasites in Thies, Senegal. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2013, 3, 135-142.	1.4	27
82	Inferring Developmental Stage Composition from Gene Expression in Human Malaria. <i>PLoS Computational Biology</i> , 2013, 9, e1003392.	1.5	45
83	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
84	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> , 2013, 110, E2838-47.	3.3	73
85	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
86	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> , 2012, 109, 13052-13057.	3.3	99
87	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> , 2012, 56, 2976-2986.	1.4	63
88	Genomic Sequencing of Plasmodium falciparum Malaria Parasites from Senegal Reveals the Demographic History of the Population. <i>Molecular Biology and Evolution</i> , 2012, 29, 3427-3439.	3.5	58
89	Halofuginone and other febrifugine derivatives inhibit prolyl-tRNA synthetase. <i>Nature Chemical Biology</i> , 2012, 8, 311-317.	3.9	301
90	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> , 2012, 111, 1541-1546.	0.6	20

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91	Application of genomics to field investigations of malaria by the international centers of excellence for malaria research. <i>Acta Tropica</i> , 2012, 121, 324-332.	0.9	33
92	Harnessing genomics and genome biology to understand malaria biology. <i>Nature Reviews Genetics</i> , 2012, 13, 315-328.	7.7	95
93	A High-Throughput Screen Targeting Malaria Transmission Stages Opens New Avenues for Drug Development. <i>Journal of Infectious Diseases</i> , 2011, 203, 1445-1453.	1.9	105
94	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.	13.9	124
95	Identification and Validation of Tetracyclic Benzothiazepines as <i>Plasmodium falciparum</i> Cytochrome bc1 Inhibitors. <i>Chemistry and Biology</i> , 2011, 18, 1602-1610.	6.2	50
96	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
97	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.	0.6	88
98	A Non-Radioactive DAPI-based High-Throughput In Vitro Assay to Assess <i>Plasmodium falciparum</i> Responsiveness to Antimalarialsâ€”Increased Sensitivity of <i>P. falciparum</i> to Chloroquine in Senegal. <i>American Journal of Tropical Medicine and Hygiene</i> , 2010, 82, 228-230.	0.6	27
99	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.	1.6	121
100	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
101	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.	1.0	47
102	Mutations in PFCRT K76T do not correlate with sulfadoxineâ€”pyrimethamineâ€”amodiaquine failure in Pikine, Senegal. <i>Parasitology Research</i> , 2008, 103, 765-769.	0.6	8
103	A general SNP-based molecular barcode for <i>Plasmodium falciparum</i> identification and tracking. <i>Malaria Journal</i> , 2008, 7, 223.	0.8	213
104	Extensive microsatellite diversity in the human malaria parasite <i>Plasmodium vivax</i> . <i>Gene</i> , 2008, 410, 105-112.	1.0	103
105	Identification and Characterization of Small Molecule Inhibitors of <i>Plasmodium falciparum</i> Dihydroorotate Dehydrogenase. <i>Journal of Biological Chemistry</i> , 2008, 283, 35078-35085.	1.6	78
106	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.	3.5	66
107	High-Throughput <i>Plasmodium falciparum</i> Growth Assay for Malaria Drug Discovery. <i>Antimicrobial Agents and Chemotherapy</i> , 2007, 51, 716-723.	1.4	150
108	Population Structure and Transmission Dynamics of <i>Plasmodium vivax</i> in Rural Amazonia. <i>Journal of Infectious Diseases</i> , 2007, 195, 1218-1226.	1.9	129

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109	Genomic heterogeneity in the density of noncoding single-nucleotide and microsatellite polymorphisms in <i>Plasmodium falciparum</i> . <i>Gene</i> , 2007, 387, 1-6.	1.0	8
110	A genome-wide map of diversity in <i>Plasmodium falciparum</i> . <i>Nature Genetics</i> , 2007, 39, 113-119.	9.4	320
111	<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.	0.5	49
112	Regulatory motifs uncovered among gene expression clusters in <i>Plasmodium falciparum</i> . <i>Molecular and Biochemical Parasitology</i> , 2007, 153, 19-30.	0.5	31
113	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.	0.5	23
114	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.	0.5	47
115	A Systematic Map of Genetic Variation in <i>Plasmodium falciparum</i> . <i>PLoS Pathogens</i> , 2006, 2, e57.	2.1	176
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.	0.6	14
117	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.	1.9	92
118	RNA polymerase II synthesizes antisense RNA in <i>Plasmodium falciparum</i> . <i>Rna</i> , 2005, 11, 365-370.	1.6	56
119	Identification of regulatory elements in the <i>Plasmodium falciparum</i> genome. <i>Molecular and Biochemical Parasitology</i> , 2004, 134, 75-88.	0.5	85
120	Widespread distribution of antisense transcripts in the <i>Plasmodium falciparum</i> genome. <i>Molecular and Biochemical Parasitology</i> , 2004, 136, 35-42.	0.5	104
121	Mapping of the <i>Plasmodium falciparum</i> multidrug resistance gene 5' upstream region, and evidence of induction of transcript levels by antimalarial drugs in chloroquine sensitive parasites. <i>Molecular Microbiology</i> , 2004, 49, 671-683.	1.2	35
122	In vivo transcriptional profiling of <i>Plasmodium falciparum</i> . <i>Malaria Journal</i> , 2004, 3, 30.	0.8	52
123	A new reporter gene for transient transfection of <i>Plasmodium falciparum</i> . <i>Parasitology Research</i> , 2003, 89, 154-157.	0.6	29
124	Linker scanning mutagenesis of the <i>Plasmodium gallinaceum</i> sexual stage specific gene <i>pgs28</i> reveals a novel downstream cis-control element. <i>Molecular and Biochemical Parasitology</i> , 2003, 129, 199-208.	0.5	19
125	Drug-induced alterations in gene expression of the asexual blood forms of <i>Plasmodium falciparum</i> . <i>Molecular Microbiology</i> , 2003, 50, 1229-1239.	1.2	48
126	Gene Conversion as a Source of Nucleotide Diversity in <i>Plasmodium falciparum</i> . <i>Molecular Biology and Evolution</i> , 2003, 20, 726-734.	3.5	51

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127	Excess Polymorphisms in Genes for Membrane Proteins in <i>Plasmodium falciparum</i> . <i>Science</i> , 2002, 298, 216-218.	6.0	80
128	In vitro chloroquine susceptibility and PCR analysis of <i>pfprt</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.	0.6	67
129	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.	1.0	131
130	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.	0.5	45
131	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.	0.5	13
132	Recent Origin of <i>Plasmodium falciparum</i> from a Single Progenitor. <i>Science</i> , 2001, 293, 482-484.	6.0	197
133	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.	0.9	139
134	The signal sequence and C-terminal hydrophobic domain are required for localization of the sexual stage antigen Pgs28 to the surface of <i>P. gallinaceum</i> ookinetes. <i>Molecular and Biochemical Parasitology</i> , 2000, 111, 425-435.	0.5	3
135	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.	0.5	28
136	Host Cell Proteins Bind Specifically to the Capsid-Cleaved 5' End of Leishmanavirus RNA. <i>Journal of Biochemistry</i> , 1999, 126, 538-544.	0.9	3
137	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.	1.1	89
138	Malaria: A 21st century solution for an ancient disease. <i>Nature Medicine</i> , 1998, 4, 1360-1362.	15.2	12
139	Stage-specific transcripts of the <i>Plasmodium falciparum</i> <i>pfmdr1</i> gene. <i>Molecular and Biochemical Parasitology</i> , 1993, 57, 203-211.	0.5	39
140	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.	0.5	263
141	Stable expression of the bacterial <i>neor</i> gene in <i>Leishmania enriettii</i> . <i>Nature</i> , 1990, 343, 572-574.	13.7	158
142	A Cloned DNA Fragment for Identification of <i>Mycobacterium tuberculosis</i> . <i>Clinical Infectious Diseases</i> , 1989, 11, S411-S419.	2.9	15
143	Comparison of Thick Films, in Vitro Culture and DNA Hybridization Probes for Detecting <i>Plasmodium falciparum</i> Malaria. <i>American Journal of Tropical Medicine and Hygiene</i> , 1989, 40, 3-6.	0.6	38
144	Characterization of the Filarial Genome. <i>Novartis Foundation Symposium</i> , 1987, 127, 107-124.	1.2	2

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145	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.	0.6	23
146	Malaria: new tools for epidemiological analysis. <i>Memorias Do Instituto Oswaldo Cruz</i> , 1986, 81, 231-234.	0.8	0
147	Sequence of the immunodominant epitope for the surface protein on sporozoites of <i>Plasmodium vivax</i> . <i>Science</i> , 1985, 230, 1381-1383.	6.0	101
148	Control of tubulin gene expression in the parasitic protozoan <i>Leishmania enriettii</i> . <i>Nature</i> , 1984, 309, 716-717.	13.7	49