Jonathan J Juliano

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Occurrence and Distribution of Nonfalciparum Malaria Parasite Species Among Adolescents and Adults in Malawi. Journal of Infectious Diseases, 2022, 225, 257-268.	4.0	12
2	Deep Sequencing to Detect Diversity of <i>Trypanosoma cruzi</i> Infection in Patients Coinfected With Human Immunodeficiency Virus and Chagas Disease. Journal of Infectious Diseases, 2022, 225, 243-247.	4.0	5
3	Household Transmission of Severe Acute Respiratory Syndrome Coronavirus 2 in the United States: Living Density, Viral Load, and Disproportionate Impact on Communities of Color. Clinical Infectious Diseases, 2022, 74, 1776-1785.	5.8	49
4	Impact of extractive industries on malaria prevalence in the Democratic Republic of the Congo: a population-based cross-sectional study. Scientific Reports, 2022, 12, 1737.	3.3	3
5	Seasonality and transmissibility of Plasmodium ovale in Bagamoyo District, Tanzania. Parasites and Vectors, 2022, 15, 56.	2.5	12
6	Permethrin-treated baby wraps for the prevention of malaria: results of a randomized controlled pilot study in rural Uganda. Malaria Journal, 2022, 21, 63.	2.3	5
7	Evaluating malaria prevalence and land cover across varying transmission intensity in Tanzania using a cross-sectional survey of school-aged children. Malaria Journal, 2022, 21, 80.	2.3	11
8	The positive effect of malaria IPTp-SP on birthweight is mediated by gestational weight gain but modifiable by maternal carriage of enteric pathogens. EBioMedicine, 2022, 77, 103871.	6.1	10
9	Amplicon Sequencing as a Potential Surveillance Tool for Complexity of Infection and Drug Resistance Markers in <i>Plasmodium falciparum</i> Asymptomatic Infections. Journal of Infectious Diseases, 2022, 226, 920-927.	4.0	4
10	Ethnoracial Disparities in SARS-CoV-2 Seroprevalence in a Large Cohort of Individuals in Central North Carolina from April to December 2020. MSphere, 2022, 7, e0084121.	2.9	6
11	Prevalence of Knock-Down Resistance F1534S Mutations in <i>Aedes albopictus</i> (Skuse) (Diptera:) Tj ETQq1	1 0.78431 1.8	4 _. rgBT /Ove
12	Low Complexity of Infection Is Associated With Molecular Persistence of Plasmodium falciparum in Kenya and Tanzania. , 2022, 2, .		3
13	SARS-CoV-2 seroprevalence and risk factors among meat packing, produce processing, and farm workers. PLOS Global Public Health, 2022, 2, e0000619.	1.6	3
14	Describing the current status of <i>Plasmodium falciparum</i> population structure and drug resistance within mainland Tanzania using molecular inversion probes. Molecular Ecology, 2021, 30, 100-113.	3.9	29
15	Under the Radar: Epidemiology of <i>Plasmodium ovale</i> in the Democratic Republic of the Congo. Journal of Infectious Diseases, 2021, 223, 1005-1014.	4.0	24
16	Analysis of <i>Treponema pallidum</i> Strains From China Using Improved Methods for Whole-Genome Sequencing From Primary Syphilis Chancres. Journal of Infectious Diseases, 2021, 223, 848-853.	4.0	15
17	Comparison of Capillary Versus Venous Blood for the Diagnosis of Plasmodium falciparum Malaria Using Rapid Diagnostic Tests. Journal of Infectious Diseases, 2021, 224, 109-113.	4.0	1
18	Association of Malnutrition with Subsequent Malaria Parasitemia among Children Younger than Three years in Kenya: A Secondary Data Analysis of the Asembo Bay Cohort Study. American Journal of Tropical Medicine and Hygiene, 2021, 104, 243-254.	1.4	4

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19	Antimalarial Drug Resistance and Implications for the WHO Global Technical Strategy. Current Epidemiology Reports, 2021, 8, 46-62.	2.4	38
20	Analysis of false-negative rapid diagnostic tests for symptomatic malaria in the Democratic Republic of the Congo. Scientific Reports, 2021, 11, 6495.	3.3	20
21	SARS-CoV-2 Infection in Health Care Personnel and Their Household Contacts at a Tertiary Academic Medical Center: Protocol for a Longitudinal Cohort Study. JMIR Research Protocols, 2021, 10, e25410.	1.0	6
22	Effectiveness of a national mass distribution campaign of long-lasting insecticide-treated nets and indoor residual spraying on clinical malaria in Malawi, 2018–2020. BMJ Global Health, 2021, 6, e005447.	4.7	11
23	A novel CRISPR-based malaria diagnostic capable of Plasmodium detection, species differentiation, and drug-resistance genotyping. EBioMedicine, 2021, 68, 103415.	6.1	52
24	The epidemiology of Plasmodium vivax among adults in the Democratic Republic of the Congo. Nature Communications, 2021, 12, 4169.	12.8	18
25	Individual, household and neighborhood risk factors for malaria in the Democratic Republic of the Congo support new approaches to programmatic intervention. Health and Place, 2021, 70, 102581.	3.3	10
26	Immune selection suppresses the emergence of drug resistance in malaria parasites but facilitates its spread. PLoS Computational Biology, 2021, 17, e1008577.	3.2	14
27	Dihydroartemisinin-piperaquine chemoprevention and malaria incidence after severe flooding: evaluation of a pragmatic intervention in rural Uganda. Clinical Infectious Diseases, 2021, , .	5.8	2
28	Plasmodium falciparum is evolving to escape malaria rapid diagnostic tests in Ethiopia. Nature Microbiology, 2021, 6, 1289-1299.	13.3	71
29	Practical strategies for SARS-CoV-2 RT-PCR testing in resource-constrained settings. Diagnostic Microbiology and Infectious Disease, 2021, 101, 115469.	1.8	2
30	Antimicrobial Resistance in Enterobacterales and Its Contribution to Sepsis in Sub-saharan Africa. Frontiers in Medicine, 2021, 8, 615649.	2.6	11
31	Genomic epidemiology of Escherichia coli isolates from a tertiary referral center in Lilongwe, Malawi. Microbial Genomics, 2021, 7, .	2.0	12
32	Rapid Diagnostic Tests to Guide Case Management of and Improve Antibiotic Stewardship for Pediatric Acute Respiratory Illnesses in Resource-Constrained Settings: a Prospective Cohort Study in Southwestern Uganda. Microbiology Spectrum, 2021, , e0169421.	3.0	5
33	Efficient Transmission of Mixed Plasmodium falciparum/vivax Infections From Humans to Mosquitoes. Journal of Infectious Diseases, 2020, 221, 428-437.	4.0	4
34	Loss of daptomycin susceptibility in clinical Staphylococcus epidermidis infection coincided with variants in WalK. Evolution, Medicine and Public Health, 2020, 2020, 219-224.	2.5	1
35	Household Prevalence of Plasmodium falciparum, Plasmodium vivax, and Plasmodium ovale in the Democratic Republic of the Congo, 2013–2014. Clinical Infectious Diseases, 2020, 73, e3966-e3969. 	5.8	6
36	Dengue in Western Uganda: a prospective cohort of children presenting with undifferentiated febrile illness. BMC Infectious Diseases, 2020, 20, 835.	2.9	5

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37	Asymptomatic Plasmodium falciparum malaria prevalence among adolescents and adults in Malawi, 2015–2016. Scientific Reports, 2020, 10, 18740.	3.3	15
38	Spatial and epidemiological drivers of <i>Plasmodium falciparum</i> malaria among adults in the Democratic Republic of the Congo. BMJ Global Health, 2020, 5, e002316.	4.7	18
39	The impact of antimalarial resistance on the genetic structure of Plasmodium falciparum in the DRC. Nature Communications, 2020, 11, 2107.	12.8	57
40	A novel multiplex qPCR assay for detection of Plasmodium falciparum with histidine-rich protein 2 and 3 (pfhrp2 and pfhrp3) deletions in polyclonal infections. EBioMedicine, 2020, 55, 102757.	6.1	41
41	Environmental modifiers of RTS,S/AS01 malaria vaccine efficacy in Lilongwe, Malawi. BMC Public Health, 2020, 20, 910.	2.9	11
42	Case reduction and cost-effectiveness of the RTS,S/AS01 malaria vaccine alongside bed nets in Lilongwe, Malawi. Vaccine, 2020, 38, 4079-4087.	3.8	15
43	Falciparum malaria from coastal Tanzania and Zanzibar remains highly connected despite effective control efforts on the archipelago. Malaria Journal, 2020, 19, 47.	2.3	30
44	Therapeutic Efficacy of Artemether–Lumefantrine for Uncomplicated Falciparum Malaria in Northern Zambia. American Journal of Tropical Medicine and Hygiene, 2020, 103, 2224-2232.	1.4	8
45	Whole blood genome-wide transcriptome profiling and metagenomics next-generation sequencing in young infants with suspected sepsis in low-and middle-income countries: A study protocol. Gates Open Research, 2020, 4, 139.	1.1	0
46	Implementation of Antibiotic Time Outs Using Quality Improvement Methodology. Infection Control and Hospital Epidemiology, 2020, 41, s275-s276.	1.8	1
47	Plasmodium vivax chloroquine resistance links to pvcrt transcription in a genetic cross. Nature Communications, 2019, 10, 4300.	12.8	35
48	Hindgut microbiota in laboratory-reared and wild Triatoma infestans. PLoS Neglected Tropical Diseases, 2019, 13, e0007383.	3.0	39
49	O01.2â€Genetic, structural, and surface antigenic variation of <i>treponema pallidum's</i> OMPeome: steps towards a global syphilis vaccine. , 2019, , .		1
50	1040. Effects of An Antimicrobial Stewardship Team-led Staphylococcus aureus Bacteremia Management Bundle: A Quasi-Experimental Study. Open Forum Infectious Diseases, 2019, 6, S366-S366.	0.9	0
51	2790. Respiratory Viral Testing and Antimicrobial De-escalation Among Hospitalized Patients at a Tertiary Care Facility, 2015–2016: A Matched Cohort Study Series. Open Forum Infectious Diseases, 2019, 6, S986-S986.	0.9	0
52	The changing landscape of Plasmodium falciparum drug resistance in the Democratic Republic of Congo. BMC Infectious Diseases, 2019, 19, 872.	2.9	20
53	High Plasmodium falciparum genetic diversity and temporal stability despite control efforts in high transmission settings along the international border between Zambia and the Democratic Republic of the Congo. Malaria Journal, 2019, 18, 400.	2.3	18
54	Prevalence of Molecular Markers of Antimalarial Drug Resistance across Altitudinal Transmission Zones in Highland Western Uganda. American Journal of Tropical Medicine and Hygiene, 2019, 101, 799-802.	1.4	2

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55	Pooled Deep Sequencing of Drug Resistance Loci from Plasmodium falciparum Parasites across Ethiopia. American Journal of Tropical Medicine and Hygiene, 2019, 101, 1139-1143.	1.4	6
56	Drug-Resistance and Population Structure of Plasmodium falciparum Across the Democratic Republic of Congo Using High-Throughput Molecular Inversion Probes. Journal of Infectious Diseases, 2018, 218, 946-955.	4.0	78
57	SeekDeep: single-base resolution de novo clustering for amplicon deep sequencing. Nucleic Acids Research, 2018, 46, e21-e21.	14.5	134
58	748. The Impact of a Positive Respiratory Viral Panel Among Hospitalized Adult Patients with Negative Rapid Influenza Testing at an Academic Tertiary Care Facility: A-matched Cohort Study. Open Forum Infectious Diseases, 2018, 5, S268-S268.	0.9	1
59	Preventable Patient Harm: a Multidisciplinary, Bundled Approach to Reducing Clostridium difficile Infections While Using a Glutamate Dehydrogenase/Toxin Immunochromatographic Assay/Nucleic Acid Amplification Test Diagnostic Algorithm. Journal of Clinical Microbiology, 2018, 56, .	3.9	10
60	Reuse of malaria rapid diagnostic tests for amplicon deep sequencing to estimate Plasmodium falciparum transmission intensity in western Uganda. Scientific Reports, 2018, 8, 10159.	3.3	21
61	Plasmodium falciparum genetic variation of var2csa in the Democratic Republic of the Congo. Malaria Journal, 2018, 17, 46.	2.3	13
62	Streamlined, PCR-based testing for pfhrp2- and pfhrp3-negative Plasmodium falciparum. Malaria Journal, 2018, 17, 137.	2.3	38
63	Matched Placental and Circulating Plasmodium falciparum Parasites are Genetically Homologous at the var2csa ID1-DBL2X Locus by Deep Sequencing. American Journal of Tropical Medicine and Hygiene, 2018, 98, 77-82.	1.4	2
64	Plasmodium vivax Infections in Duffy-Negative Individuals in the Democratic Republic of the Congo. American Journal of Tropical Medicine and Hygiene, 2018, 99, 1128-1133.	1.4	22
65	<i>Pfhrp2</i> -deleted <i>Plasmodium falciparum</i> parasites in the Democratic Republic of Congo: A national cross-sectional survey. Journal of Infectious Diseases, 2017, 216, jiw538.	4.0	100
66	Effects of community-level bed net coverage on malaria morbidity in Lilongwe, Malawi. Malaria Journal, 2017, 16, 142.	2.3	18
67	Improving the Specificity of Plasmodium falciparum Malaria Diagnosis in High-Transmission Settings with a Two-Step Rapid Diagnostic Test and Microscopy Algorithm. Journal of Clinical Microbiology, 2017, 55, 1540-1549.	3.9	14
68	A Prolonged Outbreak of KPC-3-Producing Enterobacter cloacae and Klebsiella pneumoniae Driven by Multiple Mechanisms of Resistance Transmission at a Large Academic Burn Center. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	70
69	Increased risk of low birth weight in women with placental malaria associated with P. falciparum VAR2CSA clade. Scientific Reports, 2017, 7, 7768.	3.3	29
70	Association of a Novel Mutation in the Plasmodium falciparum Chloroquine Resistance Transporter With Decreased Piperaquine Sensitivity. Journal of Infectious Diseases, 2017, 216, 468-476.	4.0	102
71	RTS,S/AS01 Malaria Vaccine Efficacy is Not Modified by Seasonal Precipitation: Results from a Phase 3 Randomized Controlled Trial in Malawi. Scientific Reports, 2017, 7, 7200.	3.3	13
72	Co-trimoxazole Prophylaxis, Asymptomatic Malaria Parasitemia, and Infectious Morbidity in Human Immunodeficiency Virus–Exposed, Uninfected Infants in Malawi: The BAN Study. Clinical Infectious Diseases, 2017, 65, 575-580.	5.8	6

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73	Surveillance for sulfadoxine-pyrimethamine resistant malaria parasites in the Lake and Southern Zones, Tanzania, using pooling and next-generation sequencing. Malaria Journal, 2017, 16, 236.	2.3	29
74	Inhaled Antibiotics for Hospital-Acquired and Ventilator-Associated Pneumonia. Clinical Infectious Diseases, 2017, 64, 386-387.	5.8	13
75	Measuring ex vivo drug susceptibility in Plasmodium vivax isolates from Cambodia. Malaria Journal, 2017, 16, 392.	2.3	18
76	A deep sequencing approach to estimate Plasmodium falciparum complexity of infection (COI) and explore apical membrane antigen 1 diversity. Malaria Journal, 2017, 16, 490.	2.3	48
77	Partner-Drug Resistance and Population Substructuring of Artemisinin-Resistant Plasmodium falciparum in Cambodia. Genome Biology and Evolution, 2017, 9, 1673-1686.	2.5	45
78	Genomic Analysis of Multidrug-Resistant Escherichia coli from North Carolina Community Hospitals: Ongoing Circulation of CTX-M-Producing ST131- <i>H</i> 30Rx and ST131- <i>H</i> 30R1 Strains. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	43
79	A deep sequencing tool for partitioning clearance rates following antimalarial treatment in polyclonal infections. Evolution, Medicine and Public Health, 2016, 2016, 21-36.	2.5	38
80	Longevity of Genotype-Specific Immune Responses to Plasmodium falciparum Merozoite Surface Protein 1 in Kenyan Children from Regions of Different Malaria Transmission Intensity. American Journal of Tropical Medicine and Hygiene, 2016, 95, 580-587.	1.4	4
81	Selective sweep suggests transcriptional regulation may underlie <i>Plasmodium vivax</i> resilience to malaria control measures in Cambodia. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E8096-E8105.	7.1	43
82	Longitudinal Pooled Deep Sequencing of the Plasmodium vivax K12 Kelch Gene in Cambodia Reveals a Lack of Selection by Artemisinin. American Journal of Tropical Medicine and Hygiene, 2016, 95, 1409-1412.	1.4	11
83	Estimation of Plasmodium falciparum Transmission Intensity in Lilongwe, Malawi, by Microscopy, Rapid Diagnostic Testing, and Nucleic Acid Detection. American Journal of Tropical Medicine and Hygiene, 2016, 95, 373-377.	1.4	16
84	Next-Generation Sequencing and Comparative Analysis of Sequential Outbreaks Caused by Multidrug-Resistant Acinetobacter baumannii at a Large Academic Burn Center. Antimicrobial Agents and Chemotherapy, 2016, 60, 1249-1257.	3.2	35
85	Incident Tick-Borne Infections in a Cohort of North Carolina Outdoor Workers. Vector-Borne and Zoonotic Diseases, 2016, 16, 302-308.	1.5	22
86	Pooled Amplicon Deep Sequencing of Candidate Plasmodium falciparum Transmission-Blocking Vaccine Antigens. American Journal of Tropical Medicine and Hygiene, 2016, 94, 143-146.	1.4	20
87	Attenuation of Plasmodium falciparum in vitro drug resistance phenotype following culture adaptation compared to fresh clinical isolates in Cambodia. Malaria Journal, 2015, 14, 486.	2.3	10
88	Use of Oropharyngeal Washes to Diagnose and Genotype Pneumocystis jirovecii. Open Forum Infectious Diseases, 2015, 2, ofv080.	0.9	10
89	Absence of Putative Artemisinin Resistance Mutations Among Plasmodium falciparum in Sub-Saharan Africa: A Molecular Epidemiologic Study. Journal of Infectious Diseases, 2015, 211, 680-688.	4.0	235
90	Impact of Daily Cotrimoxazole on Clinical Malaria and Asymptomatic Parasitemias in HIV-Exposed, Uninfected Infants. Clinical Infectious Diseases, 2015, 61, 368-374.	5.8	18

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91	Using Amplicon Deep Sequencing to Detect Genetic Signatures of <i>Plasmodium vivax</i> Relapse. Journal of Infectious Diseases, 2015, 212, 999-1008.	4.0	69
92	Dihydroartemisinin-piperaquine failure associated with a triple mutant including kelch13 C580Y in Cambodia: an observational cohort study. Lancet Infectious Diseases, The, 2015, 15, 683-691.	9.1	213
93	Variation in the Microbiota of Ixodes Ticks with Regard to Geography, Species, and Sex. Applied and Environmental Microbiology, 2015, 81, 6200-6209.	3.1	167
94	Efficacy of Two versus Three-Day Regimens of Dihydroartemisinin-Piperaquine for Uncomplicated Malaria in Military Personnel in Northern Cambodia: An Open-Label Randomized Trial. PLoS ONE, 2014, 9, e93138.	2.5	47
95	Diversity of Rickettsiales in the Microbiome of the Lone Star Tick, Amblyomma americanum. Applied and Environmental Microbiology, 2014, 80, 354-359.	3.1	82
96	Differing Patterns of Selection and Geospatial Genetic Diversity within Two Leading Plasmodium vivax Candidate Vaccine Antigens. PLoS Neglected Tropical Diseases, 2014, 8, e2796.	3.0	38
97	Multilocus Microsatellite Genotyping Array for Investigation of Genetic Epidemiology of Pneumocystis jirovecii. Journal of Clinical Microbiology, 2014, 52, 1391-1399.	3.9	26
98	Development of a Capillary Electrophoresis-Based Heteroduplex Tracking Assay To Measure In-Host Genetic Diversity of Initial and Recurrent Plasmodium vivax Infections in Cambodia. Journal of Clinical Microbiology, 2014, 52, 298-301.	3.9	6
99	Long-lasting Permethrin Impregnated Uniforms. American Journal of Preventive Medicine, 2014, 46, 473-480.	3.0	51
100	Artemisinin Combination Therapies and Malaria Parasite Drug Resistance: The Game Is Afoot. Journal of Infectious Diseases, 2014, 210, 335-337.	4.0	18
101	Ahead of the curve: next generation estimators of drug resistance in malaria infections. Trends in Parasitology, 2013, 29, 321-328.	3.3	21
102	Epidemiology of <i>Plasmodium falciparum</i> gametocytemia in India: prevalence, age structure, risk factors and the role of a predictive score for detection. Tropical Medicine and International Health, 2013, 18, 800-809.	2.3	2
103	Mefloquine Exposure Induces Cell Cycle Delay and Reveals Stage-Specific Expression of the pfmdr1 Gene. Antimicrobial Agents and Chemotherapy, 2013, 57, 833-839.	3.2	6
104	Pooled Deep Sequencing of Plasmodium falciparum Isolates: An Efficient and Scalable Tool to Quantify Prevailing Malaria Drug-Resistance Genotypes. Journal of Infectious Diseases, 2013, 208, 1998-2006.	4.0	51
105	Plasmodium vivax Isolates from Cambodia and Thailand Show High Genetic Complexity and Distinct Patterns of P. vivax Multidrug Resistance Gene 1 (pvmdr1) Polymorphisms. American Journal of Tropical Medicine and Hygiene, 2013, 88, 1116-1123.	1.4	41
106	Nonrandomized Controlled Trial of Artesunate plus Sulfadoxine-Pyrimethamine with or without Primaquine for Preventing Posttreatment Circulation of Plasmodium falciparum Gametocytes. Antimicrobial Agents and Chemotherapy, 2013, 57, 2948-2954.	3.2	10
107	Approaches to Antifungal Therapies and Their Effectiveness among Patients with Cryptococcosis. Antimicrobial Agents and Chemotherapy, 2013, 57, 2485-2495.	3.2	36
108	Plasmodium falciparum sulfadoxine resistance is geographically and genetically clustered within the DR Congo. Scientific Reports, 2013, 3, 1165.	3.3	24

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109	Comparative population structure of Plasmodium falciparum circumsporozoite protein NANP repeat lengths in Lilongwe, Malawi. Scientific Reports, 2013, 3, 1990.	3.3	22
110	Diversity of T Cell Epitopes in Plasmodium falciparum Circumsporozoite Protein Likely Due to Protein-Protein Interactions. PLoS ONE, 2013, 8, e62427.	2.5	22
111	Use of Massively Parallel Pyrosequencing to Evaluate the Diversity of and Selection on Plasmodium falciparum csp T-Cell Epitopes in Lilongwe, Malawi. Journal of Infectious Diseases, 2012, 206, 580-587.	4.0	51
112	Individual Plasmodium vivax msp1 Variants within Polyclonal P. vivax Infections Display Different Propensities for Relapse. Journal of Clinical Microbiology, 2012, 50, 1449-1451.	3.9	11
113	Acute Chagas Disease in a Returning Traveler. American Journal of Tropical Medicine and Hygiene, 2012, 87, 1038-1040.	1.4	21
114	Can pharmacogenomics improve malaria drug policy?. Bulletin of the World Health Organization, 2011, 89, 838-845.	3.3	26
115	Molecular Malaria Epidemiology: Mapping and Burden Estimates for the Democratic Republic of the Congo, 2007. PLoS ONE, 2011, 6, e16420.	2.5	68
116	Drug-Resistant Malaria: The Era of ACT. Current Infectious Disease Reports, 2010, 12, 165-173.	3.0	99
117	The perils of PCR: can we accurately †̃correct' antimalarial trials?. Trends in Parasitology, 2010, 26, 119-124.	3.3	45
118	High-Throughput Pooling and Real-Time PCR-Based Strategy for Malaria Detection. Journal of Clinical Microbiology, 2010, 48, 512-519.	3.9	136
119	Does This Patient Have Malaria?. JAMA - Journal of the American Medical Association, 2010, 304, 2048-56.	7.4	57
120	Exposing malaria in-host diversity and estimating population diversity by capture-recapture using massively parallel pyrosequencing. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 20138-20143.	7.1	110
121	Extensive Drug Resistance in Malaria and Tuberculosis. Emerging Infectious Diseases, 2010, 16, 1063-1067.	4.3	16
122	<i>Plasmodium falciparum</i> and Dihydrofolate Reductase I164L Mutations in Africa. Antimicrobial Agents and Chemotherapy, 2009, 53, 1722-1723.	3.2	1
123	Misclassification of Drug Failure in <i>Plasmodium falciparum</i> Clinical Trials in Southeast Asia. Journal of Infectious Diseases, 2009, 200, 624-628.	4.0	24
124	Polymerase Chain Reaction Adjustment in Antimalarial Trials: Molecular Malarkey?. Journal of Infectious Diseases, 2009, 200, 5-7.	4.0	19
125	Lessons learnt from the six decades of chloroquine use (1945–2005) to control malaria in Madagascar. Transactions of the Royal Society of Tropical Medicine and Hygiene, 2009, 103, 3-10. 	1.8	20
126	Nonradioactive heteroduplex tracking assay for the detection of minority-variant chloroquine-resistant Plasmodium falciparum in Madagascar. Malaria Journal, 2009, 8, 47.	2.3	9

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127	Novel dhps and pfcrt polymorphisms in Plasmodium falciparum detected by heteroduplex tracking assay. American Journal of Tropical Medicine and Hygiene, 2009, 80, 734-6.	1.4	2
128	Detection of the Dihydrofolate Reductase–164L Mutation in Plasmodium falciparum Infections from Malawi by Heteroduplex Tracking Assay. American Journal of Tropical Medicine and Hygiene, 2008, 78, 892-894.	1.4	15
129	Detection of the dihydrofolate reductase-164L mutation in Plasmodium falciparum infections from Malawi by heteroduplex tracking assay. American Journal of Tropical Medicine and Hygiene, 2008, 78, 892-4.	1.4	15
130	Minority-Variant pfcrt K76T Mutations and Chloroquine Resistance, Malawi. Emerging Infectious Diseases, 2007, 13, 873-877.	4.3	40
131	Whole blood genome-wide transcriptome profiling and metagenomics next-generation sequencing in young infants with suspected sepsis in a low-and middle-income country: A study protocol. Gates Open Research, 0, 4, 139.	1.1	0
132	Targeted Amplicon deep sequencing of ama1 and mdr1 to track within-host P. falciparum diversity throughout treatment in a clinical drug trial. Wellcome Open Research, 0, 7, 95.	1.8	0
133	Potential Opportunities and Challenges of Deploying Next Generation Sequencing and CRISPR-Cas Systems to Support Diagnostics and Surveillance Towards Malaria Control and Elimination in Africa. Frontiers in Cellular and Infection Microbiology, 0, 12, .	3.9	6