Liwang Cui

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Development of single- and multiplex immunoassays for rapid detection and quantitation of amodiaquine in ACT drugs and rat serum. Analytical and Bioanalytical Chemistry, 2022, 414, 1631-1640.	3.7	0
2	Therapeutic efficacy of chloroquine for uncomplicated Plasmodium vivax malaria in southeastern and western border areas of Myanmar. Infection, 2022, , 1.	4.7	1
3	A C-Protein-Coupled Receptor Modulates Gametogenesis via PKG-Mediated Signaling Cascade in Plasmodium berghei. Microbiology Spectrum, 2022, , e0015022.	3.0	5
4	A Leak-Free Inducible CRISPRi/a System for Gene Functional Studies in Plasmodium falciparum. Microbiology Spectrum, 2022, , e0278221.	3.0	3
5	Community structure and insecticide resistance of malaria vectors in northern-central Myanmar. Parasites and Vectors, 2022, 15, 155.	2.5	9
6	Characterization of PSOP26 as an ookinete surface antigen with improved transmission-blocking activity when fused with PSOP25. Parasites and Vectors, 2022, 15, .	2.5	1
7	Genetic diversity of Plasmodium vivax reticulocyte binding protein 2b in global parasite populations. Parasites and Vectors, 2022, 15, .	2.5	2
8	Distinct Histone Post-translational Modifications during <i>Plasmodium falciparum</i> Gametocyte Development. Journal of Proteome Research, 2022, 21, 1857-1867.	3.7	7
9	Phosphatase inhibitors BVT-948 and alexidine dihydrochloride inhibit sexual development of the malaria parasite Plasmodium berghei. International Journal for Parasitology: Drugs and Drug Resistance, 2022, 19, 81-88.	3.4	3
10	A conserved malaria parasite antigen Pb22 plays a critical role in male gametogenesis in Plasmodium berghei. Cellular Microbiology, 2021, 23, e13294.	2.1	8
11	Predictors of malaria rapid diagnostic test positivity in a high burden area of Paletwa Township, Chin State in Western Myanmar. Infectious Diseases of Poverty, 2021, 10, 6.	3.7	4
12	Genome annotation of disease-causing microorganisms. Briefings in Bioinformatics, 2021, 22, 845-854.	6.5	13
13	Effects of COVID-19 government travel restrictions on mobility in a rural border area of Northern Thailand: A mobile phone tracking study. PLoS ONE, 2021, 16, e0245842.	2.5	19
14	<i>In Vitro</i> Susceptibility of <i>Plasmodium falciparum</i> Isolates from the China-Myanmar Border Area to Piperaquine and Association with Candidate Markers. Antimicrobial Agents and Chemotherapy, 2021, 65, .	3.2	9
15	Evaluation of two sexual-stage antigens as bivalent transmission-blocking vaccines in rodent malaria. Parasites and Vectors, 2021, 14, 241.	2.5	4
16	G6PD deficiency among malaria-infected national groups at the western part of Myanmar with implications for primaquine use in malaria elimination. Tropical Medicine and Health, 2021, 49, 47.	2.8	6
17	Ownership and utilization of bed nets and reasons for use or non-use of bed nets among community members at risk of malaria along the Thai-Myanmar border. Malaria Journal, 2021, 20, 305.	2.3	18
18	A unique GCN5 histone acetyltransferase complex controls erythrocyte invasion and virulence in the malaria parasite Plasmodium falciparum. PLoS Pathogens, 2021, 17, e1009351.	4.7	24

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19	Plasmodium falciparum resistance to ACTs: Emergence, mechanisms, and outlook. International Journal for Parasitology: Drugs and Drug Resistance, 2021, 16, 102-118.	3.4	36
20	Development and application of immunoassays for rapid quality control of the antimalarial drug combination artesunate-mefloquine. Journal of Pharmaceutical and Biomedical Analysis, 2021, 207, 114342.	2.8	1
21	Evaluation of two Plasmodium vivax sexual stage antigens as transmission-blocking vaccine candidates. Parasites and Vectors, 2021, 14, 407.	2.5	1
22	Increasing proportions of relapsing parasite species among imported malaria in China's Guangxi Province from Western and Central Africa. Travel Medicine and Infectious Disease, 2021, 43, 102130.	3.0	5
23	Population genetic structure of the malaria vector Anopheles minimus in Thailand based on mitochondrial DNA markers. Parasites and Vectors, 2021, 14, 496.	2.5	6
24	Detection of Plasmodium Sporozoites in Anopheles Mosquitoes using an Enzyme-linked Immunosorbent Assay. Journal of Visualized Experiments, 2021, , .	0.3	3
25	Unraveling the Complexity of Imported Malaria Infections by Amplicon Deep Sequencing. Frontiers in Cellular and Infection Microbiology, 2021, 11, 725859.	3.9	4
26	The acceptability of targeted mass treatment with primaquine for local elimination of vivax malaria in a northern Myanmar township: a mixed-methods study. Parasites and Vectors, 2021, 14, 549.	2.5	5
27	Molecular Surveillance and Ex Vivo Drug Susceptibilities of Plasmodium vivax Isolates From the China–Myanmar Border. Frontiers in Cellular and Infection Microbiology, 2021, 11, 738075.	3.9	5
28	Molecular interactions between parasite and mosquito during midgut invasion as targets to block malaria transmission. Npj Vaccines, 2021, 6, 140.	6.0	12
29	Efficacy of directly-observed chloroquine-primaquine treatment for uncomplicated acute Plasmodium vivax malaria in northeast Myanmar: A prospective open-label efficacy trial. Travel Medicine and Infectious Disease, 2020, 36, 101499.	3.0	19
30	Rapid quantification of artemisinin derivatives in antimalarial drugs with dipstick immunoassays. Journal of Pharmaceutical and Biomedical Analysis, 2020, 191, 113605.	2.8	6
31	Efficacy and Safety of a Naphthoquine-Azithromycin Co-Formulation for Malaria Prophylaxis in Southeast Asia: A Phase 3, Double-Blind, Randomized, Placebo-Controlled Trial. Clinical Infectious Diseases, 2020, 73, e2470-e2476.	5.8	4
32	Seasonal dynamics and molecular differentiation of three natural Anopheles species (Diptera:) Tj ETQq0 0 0 rgBT and Vectors, 2020, 13, 574.	/Overlock 2.5	10 Tf 50 227 11
33	Population genomics identifies a distinct Plasmodium vivax population on the China-Myanmar border of Southeast Asia. PLoS Neglected Tropical Diseases, 2020, 14, e0008506.	3.0	18
34	New Plasmodium vivax Genomes From the China-Myanmar Border. Frontiers in Microbiology, 2020, 11, 1930.	3.5	5
35	Efficacy of artemether-lumefantrine for treating uncomplicated Plasmodium falciparum cases and molecular surveillance of drug resistance genes in Western Myanmar. Malaria Journal, 2020, 19, 304.	2.3	8
36	Spatial heterogeneity and temporal dynamics of mosquito population density and community structure in Hainan Island, China. Parasites and Vectors, 2020, 13, 444.	2.5	16

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37	Molecular surveillance for drug resistance markers in Plasmodium vivax isolates from symptomatic and asymptomatic infections at the China–Myanmar border. Malaria Journal, 2020, 19, 281.	2.3	15
38	A novel multistage antiplasmodial inhibitor targeting Plasmodium falciparum histone deacetylase 1. Cell Discovery, 2020, 6, 93.	6.7	23
39	Lineage-Specific Expansion of Plasmodium falciparum Parasites With pfhrp2 Deletion in the Greater Mekong Subregion. Journal of Infectious Diseases, 2020, 222, 1561-1569.	4.0	9
40	Role of Plasmodium falciparum Kelch 13 Protein Mutations in P. falciparum Populations from Northeastern Myanmar in Mediating Artemisinin Resistance. MBio, 2020, 11, .	4.1	56
41	Quantification of glucose-6-phosphate dehydrogenase activity by spectrophotometry: A systematic review and meta-analysis. PLoS Medicine, 2020, 17, e1003084.	8.4	31
42	Genomic Variant Analyses in Pyrethroid Resistant and Susceptible Malaria Vector, <i>Anopheles sinensis</i> . G3: Genes, Genomes, Genetics, 2020, 10, 2185-2193.	1.8	4
43	Ex vivo susceptibilities of Plasmodium vivax isolates from the China-Myanmar border to antimalarial drugs and association with polymorphisms in Pvmdr1 and Pvcrt-o genes. PLoS Neglected Tropical Diseases, 2020, 14, e0008255.	3.0	18
44	Blood-stage malaria parasites manipulate host innate immune responses through the induction of sFGL2. Science Advances, 2020, 6, eaay9269.	10.3	15
45	Characterization of a Sulfhydryl Oxidase From Plasmodium berghei as a Target for Blocking Parasite Transmission. Frontiers in Cellular and Infection Microbiology, 2020, 10, 311.	3.9	1
46	Evaluation of Plasmodium vivax HAP2 as a transmission-blocking vaccine candidate. Vaccine, 2020, 38, 2841-2848.	3.8	21
47	Evolution of the Plasmodium vivax multidrug resistance 1 gene in the Greater Mekong Subregion during malaria elimination. Parasites and Vectors, 2020, 13, 67.	2.5	13
48	The Blood Stage Antigen RBP2-P1 of Plasmodium vivax Binds Reticulocytes and Is a Target of Naturally Acquired Immunity. Infection and Immunity, 2020, 88, .	2.2	6
49	Dynamics of Plasmodium vivax populations in border areas of the Greater Mekong sub-region during malaria elimination. Malaria Journal, 2020, 19, 145.	2.3	7
50	Plasmodium vivax HAP2/GCS1 gene exhibits limited genetic diversity among parasite isolates from the Greater Mekong Subregion. Parasites and Vectors, 2020, 13, 175.	2.5	1
51	PfAP2-G2 Is Associated to Production and Maturation of Gametocytes in Plasmodium falciparum via Regulating the Expression of PfMDV-1. Frontiers in Microbiology, 2020, 11, 631444.	3.5	15
52	Malaria Risk Map Using Spatial Multi-Criteria Decision Analysis along Yunnan Border During the Pre-elimination Period. American Journal of Tropical Medicine and Hygiene, 2020, 103, 793-809.	1.4	10
53	Molecular Surveillance and in vitro Drug Sensitivity Study of Plasmodium falciparum Isolates from the China–Myanmar Border. American Journal of Tropical Medicine and Hygiene, 2020, 103, 1100-1106.	1.4	6
54	Associations among Soil-Transmitted Helminths, G6PD Deficiency and Asymptomatic Malaria Parasitemia, and Anemia in Schoolchildren from a Conflict Zone of Northeast Myanmar. American Journal of Tropical Medicine and Hygiene, 2020, 102, 851-856.	1.4	8

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64	Title is missing!. , 2020, 14, e0008506.		0
65	Title is missing!. , 2020, 14, e0008506.		0
66	Multiple relapses of Plasmodium vivax malaria acquired from West Africa and association with poor metabolizer CYP2D6 variant: a case report. BMC Infectious Diseases, 2019, 19, 704.	2.9	20
67	The glucose-6-phosphate dehydrogenase Mahidol variant protects against uncomplicated Plasmodium vivax infection and reduces disease severity in a Kachin population from northeast Myanmar. Infection, Genetics and Evolution, 2019, 75, 103980.	2.3	14
68	A glance of the blood stage transcriptome of a Southeast Asian Plasmodium ovale isolate. PLoS Neglected Tropical Diseases, 2019, 13, e0007850.	3.0	5
69	Increasing trends of malaria in a border area of the Greater Mekong Subregion. Malaria Journal, 2019, 18, 309.	2.3	38
70	An MFS-Domain Protein Pb115 Plays a Critical Role in Gamete Fertilization of the Malaria Parasite Plasmodium berghei. Frontiers in Microbiology, 2019, 10, 2193.	3.5	11
71	Genetic Variations Associated with Drug Resistance Markers in Asymptomatic Plasmodium falciparum Infections in Myanmar. Genes, 2019, 10, 692.	2.4	20
72	Study of the whole genome, methylome and transcriptome of Cordyceps militaris. Scientific Reports, 2019, 9, 898.	3.3	17

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73	Geometric morphometrics approach towards discrimination of three member species of Maculatus group in Thailand. Acta Tropica, 2019, 192, 66-74.	2.0	19
74	Insecticide Resistance Status and Mechanisms of Anopheles sinensis (Diptera: Culicidae) in Wenzhou, an Important Coastal Port City in China. Journal of Medical Entomology, 2019, 56, 803-810.	1.8	6
75	Plasmodium berghei serine/threonine protein phosphatase PP5 plays a critical role in male gamete fertility. International Journal for Parasitology, 2019, 49, 685-695.	3.1	13
76	Development of a lateral flow dipstick for simultaneous and semiâ€quantitative analysis of dihydroartemisinin and piperaquine in an artemisinin combination therapy. Drug Testing and Analysis, 2019, 11, 1444-1452.	2.6	6
77	Efficient synchronization of Plasmodium knowlesi in vitro cultures using guanidine hydrochloride. Malaria Journal, 2019, 18, 148.	2.3	12
78	Characterization of protein arginine methyltransferase of TgPRMT5 in Toxoplasma gondii. Parasites and Vectors, 2019, 12, 221.	2.5	7
79	In vitro susceptibility of Plasmodium falciparum isolates from the China-Myanmar border area to artemisinins and correlation with K13 mutations. International Journal for Parasitology: Drugs and Drug Resistance, 2019, 10, 20-27.	3.4	20
80	Epidemiological profiles of recurrent malaria episodes in an endemic area along the Thailand-Myanmar border: a prospective cohort study. Malaria Journal, 2019, 18, 124.	2.3	25
81	Odorant ligands for the CO2 receptor in two Anopheles vectors of malaria. Scientific Reports, 2019, 9, 2549.	3.3	12
82	DNA helicase RecQ1 regulates mutually exclusive expression of virulence genes in <i>Plasmodium falciparum</i> via heterochromatin alteration. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 3177-3182.	7.1	16
83	Geographical heterogeneity in prevalence of subclinical malaria infections at sentinel endemic sites of Myanmar. Parasites and Vectors, 2019, 12, 83.	2.5	20
84	Epigenetic reader complexes of the human malaria parasite, Plasmodium falciparum. Nucleic Acids Research, 2019, 47, 11574-11588.	14.5	45
85	Health education through mass media announcements by loudspeakers about malaria care: prevention and practice among people living in a malaria endemic area of northern Myanmar. Malaria Journal, 2019, 18, 362.	2.3	15
86	Genetic diversity, natural selection and haplotype grouping of Plasmodium vivax Duffy-binding protein genes from eastern and western Myanmar borders. Parasites and Vectors, 2019, 12, 546.	2.5	7
87	Epigenetic editing by CRISPR/dCas9 in <i>Plasmodium falciparum</i> . Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 255-260.	7.1	50
88	Case Report: Case Series of Human Plasmodium knowlesi Infection on the Southern Border of Thailand. American Journal of Tropical Medicine and Hygiene, 2019, 101, 1397-1401.	1.4	22
89	Indigenous Plasmodium malariae Infection in an Endemic Population at the Thai–Myanmar Border. American Journal of Tropical Medicine and Hygiene, 2019, 100, 1164-1169.	1.4	6
90	Puf3 participates in ribosomal biogenesis in malaria parasites. Journal of Cell Science, 2018, 131, .	2.0	8

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91	Plasmodium falciparum Falcipain-2a Polymorphisms in Southeast Asia and Their Association With Artemisinin Resistance. Journal of Infectious Diseases, 2018, 218, 434-442.	4.0	32
92	Genetic diversity of the Plasmodium vivax phosphatidylinositol 3-kinase gene in two regions of the China-Myanmar border. Infection, Genetics and Evolution, 2018, 61, 45-52.	2.3	4
93	Fitness Loss under Amino Acid Starvation in Artemisinin-Resistant Plasmodium falciparum Isolates from Cambodia. Scientific Reports, 2018, 8, 12622.	3.3	21
94	The Plasmodium falciparum male gametocyte protein P230p, a paralog of P230, is vital for ookinete formation and mosquito transmission. Scientific Reports, 2018, 8, 14902.	3.3	37
95	The Glycosylphosphatidylinositol Transamidase Complex Subunit PbGPI16 of Plasmodium berghei Is Important for Inducing Experimental Cerebral Malaria. Infection and Immunity, 2018, 86, .	2.2	7
96	Longitudinal surveillance of drug resistance in Plasmodium falciparum isolates from the China-Myanmar border reveals persistent circulation of multidrug resistant parasites. International Journal for Parasitology: Drugs and Drug Resistance, 2018, 8, 320-328.	3.4	22
97	Sample-to-answer palm-sized nucleic acid testing device towards low-cost malaria mass screening. Biosensors and Bioelectronics, 2018, 115, 83-90.	10.1	46
98	Development of monoclonal antibody-based immunoassays for quantification and rapid assessment of dihydroartemisinin contents in antimalarial drugs. Journal of Pharmaceutical and Biomedical Analysis, 2018, 159, 66-72.	2.8	7
99	Genetic diversity of the Plasmodium vivax multidrug resistance 1 gene in Thai parasite populations. Infection, Genetics and Evolution, 2018, 64, 168-177.	2.3	10
100	Hemoglobin E protects against acute Plasmodium vivax infections in a Kachin population at the China–Myanmar border. Journal of Infection, 2018, 77, 435-439.	3.3	4
101	Randomized, Double-Blind, Placebo-Controlled Studies to Assess Safety and Prophylactic Efficacy of Naphthoquine-Azithromycin Combination for Malaria Prophylaxis in Southeast Asia. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	5
102	Risk factors for asymptomatic malaria infections from seasonal cross-sectional surveys along the China–Myanmar border. Malaria Journal, 2018, 17, 247.	2.3	37
103	Molecular approaches to determine the multiplicity of Plasmodium infections. Malaria Journal, 2018, 17, 172.	2.3	42
104	Characterization of Plasmodium berghei Pbg37 as Both a Pre- and Postfertilization Antigen with Transmission-Blocking Potential. Infection and Immunity, 2018, 86, .	2.2	14
105	Infectivity of symptomatic and asymptomatic Plasmodium vivax infections to a Southeast Asian vector, Anopheles dirus. International Journal for Parasitology, 2017, 47, 163-170.	3.1	76
106	Sex-Specific Biology of the Human Malaria Parasite Revealed from the Proteomes of Mature Male and Female Gametocytes. Molecular and Cellular Proteomics, 2017, 16, 537-551.	3.8	41
107	Variable number of tandem repeats of 9 Plasmodium vivax genes among Southeast Asian isolates. Acta Tropica, 2017, 170, 161-168.	2.0	3
108	Artesunate and erythropoietin synergistically improve the outcome of experimental cerebral malaria. International Immunopharmacology, 2017, 48, 219-230.	3.8	22

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109	Interactions between tafenoquine and artemisinin-combination therapy partner drug in asexual and sexual stage Plasmodium falciparum. International Journal for Parasitology: Drugs and Drug Resistance, 2017, 7, 131-137.	3.4	18
110	Frequent Spread of Plasmodium vivax Malaria Maintains High Genetic Diversity at the Myanmar-China Border, Without Distance and Landscape Barriers. Journal of Infectious Diseases, 2017, 216, 1254-1263.	4.0	32
111	Significant Divergence in Sensitivity to Antimalarial Drugs between Neighboring Plasmodium falciparum Populations along the Eastern Border of Myanmar. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	12
112	A young man with severe acute haemolytic anaemia. BMJ: British Medical Journal, 2017, 359, j4263.	2.3	9
113	High-throughput and label-free parasitemia quantification and stage differentiation for malaria-infected red blood cells. Biosensors and Bioelectronics, 2017, 98, 408-414.	10.1	26
114	Tryptophan-rich domains of Plasmodium falciparum SURFIN4.2 and Plasmodium vivax PvSTP2 interact with membrane skeleton of red blood cell. Malaria Journal, 2017, 16, 121.	2.3	10
115	Asymptomatic and sub-microscopic malaria infection in Kayah State, eastern Myanmar. Malaria Journal, 2017, 16, 138.	2.3	41
116	Comparison of methods for detecting asymptomatic malaria infections in the China–Myanmar border area. Malaria Journal, 2017, 16, 159.	2.3	22
117	Further evaluation of the NWF filter for the purification of Plasmodium vivax-infected erythrocytes. Malaria Journal, 2017, 16, 201.	2.3	12
118	Imported Plasmodium falciparum and locally transmitted Plasmodium vivax: cross-border malaria transmission scenario in northwestern Thailand. Malaria Journal, 2017, 16, 258.	2.3	41
119	Proteomic Analysis of Differentially Expressed Proteins in Intracranial <i>Angiostrongylus cantonensis</i> Larvae in Permissive and Non-Permissive Hosts. Journal of Parasitology, 2017, 103, 718-726.	0.7	1
120	Genetic diversity of Plasmodium falciparum populations in southeast and western Myanmar. Parasites and Vectors, 2017, 10, 322.	2.5	26
121	Characterization of Pb51 in Plasmodium berghei as a malaria vaccine candidate targeting both asexual erythrocytic proliferation and transmission. Malaria Journal, 2017, 16, 458.	2.3	8
122	Functional characterization of Plasmodium berghei PSOP25 during ookinete development and as a malaria transmission-blocking vaccine candidate. Parasites and Vectors, 2017, 10, 8.	2.5	29
123	Substantial population structure of Plasmodium vivax in Thailand facilitates identification of the sources of residual transmission. PLoS Neglected Tropical Diseases, 2017, 11, e0005930.	3.0	14
124	Co-inheritance of glucose-6-phosphate dehydrogenase deficiency mutations and hemoglobin E in a Kachin population in a malaria-endemic region of Southeast Asia. PLoS ONE, 2017, 12, e0177917.	2.5	15
125	Quality Testing of Artemisinin-Based Antimalarial Drugs in Myanmar. American Journal of Tropical Medicine and Hygiene, 2017, 97, 1198-1203.	1.4	15
126	Microgeographic Heterogeneity of Border Malaria During Elimination Phase, Yunnan Province, China, 2011–2013. Emerging Infectious Diseases, 2016, 22, 1363-1370.	4.3	13

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127	Arbitrarily Accessible 3D Microfluidic Device for Combinatorial High-Throughput Drug Screening. Sensors, 2016, 16, 1616.	3.8	19
128	Common asymptomatic and submicroscopic malaria infections in Western Thailand revealed in longitudinal molecular and serological studies: a challenge to malaria elimination. Malaria Journal, 2016, 15, 333.	2.3	70
129	Impact of interventions on malaria in internally displaced persons along the China–Myanmar border: 2011–2014. Malaria Journal, 2016, 15, 471.	2.3	34
130	Limited genetic diversity in the PvK12 Kelch protein in Plasmodium vivax isolates from Southeast Asia. Malaria Journal, 2016, 15, 537.	2.3	21
131	Genetic diversity of the Pvk12 gene in Plasmodium vivax from the China-Myanmar border area. Malaria Journal, 2016, 15, 528.	2.3	16
132	Effects of transmission-blocking vaccines simultaneously targeting pre- and post-fertilization antigens in the rodent malaria parasite Plasmodium yoelii. Parasites and Vectors, 2016, 9, 433.	2.5	4
133	Effects of Microclimate Condition Changes Due to Land Use and Land Cover Changes on the Survivorship of Malaria Vectors in China-Myanmar Border Region. PLoS ONE, 2016, 11, e0155301.	2.5	23
134	The RNA-binding protein PfPuf1 functions in the maintenance of gametocytes in <i>Plasmodium falciparum</i> . Journal of Cell Science, 2016, 129, 3144-52.	2.0	29
135	Plasmodium malariae and Plasmodium ovale infections in the China–Myanmar border area. Malaria Journal, 2016, 15, 557.	2.3	28
136	Identification of three ookinete-specific genes and evaluation of their transmission-blocking potentials in Plasmodium berghei. Vaccine, 2016, 34, 2570-2578.	3.8	26
137	Rapid evaluation of artesunate quality with a specific monoclonal antibody-based lateral flow dipstick. Analytical and Bioanalytical Chemistry, 2016, 408, 6003-6008.	3.7	13
138	A field-deployable mobile molecular diagnostic system for malaria at the point of need. Lab on A Chip, 2016, 16, 4341-4349.	6.0	39
139	TLR4 and TLR9 signals stimulate protective immunity against blood-stage Plasmodium yoelii infection in mice. Experimental Parasitology, 2016, 170, 73-81.	1.2	16
140	Microgeographically diverse Plasmodium vivax populations at the Thai-Myanmar border. Infection, Genetics and Evolution, 2016, 45, 341-346.	2.3	3
141	Genome-wide association analysis identifies genetic loci associated with resistance to multiple antimalarials in Plasmodium falciparum from China-Myanmar border. Scientific Reports, 2016, 6, 33891.	3.3	100
142	Life-table studies revealed significant effects of deforestation on the development and survivorship of Anopheles minimus larvae. Parasites and Vectors, 2016, 9, 323.	2.5	18
143	Pilot testing of dipsticks as point-of-care assays for rapid diagnosis of poor-quality artemisinin drugs in endemic settings. Tropical Medicine and Health, 2016, 44, 15.	2.8	7
144	Analysis of Pvama1 genes from China-Myanmar border reveals little regional genetic differentiation of Plasmodium vivax populations. Parasites and Vectors, 2016, 9, 614.	2.5	13

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145	Examining Plasmodium falciparum and P. vivax clearance subsequent to antimalarial drug treatment in the Myanmar-China border area based on quantitative real-time polymerase chain reaction. BMC Infectious Diseases, 2016, 16, 154.	2.9	14
146	Population genomics studies identify signatures of global dispersal and drug resistance in Plasmodium vivax. Nature Genetics, 2016, 48, 953-958.	21.4	194
147	A Worldwide Map of <i>Plasmodium falciparum</i> K13-Propeller Polymorphisms. New England Journal of Medicine, 2016, 374, 2453-2464.	27.0	449
148	Characterization of a Plasmodium berghei sexual stage antigen PbPH as a new candidate for malaria transmission-blocking vaccine. Parasites and Vectors, 2016, 9, 190.	2.5	20
149	Development of a Specific Monoclonal Antibody for the Quantification of Artemisinin in <i>Artemisia annua</i> and Rat Serum. Analytical Chemistry, 2016, 88, 2701-2706.	6.5	20
150	Natural human Plasmodium infections in major Anopheles mosquitoes in western Thailand. Parasites and Vectors, 2016, 9, 17.	2.5	54
151	Genetic diversity of the Plasmodium falciparum apical membrane antigen I gene in parasite population from the China–Myanmar border area. Infection, Genetics and Evolution, 2016, 39, 155-162.	2.3	20
152	A more appropriate white blood cell count for estimating malaria parasite density in Plasmodium vivax patients in northeastern Myanmar. Acta Tropica, 2016, 156, 152-156.	2.0	10
153	Seasonal dynamics and microgeographical spatial heterogeneity of malaria along the China–Myanmar border. Acta Tropica, 2016, 157, 12-19.	2.0	29
154	Naturally Acquired Antibody Responses to Plasmodium vivax and Plasmodium falciparum Merozoite Surface Protein 1 (MSP1) C-Terminal 19 kDa Domains in an Area of Unstable Malaria Transmission in Southeast Asia. PLoS ONE, 2016, 11, e0151900.	2.5	22
155	Evaluation of CDC light traps for mosquito surveillance in a malaria endemic area on the Thai-Myanmar border. Parasites and Vectors, 2015, 8, 636.	2.5	58
156	A bioinformatic survey of RNA-binding proteins in Plasmodium. BMC Genomics, 2015, 16, 890.	2.8	79
157	Microgeography and molecular epidemiology of malaria at the Thailand-Myanmar border in the malaria pre-elimination phase. Malaria Journal, 2015, 14, 198.	2.3	47
158	Improvement of culture conditions for long-term in vitro culture of Plasmodium vivax. Malaria Journal, 2015, 14, 297.	2.3	41
159	L-Arginine supplementation in mice enhances NO production in spleen cells and inhibits Plasmodium yoelii transmission in mosquitoes. Parasites and Vectors, 2015, 8, 326.	2.5	13
160	Population dynamics and community structure of Anopheles mosquitoes along the China-Myanmar border. Parasites and Vectors, 2015, 8, 445.	2.5	27
161	Genetic diversity of transmission-blocking vaccine candidate Pvs48/45 in Plasmodium vivax populations in China. Parasites and Vectors, 2015, 8, 615.	2.5	12
162	Prevalence and Molecular Characterization of Glucose-6-Phosphate Dehydrogenase Deficiency at the China-Myanmar Border. PLoS ONE, 2015, 10, e0134593.	2.5	39

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163	Molecular Evolution of PvMSP3α Block II in Plasmodium vivax from Diverse Geographic Origins. PLoS ONE, 2015, 10, e0135396.	2.5	13
164	Prevalence of K13-propeller polymorphisms in Plasmodium falciparum from China-Myanmar border in 2007–2012. Malaria Journal, 2015, 14, 168.	2.3	71
165	Clinical Efficacy of Dihydroartemisinin–Piperaquine for the Treatment of Uncomplicated Plasmodium falciparum Malaria at the China–Myanmar Border. American Journal of Tropical Medicine and Hygiene, 2015, 93, 577-583.	1.4	29
166	Molecular inference of sources and spreading patterns of Plasmodium falciparum malaria parasites in internally displaced persons settlements in Myanmar–China border area. Infection, Genetics and Evolution, 2015, 33, 189-196.	2.3	20
167	Submicroscopic and asymptomatic Plasmodium falciparum and Plasmodium vivax infections are common in western Thailand - molecular and serological evidence. Malaria Journal, 2015, 14, 95.	2.3	82
168	<i>In Vitro</i> Activities of Primaquine-Schizonticide Combinations on Asexual Blood Stages and Gametocytes of Plasmodium falciparum. Antimicrobial Agents and Chemotherapy, 2015, 59, 7650-7656.	3.2	20
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