Liwang Cui

List of Publications by Year
in descending order

292 papers	11,900 citations	36303 51 h-index	42399 92 g-index
295 all docs	295 docs citations	295 times ranked	10373 citing authors

#	Article	IF	Citations
1	A Metagenomic Survey of Microbes in Honey Bee Colony Collapse Disorder. Science, 2007, 318, 283-287.	12.6	1,481
2	A Worldwide Map ofPlasmodium falciparumK13-Propeller Polymorphisms. New England Journal of Medicine, 2016, 374, 2453-2464.	27.0	449
3	Discovery, mechanisms of action and combination therapy of artemisinin. Expert Review of Anti-Infective Therapy, 2009, 7, 999-1013.	4.4	283
4	Antimalarial Drug Resistance: Literature Review and Activities and Findings of the ICEMR Network. American Journal of Tropical Medicine and Hygiene, 2015, 93, 57-68.	1.4	250
5	Malaria in the Greater Mekong Subregion: Heterogeneity and complexity. Acta Tropica, 2012, 121, 227-239.	2.0	219
6	Cytotoxic Effect of Curcumin on Malaria Parasite Plasmodium falciparum: Inhibition of Histone Acetylation and Generation of Reactive Oxygen Species. Antimicrobial Agents and Chemotherapy, 2007, 51, 488-494.	3.2	216
7	The role of varroa mites in infections of Kashmir bee virus (KBV) and deformed wing virus (DWV) in honey bees. Virology, 2005, 342, 141-149.	2.4	211
8	Population genomics studies identify signatures of global dispersal and drug resistance in Plasmodium vivax. Nature Genetics, 2016, 48, 953-958.	21.4	194
9	Plasmodium falciparum genome-wide scans for positive selection, recombination hot spots and resistance to antimalarial drugs. Nature Genetics, 2010, 42, 268-271.	21.4	178
10	Intricate transmission routes and interactions between picorna-like viruses (Kashmir bee virus and) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2005, 86, 2281-2289.	2.9	172
11	The malaria parasite Plasmodium falciparum histones: Organization, expression, and acetylation. Gene, 2006, 369, 53-65.	2.2	166
12	Plasmodium vivax Invasion of Human Erythrocytes Inhibited by Antibodies Directed against the Duffy Binding Protein. PLoS Medicine, 2007, 4, e337.	8.4	161
13	Differential Prevalence ofPlasmodiumInfections and CrypticPlasmodium knowlesiMalaria in Humans in Thailand. Journal of Infectious Diseases, 2009, 199, 1143-1150.	4.0	159
14	Histone lysine methyltransferases and demethylases in Plasmodium falciparum. International Journal for Parasitology, 2008, 38, 1083-1097.	3.1	128
15	Plasmodium vivax transmission: chances for control?. Trends in Parasitology, 2004, 20, 192-198.	3.3	122
16	GENETIC DIVERSITY AND MULTIPLE INFECTIONS OF PLASMODIUM VIVAX MALARIA IN WESTERN THAILAND. American Journal of Tropical Medicine and Hygiene, 2003, 68, 613-619.	1.4	117
17	The genetic diversity of Plasmodium vivax populations. Trends in Parasitology, 2003, 19, 220-226.	3.3	115
18	PfGCN5-Mediated Histone H3 Acetylation Plays a Key Role in Gene Expression in Plasmodium falciparum. Eukaryotic Cell, 2007, 6, 1219-1227.	3.4	113

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19	The Evolutionary History of Plasmodium vivax as Inferred from Mitochondrial Genomes: Parasite Genetic Diversity in the Americas. Molecular Biology and Evolution, 2013, 30, 2050-2064.	8.9	110
20	Chromatin-Mediated Epigenetic Regulation in the Malaria Parasite Plasmodium falciparum. Eukaryotic Cell, 2010, 9, 1138-1149.	3.4	108
21	Establishment of a human hepatocyte line that supports in vitro development of the exo-erythrocytic stages of the malaria parasites Plasmodium falciparum and P. vivax. American Journal of Tropical Medicine and Hygiene, 2006, 74, 708-15.	1.4	104
22	Plasmodium falciparum Histone Acetyltransferase, a Yeast GCN5 Homologue Involved in Chromatin Remodeling. Eukaryotic Cell, 2004, 3, 264-276.	3.4	103
23	Histone Acetyltransferase Inhibitor Anacardic Acid Causes Changes in Global Gene Expression during In Vitro Plasmodium falciparum Development. Eukaryotic Cell, 2008, 7, 1200-1210.	3.4	101
24	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
25	The Puf-family RNA-binding protein PfPuf2 regulates sexual development and sex differentiation in the malaria parasitePlasmodium falciparum. Journal of Cell Science, 2010, 123, 1039-1049.	2.0	88
26	Extensive lysine acetylation occurs in evolutionarily conserved metabolic pathways and parasiteâ€specific functions during <scp>P</scp>lasmodium falciparum intraerythrocytic development. Molecular Microbiology, 2013, 89, 660-675.	2.5	86
27	Artemisinin Resistance at the China-Myanmar Border and Association with Mutations in the K13 Propeller Gene. Antimicrobial Agents and Chemotherapy, 2015, 59, 6952-6959.	3.2	84
28	Mechanisms of in vitro resistance to dihydroartemisinin in Plasmodium falciparum. Molecular Microbiology, 2012, 86, 111-128.	2.5	83
29	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
30	SPATIO-TEMPORAL DISTRIBUTION OF PLASMODIUM FALCIPARUM AND P. VIVAX MALARIA IN THAILAND. American Journal of Tropical Medicine and Hygiene, 2005, 72, 256-262.	1.4	82
31	Plasmodium vivax parasites alter the balance of myeloid and plasmacytoid dendritic cells and the induction of regulatory T cells. European Journal of Immunology, 2008, 38, 2697-2705.	2.9	81
32	Malaria Molecular Epidemiology: Lessons from the International Centers of Excellence for Malaria Research Network. American Journal of Tropical Medicine and Hygiene, 2015, 93, 79-86.	1.4	80
33	A bioinformatic survey of RNA-binding proteins in Plasmodium. BMC Genomics, 2015, 16, 890.	2.8	79
34	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
35	The malaria parasite Plasmodium falciparum encodes members of the Puf RNA-binding protein family with conserved RNA binding activity. Nucleic Acids Research, 2002, 30, 4607-4617.	14.5	74
36	Production of erythropoietic cells in vitro for continuous culture of Plasmodium vivax. International Journal for Parasitology, 2007, 37, 1551-1557.	3.1	72

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37	Induction of specific immune responses against the Plasmodium vivax liver-stage via in vitro activation by dendritic cells. Parasitology International, 2006, 55, 187-193.	1.3	71
38	Natural human humoral response to salivary gland proteins of Anopheles mosquitoes in Thailand. Acta Tropica, 2006, 98, 66-73.	2.0	71
39	Prevalence of K13-propeller polymorphisms in Plasmodium falciparum from China-Myanmar border in 2007â€"2012. Malaria Journal, 2015, 14, 168.	2.3	71
40	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
41	Genome-wide nucleosome mapping of Plasmodium falciparum reveals histone-rich coding and histone-poor intergenic regions and chromatin remodeling of core and subtelomeric genes. BMC Genomics, 2009, 10, 610.	2.8	67
42	The MYST family histone acetyltransferase regulates gene expression and cell cycle in malaria parasite Plasmodium falciparum. Molecular Microbiology, 2010, 78, 883-902.	2.5	66
43	Puf Mediates Translation Repression of Transmission-Blocking Vaccine Candidates in Malaria Parasites. PLoS Pathogens, 2013, 9, e1003268.	4.7	66
44	Short-term in vitro culture of field isolates of Plasmodium vivax using umbilical cord blood. Parasitology International, 2007, 56, 65-69.	1.3	65
45	Relationship between Knockdown Resistance, Metabolic Detoxification and Organismal Resistance to Pyrethroids in Anopheles sinensis. PLoS ONE, 2013, 8, e55475.	2.5	61
46	Vitamin D Inhibits the Occurrence of Experimental Cerebral Malaria in Mice by Suppressing the Host Inflammatory Response. Journal of Immunology, 2014, 193, 1314-1323.	0.8	60
47	A nonspecific nucleoside hydrolase from Leishmania donovani : implications for purine salvage by the parasite. Gene, 2001, 280, 153-162.	2.2	59
48	Translational regulation during stage transitions in malaria parasites. Annals of the New York Academy of Sciences, 2015, 1342, 1-9.	3.8	59
49	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
50	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
51	Plasmodium falciparum Genetic Diversity in Western Kenya Highlands. American Journal of Tropical Medicine and Hygiene, 2007, 77, 1043-1050.	1.4	56
52	Expression and hemocyte-targeting of aCampoletis sonorensis polydnavirus cysteine-rich gene inHeliothis virescens larvae. , 1997, 36, 251-271.		55
53	Nested PCR detection of malaria directly using blood filter paper samples from epidemiological surveys. Malaria Journal, 2014, 13, 175.	2.3	55
54	Profiling the humoral immune responses to Plasmodium vivax infection and identification of candidate immunogenic rhoptry-associated membrane antigen (RAMA). Journal of Proteomics, 2014, 102, 66-82.	2.4	55

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55	In Vitro Sensitivity of Plasmodium falciparum Clinical Isolates from the China-Myanmar Border Area to Quinine and Association with Polymorphism in the Na + /H + Exchanger. Antimicrobial Agents and Chemotherapy, 2010, 54, 4306-4313.	3.2	54
56	Natural human Plasmodium infections in major Anopheles mosquitoes in western Thailand. Parasites and Vectors, 2016, 9, 17.	2.5	54
57	Relationships between polydnavirus gene expression and host range of the parasitoid wasp Campoletis sonorensis. Journal of Insect Physiology, 2000, 46, 1397-1407.	2.0	53
58	Epigenetic editing by CRISPR/dCas9 in Plasmodium falciparum. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 255-260.	7.1	50
59	Spatio-temporal distribution of Plasmodium falciparum and p. Vivax malaria in Thailand. American Journal of Tropical Medicine and Hygiene, 2005, 72, 256-62.	1.4	50
60	Characterization of PRMT1 from Plasmodium falciparum. Biochemical Journal, 2009, 421, 107-118.	3.7	49
61	Genetic diversity of Plasmodium falciparum histidine-rich protein 2 in the Chinaâ€"Myanmar border area. Acta Tropica, 2015, 152, 26-31.	2.0	49
62	Therapeutic Responses of Plasmodium vivax Malaria to Chloroquine and Primaquine Treatment in Northeastern Myanmar. Antimicrobial Agents and Chemotherapy, 2015, 59, 1230-1235.	3.2	48
63	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
64	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
65	Plasmodium falciparum: Development of a transgenic line for screening antimalarials using firefly luciferase as the reporter. Experimental Parasitology, 2008, 120, 80-87.	1.2	45
66	Epigenetic reader complexes of the human malaria parasite, Plasmodium falciparum. Nucleic Acids Research, 2019, 47, 11574-11588.	14.5	45
67	Relationships between polydnavirus genomes and viral gene expression. Journal of Insect Physiology, 1998, 44, 785-793.	2.0	44
68	CHARACTERIZATION OF A SALIVARY LYSOZYME IN LARVAL Helicoverpa zea. Journal of Chemical Ecology, 2004, 30, 2439-2457.	1.8	42
69	Molecular Systematics of Nuclear Gene <I>period</I> in Genus <I>Anastrepha</I> (Tephritidae). Annals of the Entomological Society of America, 2005, 98, 173-180.	2.5	42
70	Rapid isolation of single malaria parasiteâ€"infected red blood cells by cell sorting. Nature Protocols, 2011, 6, 140-146.	12.0	42
71	Challenges and prospects for malaria elimination in the Greater Mekong Subregion. Acta Tropica, 2012, 121, 240-245.	2.0	42
72	Molecular approaches to determine the multiplicity of Plasmodium infections. Malaria Journal, 2018, 17, 172.	2.3	42

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73	PfADA2, a Plasmodium falciparum homologue of the transcriptional coactivator ADA2 and its in vivo association with the histone acetyltransferase PfGCN5. Gene, 2004, 336, 251-261.	2.2	41
74	Improvement of culture conditions for long-term in vitro culture of Plasmodium vivax. Malaria Journal, 2015, 14, 297.	2.3	41
75	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
76	Asymptomatic and sub-microscopic malaria infection in Kayah State, eastern Myanmar. Malaria Journal, 2017, 16, 138.	2.3	41
77	Imported Plasmodium falciparum and locally transmitted Plasmodium vivax: cross-border malaria transmission scenario in northwestern Thailand. Malaria Journal, 2017, 16, 258.	2.3	41
78	Molecular analysis of chloroquine resistance in Plasmodium falciparum in Yunnan Province, China. Tropical Medicine and International Health, 2007, 12, 1051-1060.	2.3	39
79	Prevalence and Molecular Characterization of Glucose-6-Phosphate Dehydrogenase Deficiency at the China-Myanmar Border. PLoS ONE, 2015, 10, e0134593.	2.5	39
80	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
81	Gametocytogenesis in malaria parasite: commitment, development and regulation. Future Microbiology, 2011, 6, 1351-1369.	2.0	38
82	Lack of Association of the S769N Mutation in Plasmodium falciparum SERCA (PfATP6) with Resistance to Artemisinins. Antimicrobial Agents and Chemotherapy, 2012, 56, 2546-2552.	3.2	38
83	Plasmodium falciparum: Generation of pure gametocyte culture by heparin treatment. Experimental Parasitology, 2013, 135, 541-545.	1.2	38
84	Plasmodium falciparum populations from northeastern Myanmar display high levels of genetic diversity at multiple antigenic loci. Acta Tropica, 2013, 125, 53-59.	2.0	38
85	Increasing trends of malaria in a border area of the Greater Mekong Subregion. Malaria Journal, 2019, 18, 309.	2.3	38
86	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
87	Risk factors for asymptomatic malaria infections from seasonal cross-sectional surveys along the Chinaâ€“Myanmar border. Malaria Journal, 2018, 17, 247.	2.3	37
88	In Vitro Sensitivity of Plasmodium falciparum from China-Myanmar Border Area to Major ACT Drugs and Polymorphisms in Potential Target Genes. PLoS ONE, 2012, 7, e30927.	2.5	37
89	Plasmodium falciparum resistance to ACTs: Emergence, mechanisms, and outlook. International Journal for Parasitology: Drugs and Drug Resistance, 2021, 16, 102-118.	3.4	36
90	Plasmodium falciparum genetic diversity in western Kenya highlands. American Journal of Tropical Medicine and Hygiene, 2007, 77, 1043-50.	1.4	36

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91	Determination of the Plasmodium vivax schizont stage proteome. Journal of Proteomics, 2011, 74, 1701-1710.	2.4	35
92	Risk factors associated with slide positivity among febrile patients in a conflict zone of north-eastern Myanmar along the China-Myanmar border. Malaria Journal, 2013, 12, 361.	2.3	35
93	Performance of two rapid diagnostic tests for malaria diagnosis at the China-Myanmar border area. Malaria Journal, 2013, 12, 73.	2.3	34
94	Malaria Epidemiology and Control Within the International Centers of Excellence for Malaria Research. American Journal of Tropical Medicine and Hygiene, 2015, 93, 5-15.	1.4	34
95	Impact of interventions on malaria in internally displaced persons along the Chinaâ€“Myanmar border: 2011â€“2014. Malaria Journal, 2016, 15, 471.	2.3	34
96	Genetic structures of geographically distinct Plasmodium vivax populations assessed by PCR/RFLP analysis of the merozoite surface protein 3Î² gene. Acta Tropica, 2006, 100, 205-212.	2.0	32
97	Nucleotide sequence polymorphism at the apical membrane antigen-1 locus reveals population history of Plasmodium vivax in Thailand. Infection, Genetics and Evolution, 2009, 9, 1295-1300.	2.3	32
98	In Vitro Sensitivities of Plasmodium falciparum Isolates from the China-Myanmar Border to Piperaquine and Association with Polymorphisms in Candidate Genes. Antimicrobial Agents and Chemotherapy, 2013, 57, 1723-1729.	3.2	32
99	A Flow Cytometry-Based Quantitative Drug Sensitivity Assay for All Plasmodium falciparum Gametocyte Stages. PLoS ONE, 2014, 9, e93825.	2.5	32
100	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
101	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
102	Mutually exclusive var gene expression in the malaria parasite: multiple layers of regulation. Trends in Parasitology, 2008, 24, 455-461.	3.3	31
103	Development of a colloidal gold-based lateral flow dipstick immunoassay for rapid qualitative and semi-quantitative analysis of artesunate and dihydroartemisinin. Malaria Journal, 2014, 13, 127.	2.3	31
104	Quantification of glucose-6-phosphate dehydrogenase activity by spectrophotometry: A systematic review and meta-analysis. PLoS Medicine, 2020, 17, e1003084.	8.4	31
105	Optimisation of an ELISA for the serodiagnosis of visceral leishmaniasis using in vitro derived promastigote antigens. Journal of Immunological Methods, 2001, 252, 105-119.	1.4	29
106	Clinical Malaria along the Chinaâ€“Myanmar Border, Yunnan Province, China, January 2011â€“August 2012. Emerging Infectious Diseases, 2014, 20, 681-684.	4.3	29
107	Clinical Efficacy of Dihydroartemisininâ€“Piperaquine for the Treatment of Uncomplicated Plasmodium falciparum Malaria at the Chinaâ€“Myanmar Border. American Journal of Tropical Medicine and Hygiene, 2015, 93, 577-583.	1.4	29
108	The RNA-binding protein PfPuf1 functions in the maintenance of gametocytes in Plasmodium falciparum. Journal of Cell Science, 2016, 129, 3144-52.	2.0	29

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109	Seasonal dynamics and microgeographical spatial heterogeneity of malaria along the Chinaâ€"Myanmar border. Acta Tropica, 2016, 157, 12-19.	2.0	29
110	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
111	Penetration of Steinernematid Nematodes (Nematoda: Steinernematidae) into Japanese Beetle Larvae, Popillia japonica (Coleoptera: Scarabaeidae). Journal of Invertebrate Pathology, 1993, 62, 73-78.	3.2	28
112	Characterization of PfPuf2, Member of the Puf Family RNA-Binding Proteins from the Malaria Parasite Plasmodium falciparum. DNA and Cell Biology, 2004, 23, 753-760.	1.9	28
113	Genetic diversity of Plasmodium vivax malaria in China and Myanmar. Infection, Genetics and Evolution, 2011, 11, 1419-1425.	2.3	28
114	Plasmodium malariae and Plasmodium ovale infections in the Chinaâ€"Myanmar border area. Malaria Journal, 2016, 15, 557.	2.3	28
115	Diversity and Phylogeny of <I>Wolbachia</I> Infecting <I>Bactrocera dorsalis</I> (Diptera: Tephritidae) Populations from China. Environmental Entomology, 2007, 36, 1283-1289.	1.4	27
116	Population dynamics and community structure of Anopheles mosquitoes along the China-Myanmar border. Parasites and Vectors, 2015, 8, 445.	2.5	27
117	Malaria Diagnosis Across the International Centers of Excellence for Malaria Research: Platforms, Performance, and Standardization. American Journal of Tropical Medicine and Hygiene, 2015, 93, 99-109.	1.4	27
118	The genome sequence of the multinucleocapsid nucleopolyhedrovirus of the Chinese oak silkworm Antheraea pernyi. Virology, 2007, 366, 304-315.	2.4	26
119	Identification of three ookinete-specific genes and evaluation of their transmission-blocking potentials in Plasmodium berghei. Vaccine, 2016, 34, 2570-2578.	3.8	26
120	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
121	Genetic diversity of Plasmodium falciparum populations in southeast and western Myanmar. Parasites and Vectors, 2017, 10, 322.	2.5	26
122	Genetic diversity of the Plasmodium vivax merozoite surface protein-5 locus from diverse geographic origins. Gene, 2010, 456, 24-35.	2.2	25
123	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
124	Plasmodium falciparum: Differential Display Analysis of Gene Expression during Gametocytogenesis. Experimental Parasitology, 2001, 99, 244-254.	1.2	24
125	Gene discovery in Plasmodium vivax through sequencing of ESTs from mixed blood stages. Molecular and Biochemical Parasitology, 2005, 144, 1-9.	1.1	24
126	Memory T cells protect against Plasmodium vivax infection. Microbes and Infection, 2006, 8, 680-686.	1.9	24

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127	Genetic diversity of transmission-blocking vaccine candidates Pvs25 and Pvs28 in Plasmodium vivax isolates from Yunnan Province, China. Parasites and Vectors, 2011, 4, 224.	2.5	24
128	Plasmodium falciparum multidrug resistance protein 1 (pfmrp1) gene and its association with in vitro drug susceptibility of parasite isolates from north-east Myanmar. Journal of Antimicrobial Chemotherapy, 2014, 69, 2110-2117.	3.0	24
129	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
130	Malaria and Hepatocystis species in wild macaques, southern Thailand. American Journal of Tropical Medicine and Hygiene, 2008, 78, 646-53.	1.4	24
131	Validating a Firefly Luciferase-Based High-Throughput Screening Assay for Antimalarial Drug Discovery. Assay and Drug Development Technologies, 2012, 10, 61-68.	1.2	23
132	Erythropoietin Protects against Murine Cerebral Malaria through Actions on Host Cellular Immunity. Infection and Immunity, 2014, 82, 165-173.	2.2	23
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	A novel multistage antiplasmodial inhibitor targeting Plasmodium falciparum histone deacetylase 1. Cell Discovery, 2020, 6, 93.	6.7	23
135	Population Genetics, Evolutionary Genomics, and Genome-Wide Studies of Malaria: A View Across the International Centers of Excellence for Malaria Research. American Journal of Tropical Medicine and Hygiene, 2015, 93, 87-98.	1.4	22
136	Artesunate and erythropoietin synergistically improve the outcome of experimental cerebral malaria. International Immunopharmacology, 2017, 48, 219-230.	3.8	22
137	Comparison of methods for detecting asymptomatic malaria infections in the Chinaâ€"Myanmar border area. Malaria Journal, 2017, 16, 159.	2.3	22
138	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
139	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
140	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
141	Multidrug-Resistant Genotypes ofPlasmodium falciparum, Myanmar. Emerging Infectious Diseases, 2011, 17, 498-501.	4.3	21
142	Limited genetic diversity in the PvK12 Kelch protein in Plasmodium vivax isolates from Southeast Asia. Malaria Journal, 2016, 15, 537.	2.3	21
143	Fitness Loss under Amino Acid Starvation in Artemisinin-Resistant Plasmodium falciparum Isolates from Cambodia. Scientific Reports, 2018, 8, 12622.	3.3	21
144	Evaluation of Plasmodium vivax HAP2 as a transmission-blocking vaccine candidate. Vaccine, 2020, 38, 2841-2848.	3.8	21

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145	Limited global diversity of the Plasmodium vivax merozoite surface protein 4 gene. Infection, Genetics and Evolution, 2009, 9, 821-826.	2.3	20
146	Molecular inference of sources and spreading patterns of Plasmodium falciparum malaria parasites in internally displaced persons settlements in Myanmarâ€"China border area. Infection, Genetics and Evolution, 2015, 33, 189-196.	2.3	20
147	In Vitro 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
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 Artemisia annua and Rat Serum. Analytical Chemistry, 2016, 88, 2701-2706.	6.5	20
150	Genetic diversity of the Plasmodium falciparum apical membrane antigen I gene in parasite population from the Chinaâ€"Myanmar border area. Infection, Genetics and Evolution, 2016, 39, 155-162.	2.3	20
151	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
152	Genetic Variations Associated with Drug Resistance Markers in Asymptomatic Plasmodium falciparum Infections in Myanmar. Genes, 2019, 10, 692.	2.4	20
153	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
154	Geographical heterogeneity in prevalence of subclinical malaria infections at sentinel endemic sites of Myanmar. Parasites and Vectors, 2019, 12, 83.	2.5	20
155	Immune responses in mice induced by prime-boost schemes of the Plasmodium falciparum apical membrane antigen 1 (PfAMA1)-based DNA, protein and recombinant modified vaccinia Ankara vaccines. Vaccine, 2006, 24, 6187-6198.	3.8	19
156	Sarcocystis cruzi: Comparative studies confirm natural infections of buffaloes. Experimental Parasitology, 2011, 127, 460-466.	1.2	19
157	Plasmodium vivax populations revisited: mitochondrial genomes of temperate strains in Asia suggest ancient population expansion. BMC Evolutionary Biology, 2012, 12, 22.	3.2	19
158	Arbitrarily Accessible 3D Microfluidic Device for Combinatorial High-Throughput Drug Screening. Sensors, 2016, 16, 1616.	3.8	19
159	Geometric morphometrics approach towards discrimination of three member species of Maculatus group in Thailand. Acta Tropica, 2019, 192, 66-74.	2.0	19
160	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
161	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
162	Novel Glycosidic Linkage in Aedes aegypti Chorion Peroxidase. Journal of Biological Chemistry, 2005, 280, 38513-38521.	3.4	18

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164	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
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