## Xin-zhuan Su

## List of Publications by Year in descending order

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		14655	15266
179	17,581	66	126
papers	citations	h-index	g-index
100	100	100	1222
182	182	182	12233
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Mutations in the P. falciparum Digestive Vacuole Transmembrane Protein PfCRT and Evidence for Their Role in Chloroquine Resistance. Molecular Cell, 2000, 6, 861-871.	9.7	1,268
2	The large diverse gene family var encodes proteins involved in cytoadherence and antigenic variation of plasmodium falciparum-infected erythrocytes. Cell, 1995, 82, 89-100.	28.9	1,143
3	A Molecular Marker for Chloroquine-Resistant Falciparum Malaria. New England Journal of Medicine, 2001, 344, 257-263.	27.0	873
4	Genetic diversity and chloroquine selective sweeps in Plasmodium falciparum. Nature, 2002, 418, 320-323.	27.8	663
5	Malaria biology and disease pathogenesis: insights for new treatments. Nature Medicine, 2013, 19, 156-167.	30.7	456
6	Analysis of Plasmodium falciparum diversity in natural infections by deep sequencing. Nature, 2012, 487, 375-379.	27.8	450
7	Multiple populations of artemisinin-resistant Plasmodium falciparum in Cambodia. Nature Genetics, 2013, 45, 648-655.	21.4	424
8	Early Origin and Recent Expansion of Plasmodium falciparum. Science, 2003, 300, 318-321.	12.6	365
9	Complex Polymorphisms in an $\hat{a}^{1}/4330$ kDa Protein Are Linked to Chloroquine-Resistant P. falciparum in Southeast Asia and Africa. Cell, 1997, 91, 593-603.	28.9	347
10	Transfection of Plasmodium falciparum within human red blood cells Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 973-977.	7.1	346
11	Artemisinin: Discovery from the Chinese Herbal Garden. Cell, 2011, 146, 855-858.	28.9	336
12	A Genetic Map and Recombination Parameters of the Human Malaria Parasite Plasmodium falciparum. Science, 1999, 286, 1351-1353.	12.6	326
13	Twelve microsatellite markers for characterization of Plasmodium falciparum from finger-prick blood samples. Parasitology, 1999, 119, 113-125.	1.5	320
14	Directional gene expression and antisense transcripts in sexual and asexual stages of Plasmodium falciparum. BMC Genomics, 2011, 12, 587.	2.8	309
15	Artemisinin-resistant Plasmodium falciparum in Pursat province, western Cambodia: a parasite clearance rate study. Lancet Infectious Diseases, The, 2012, 12, 851-858.	9.1	294
16	Discovery, mechanisms of action and combination therapy of artemisinin. Expert Review of Anti-Infective Therapy, 2009, 7, 999-1013.	4.4	283
17	Increased Tolerance to Artemisinin in <i>Plasmodium falciparum</i> Is Mediated by a Quiescence Mechanism. Antimicrobial Agents and Chemotherapy, 2010, 54, 1872-1877.	3.2	258
18	Genetic loci associated with delayed clearance of <i>Plasmodium falciparum</i> following artemisinin treatment in Southeast Asia. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 240-245.	7.1	242

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19	Multiple transporters associated with malaria parasite responses to chloroquine and quinine. Molecular Microbiology, 2003, 49, 977-989.	2.5	237
20	Alternative Mutations at Position 76 of the Vacuolar Transmembrane Protein PfCRT Are Associated with Chloroquine Resistance and Unique Stereospecific Quinine and Quinidine Responses inPlasmodium falciparum. Molecular Pharmacology, 2002, 61, 35-42.	2.3	222
21	Malaria in the Greater Mekong Subregion: Heterogeneity and complexity. Acta Tropica, 2012, 121, 227-239.	2.0	219
22	Dissecting the loci of low-level quinine resistance in malaria parasites. Molecular Microbiology, 2004, 52, 985-997.	2.5	215
23	Genome-wide variation and identification of vaccine targets in the Plasmodium falciparum genome. Nature Genetics, 2007, 39, 126-130.	21.4	212
24	Host Switch Leads to Emergence of Plasmodium vivax Malaria in Humans. Molecular Biology and Evolution, 2005, 22, 1686-1693.	8.9	199
25	Bone-Marrow-Resident NK Cells Prime Monocytes for Regulatory Function during Infection. Immunity, 2015, 42, 1130-1142.	14.3	199
26	The discovery of artemisinin and the Nobel Prize in Physiology or Medicine. Science China Life Sciences, 2015, 58, 1175-1179.	4.9	189
27	Indels, structural variation, and recombination drive genomic diversity in <i>Plasmodium falciparum</i> . Genome Research, 2016, 26, 1288-1299.	5.5	180
28	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
29	Recombination Hotspots and Population Structure in Plasmodium falciparum. PLoS Biology, 2005, 3, e335.	5.6	173
30	Toward a High-ResolutionPlasmodium falciparumLinkage Map: Polymorphic Markers from Hundreds of Simple Sequence Repeats. Genomics, 1996, 33, 430-444.	2.9	161
31	Global genetic diversity and evolution of var genes associated with placental and severe childhood malariaâ~†. Molecular and Biochemical Parasitology, 2006, 148, 169-180.	1.1	147
32	Chromosome-wide SNPs reveal an ancient origin for Plasmodium falciparum. Nature, 2002, 418, 323-324.	27.8	141
33	Chemical Genomic Profiling for Antimalarial Therapies, Response Signatures, and Molecular Targets. Science, 2011, 333, 724-729.	12.6	130
34	Disruption of a Plasmodium falciparum Multidrug Resistance-associated Protein (PfMRP) Alters Its Fitness and Transport of Antimalarial Drugs and Glutathione. Journal of Biological Chemistry, 2009, 284, 7687-7696.	3.4	122
35	Two cases of autochthonous Plasmodium falciparum malaria in Germany with evidence for local transmission by indigenous Anopheles plumbeus. Tropical Medicine and International Health, 2001, 6, 983-985.	2.3	121
36	Efficient Editing of Malaria Parasite Genome Using the CRISPR/Cas9 System. MBio, 2014, 5, e01414-14.	4.1	119

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37	Local Adaptation and Vector-Mediated Population Structure in Plasmodium vivax Malaria. Molecular Biology and Evolution, 2008, 25, 1245-1252.	8.9	115
38	Plasmodium falciparum Gametocyte Development 1 (Pfgdv1) and Gametocytogenesis Early Gene Identification and Commitment to Sexual Development. PLoS Pathogens, 2012, 8, e1002964.	4.7	115
39	PfGCN5-Mediated Histone H3 Acetylation Plays a Key Role in Gene Expression in Plasmodium falciparum. Eukaryotic Cell, 2007, 6, 1219-1227.	3.4	113
40	Structural polymorphism and diversifying selection on the pregnancy malaria vaccine candidate VAR2CSA. Molecular and Biochemical Parasitology, 2007, 155, 103-112.	1.1	111
41	Reduced extension temperatures required for PCR amplification of extremely A+T-rich DNA. Nucleic Acids Research, 1996, 24, 1574-1575.	14.5	108
42	Polymorphism in a Plasmodium falciparum Erythrocyte-binding Ligand Changes Its Receptor Specificity. Journal of Experimental Medicine, 2002, 196, 1523-1528.	8.5	105
43	Erythrocytic ferroportin reduces intracellular iron accumulation, hemolysis, and malaria risk. Science, 2018, 359, 1520-1523.	12.6	104
44	Histone Acetyltransferase Inhibitor Anacardic Acid Causes Changes in Global Gene Expression during In Vitro <i>Plasmodium falciparum</i> Development. Eukaryotic Cell, 2008, 7, 1200-1210.	3.4	101
45	Cross-Regulation of Two Type I Interferon Signaling Pathways in Plasmacytoid Dendritic Cells Controls Anti-malaria Immunity and Host Mortality. Immunity, 2016, 45, 1093-1107.	14.3	100
46	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
47	An open dataset of Plasmodium falciparum genome variation in 7,000 worldwide samples. Wellcome Open Research, 2021, 6, 42.	1.8	97
48	High-throughput matrix screening identifies synergistic and antagonistic antimalarial drug combinations. Scientific Reports, 2015, 5, 13891.	3.3	92
49	DECREASED PREVALENCE OF THE PLASMODIUM FALCIPARUM CHLOROQUINE RESISTANCE TRANSPORTER 76T MARKER ASSOCIATED WITH CESSATION OF CHLOROQUINE USE AGAINST P. FALCIPARUM MALARIA IN HAINAN, PEOPLE'S REPUBLIC OF CHINA. American Journal of Tropical Medicine and Hygiene, 2005, 72, 410-414.	1.4	92
50	Single-nucleotide polymorphisms and genome diversity inPlasmodium vivax. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 8502-8507.	7.1	91
51	Polymorphism in the Plasmodium falciparum erythrocyte-binding ligand JESEBL/EBA-181 alters its receptor specificity. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 2518-2523.	7.1	91
52	Mutations in transmembrane domains 1, 4 and 9 of the Plasmodium falciparum chloroquine resistance transporter alter susceptibility to chloroquine, quinine and quinidine. Molecular Microbiology, 2007, 63, 270-282.	2.5	87
53	Identification of a subtelomeric gene family expressed during the asexual–sexual stage transition in Plasmodium falciparum. Molecular and Biochemical Parasitology, 2005, 143, 90-99.	1.1	84
54	Population structure of the genes encoding the polymorphic <i>Plasmodium falciparum</i> apical membrane antigen 1: Implications for vaccine design. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 7857-7862.	7.1	83

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55	Mechanisms of <i>in vitro</i> resistance to dihydroartemisinin in <i>Plasmodium falciparum</i> Molecular Microbiology, 2012, 86, 111-128.	2.5	83
56	A Specific Inhibitor of PfCDPK4 Blocks Malaria Transmission: Chemical-genetic Validation. Journal of Infectious Diseases, 2014, 209, 275-284.	4.0	83
57	Artemisinin and its derivatives in treating protozoan infections beyond malaria. Pharmacological Research, 2017, 117, 192-217.	7.1	82
58	Genetic linkage and association analyses for trait mapping in Plasmodium falciparum. Nature Reviews Genetics, 2007, 8, 497-506.	16.3	80
59	High recombination rates and hotspots in a Plasmodium falciparum genetic cross. Genome Biology, 2011, 12, R33.	8.8	80
60	Allelic modifications of the cg2 and cg1 genes do not alter the chloroquine response of drug-resistant Plasmodium falciparum. Molecular and Biochemical Parasitology, 2000, 110, 1-10.	1.1	77
61	Strain-specific innate immune signaling pathways determine malaria parasitemia dynamics and host mortality. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E511-20.	7.1	74
62	Gene structure and expression of a Plasmodium falciparum 220-kDa protein homologous to the Plasmodium vivax reticulocyte binding proteins. Molecular and Biochemical Parasitology, 2002, 121, 275-278.	1.1	73
63	pfcrtPolymorphism and the Spread of Chloroquine Resistance inPlasmodium falciparumPopulations across the Amazon Basin. Journal of Infectious Diseases, 2004, 190, 417-424.	4.0	<b>7</b> 3
64	Disruption of a Plasmodium falciparum gene linked to male sexual development causes early arrest in gametocytogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 16813-16818.	7.1	73
65	Complex mutations in a high proportion of microsatellite loci from the protozoan parasitePlasmodium falciparum. Molecular Ecology, 2000, 9, 1599-1608.	3.9	71
66	Genome-Wide Compensatory Changes Accompany Drug- Selected Mutations in the Plasmodium falciparum crt Gene. PLoS ONE, 2008, 3, e2484.	2.5	70
67	Decreased prevalence of the Plasmodium falciparum chloroquine resistance transporter 76T marker associated with cessation of chloroquine use against P. falciparum malaria in Hainan, People's Republic of China. American Journal of Tropical Medicine and Hygiene, 2005, 72, 410-4.	1.4	70
68	Angiogenesis inhibitors specific for methionine aminopeptidase 2 as drugs for Malaria and Leishmaniasis. Journal of Biomedical Science, 2002, 9, 34-40.	7.0	69
69	Systematic CRISPR-Cas9-Mediated Modifications of <i>Plasmodium yoelii</i> ApiAP2 Genes Reveal Functional Insights into Parasite Development. MBio, 2017, 8, .	4.1	66
70	<i>Plasmodium</i> Genomics and Genetics: New Insights into Malaria Pathogenesis, Drug Resistance, Epidemiology, and Evolution. Clinical Microbiology Reviews, 2019, 32, .	13.6	65
71	Upregulation of expression of the reticulocyte homology gene 4 in the Plasmodium falciparum clone Dd2 is associated with a switch in the erythrocyte invasion pathway. Molecular and Biochemical Parasitology, 2006, 145, 205-215.	1.1	63
72	Population Genetic Analysis of Plasmodium falciparum Parasites Using a Customized Illumina GoldenGate Genotyping Assay. PLoS ONE, 2011, 6, e20251.	2.5	63

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73	Lack of allele-specific efficacy of a bivalent AMA1 malaria vaccine. Malaria Journal, 2010, 9, 175.	2.3	61
74	Genetic mapping of targets mediating differential chemical phenotypes in Plasmodium falciparum. Nature Chemical Biology, 2009, 5, 765-771.	8.0	59
75	Drug resistance and genetic mapping in PlasmodiumÂfalciparum. Current Genetics, 2008, 54, 223-239.	1.7	56
76	Current status of the Plasmodium falciparum genome project. Molecular and Biochemical Parasitology, 1996, 79, 1-12.	1.1	55
77	Detection of genome-wide polymorphisms in the AT-rich Plasmodium falciparum genome using a high-density microarray. BMC Genomics, 2008, 9, 398.	2.8	54
78	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
79	ISP1-Anchored Polarization of $GC\hat{l}^2/CDC50A$ Complex Initiates Malaria Ookinete Gliding Motility. Current Biology, 2018, 28, 2763-2776.e6.	3.9	54
80	Diversity-Oriented Synthesis Yields a Novel Lead for the Treatment of Malaria. ACS Medicinal Chemistry Letters, 2012, 3, 112-117.	2.8	52
81	An open dataset of Plasmodium falciparum genome variation in 7,000 worldwide samples. Wellcome Open Research, 2021, 6, 42.	1.8	51
82	cDNA sequences reveal considerable gene prediction inaccuracy in the Plasmodium falciparum genome. BMC Genomics, 2007, 8, 255.	2.8	50
83	Cloning and expression of complementary DNA encoding an antigen of Trichinella spiralis. Molecular and Biochemical Parasitology, 1991, 45, 331-336.	1.1	49
84	Genomeâ€wide profiling of chromosome interactions in <i><scp>P</scp>lasmodium falciparum</i> characterizes nuclear architecture and reconfigurations associated with antigenic variation. Molecular Microbiology, 2013, 90, 519-537.	2.5	48
85	CRISPR/Cas9 mediated sequential editing of genes critical for ookinete motility in Plasmodium yoelii. Molecular and Biochemical Parasitology, 2017, 212, 1-8.	1.1	47
86	Inflammasome activation negatively regulates MyD88-IRF7 type I IFN signaling and anti-malaria immunity. Nature Communications, 2018, 9, 4964.	12.8	46
87	Artemisinin resistance phenotypes and K13 inheritance in a <i>Plasmodium falciparum</i> cross and <i>Aotus</i> model. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 12513-12518.	7.1	46
88	Changes in the Plasmodial Surface Anion Channel Reduce Leupeptin Uptake and Can Confer Drug Resistance in <i>Plasmodium falciparum</i> -Infected Erythrocytes. Antimicrobial Agents and Chemotherapy, 2008, 52, 2346-2354.	3.2	45
89	Linkage maps from multiple genetic crosses and loci linked to growth-related virulent phenotype in Plasmodium yoelii. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E374-E382.	7.1	45
90	Plasmodium falciparum:Parasite Typing by Using a Multicopy Microsatellite Marker, PfRRM. Experimental Parasitology, 1998, 89, 262-265.	1.2	43

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91	Sequence, transcript characterization and polymorphisms of a Plasmodium falciparum gene belonging to the heat-shock protein (HSP) 90 family. Gene, 1994, 151, 225-230.	2.2	42
92	Diversity and evolution of the rhoph $1/c$ lag multigene family of Plasmodium falciparum. Molecular and Biochemical Parasitology, 2008, 158, 11-21.	1.1	42
93	Discovery of new antimalarial chemotypes through chemical methodology and library development. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 6775-6780.	7.1	42
94	Challenges and prospects for malaria elimination in the Greater Mekong Subregion. Acta Tropica, 2012, 121, 240-245.	2.0	42
95	Effects of Plasmodium falciparum Mixed Infections on In Vitro Antimalarial Drug Tests and Genotyping. American Journal of Tropical Medicine and Hygiene, 2008, 79, 178-184.	1.4	42
96	Host-Malaria Parasite Interactions and Impacts on Mutual Evolution. Frontiers in Cellular and Infection Microbiology, 2020, 10, 587933.	3.9	41
97	Large-scale Artemisinin–Piperaquine Mass Drug Administration With or Without Primaquine Dramatically Reduces Malaria in a Highly Endemic Region of Africa. Clinical Infectious Diseases, 2018, 67, 1670-1676.	5.8	39
98	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
99	FOSL1 Inhibits Type I Interferon Responses to Malaria and Viral Infections by Blocking TBK1 and TRAF3/TRIF Interactions. MBio, 2017, 8, .	4.1	38
100	Melaleuca alternifolia (tea tree) oil and its monoterpene constituents in treating protozoan and helminthic infections. Biomedicine and Pharmacotherapy, 2020, 130, 110624.	5.6	38
101	The roles of galectins in parasitic infections. Acta Tropica, 2018, 177, 97-104.	2.0	38
102	Plasmodium falciparum:Isolation of Large Numbers of Parasite Clones from Infected Blood Samples. Experimental Parasitology, 1996, 83, 147-149.	1.2	37
103	Genetic mapping in the human malaria parasite Plasmodium falciparum. Molecular Microbiology, 2004, 53, 1573-1582.	2.5	36
104	Leveraging crowdsourcing to accelerate global health solutions. Nature Biotechnology, 2019, 37, 848-850.	17.5	36
105	<i>Ex Vivo</i> Susceptibility of Plasmodium falciparum to Antimalarial Drugs in Western, Northern, and Eastern Cambodia, 2011-2012: Association with Molecular Markers. Antimicrobial Agents and Chemotherapy, 2013, 57, 5277-5283.	3.2	34
106	An intracellular membrane protein GEP1 regulates xanthurenic acid induced gametogenesis of malaria parasites. Nature Communications, 2020, 11, 1764.	12.8	34
107	Artemisinin and its derivatives in treating helminthic infections beyond schistosomiasis. Pharmacological Research, 2018, 133, 77-100.	7.1	33
108	Effects of Plasmodium falciparum mixed infections on in vitro antimalarial drug tests and genotyping. American Journal of Tropical Medicine and Hygiene, 2008, 79, 178-84.	1.4	33

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109	Ambient glucose concentration and gene expression in Plasmodium falciparum. Molecular and Biochemical Parasitology, 2004, 133, 125-129.	1.1	32
110	A Class of Tricyclic Compounds Blocking Malaria Parasite Oocyst Development and Transmission. Antimicrobial Agents and Chemotherapy, 2013, 57, 425-435.	3.2	32
111	The "Malaria's Eve―hypothesis and the debate concerning the origin of the human malaria parasite Plasmodium falciparum. Microbes and Infection, 2003, 5, 891-896.	1.9	31
112	RTP4 inhibits IFN-I response and enhances experimental cerebral malaria and neuropathology. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 19465-19474.	7.1	31
113	Actinoramide A Identified as a Potent Antimalarial from Titration-Based Screening of Marine Natural Product Extracts. Journal of Natural Products, 2015, 78, 2411-2422.	3.0	30
114	Polymorphisms of the artemisinin resistant marker (K13) in Plasmodium falciparum parasite populations of Grande Comore Island 10Âyears after artemisinin combination therapy. Parasites and Vectors, 2015, 8, 634.	2.5	29
115	Increased CD40 Expression Enhances Early STING-Mediated Type I Interferon Response and Host Survival in a Rodent Malaria Model. PLoS Pathogens, 2016, 12, e1005930.	4.7	29
116	Type I Interferons and Malaria: A Double-Edge Sword Against a Complex Parasitic Disease. Frontiers in Cellular and Infection Microbiology, 2020, 10, 594621.	3.9	29
117	P. falciparum CG2, Linked to Chloroquine Resistance, Does Not Resemble Na+/H+ Exchangers. Cell, 1998, 94, 285-286.	28.9	27
118	The E3 ubiquitin ligase MARCH1 regulates antimalaria immunity through interferon signaling and T cell activation. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 16567-16578.	7.1	26
119	Molecular surveillance of pvdhfr, pvdhps, and pvmdr-1 mutations in Plasmodium vivax isolates from Yunnan and Anhui provinces of China. Malaria Journal, 2014, 13, 346.	2.3	25
120	Peripheral blood stem cell transplant–related <i>Plasmodium falciparum</i> infection in a patient with sickle cell disease. Transfusion, 2012, 52, 2677-2682.	1.6	23
121	The Gametocytes of Leucocytozoon sabrazesi Infect Chicken Thrombocytes, Not Other Blood Cells. PLoS ONE, 2015, 10, e0133478.	2.5	22
122	Malaria: Therapy, Genes and Vaccines. Current Molecular Medicine, 2006, 6, 309-326.	1.3	21
123	Molecular and epidemiological characterization of Plasmodium vivax recurrent infections in southern Mexico. Parasites and Vectors, 2013, 6, 109.	2.5	21
124	Genome-wide Analysis of Host-Plasmodium yoelii Interactions Reveals Regulators of the Type I Interferon Response. Cell Reports, 2015, 12, 661-672.	6.4	21
125	Typing Plasmodium yoelii microsatellites using a simple and affordable fluorescent labeling method. Molecular and Biochemical Parasitology, 2007, 155, 94-102.	1.1	20
126	Prevalence of crt and mdr-1 mutations in Plasmodium falciparum isolates from Grande Comore island after withdrawal of chloroquine. Malaria Journal, 2016, 15, 414.	2.3	20

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127	â€~Artemisinin Resistance': Something New or Old? Something of a Misnomer?. Trends in Parasitology, 2020, 36, 735-744.	3.3	20
128	Recent Progress in Functional Genomic Research in Plasmodium falciparum. Current Genomics, 2010, 11, 279-286.	1.6	19
129	Effect of PCR extension temperature on high-throughput sequencing. Molecular and Biochemical Parasitology, 2011, 176, 64-67.	1.1	19
130	Genetic diversity of Plasmodium vivax population in Anhui province of China. Malaria Journal, 2014, 13, 13.	2.3	19
131	Mechanism of splenic cell death and host mortality in a Plasmodium yoelii malaria model. Scientific Reports, 2017, 7, 10438.	3.3	19
132	CD4+ T-Cell Response to Mitochondrial Cytochrome b in Human Melanoma. Cancer Research, 2006, 66, 5919-5926.	0.9	18
133	A Plasmodium yoelii HECT-like E3 ubiquitin ligase regulates parasite growth and virulence. Nature Communications, 2017, 8, 223.	12.8	18
134	Anti-Pfs25 Human Plasma Reduces Transmission of Plasmodium falciparum Isolates That Have Diverse Genetic Backgrounds. Infection and Immunity, 2013, 81, 1984-1989.	2.2	17
135	Blockage of Galectin-receptor Interactions by $\hat{l}_{\pm}$ -lactose Exacerbates Plasmodium berghei-induced Pulmonary Immunopathology. Scientific Reports, 2016, 6, 32024.	3.3	17
136	A Cas9 transgenic Plasmodium yoelii parasite for efficient gene editing. Molecular and Biochemical Parasitology, 2018, 222, 21-28.	1.1	16
137	PfCRT and PfMDR1 modulate interactions of artemisinin derivatives and ion channel blockers. Scientific Reports, 2016, 6, 25379.	3.3	15
138	Detection of host pathways universally inhibited after Plasmodium yoelii infection for immune intervention. Scientific Reports, 2018, 8, 15280.	3.3	15
139	Temporal changes in genetic diversity of msp-1, msp-2, and msp-3 in Plasmodium falciparum isolates from Grande Comore Island after introduction of ACT. Malaria Journal, 2018, 17, 83.	2.3	15
140	Plasmodium falciparum:Assignment of Microsatellite Markers to Chromosomes by PFG–PCR. Experimental Parasitology, 1999, 91, 367-369.	1.2	14
141	Genome projects, genetic analysis, and the changing landscape of malaria research. Current Opinion in Microbiology, 1999, 2, 415-419.	5.1	14
142	Hundreds of microsatellites for genotyping Plasmodium yoelii parasites. Molecular and Biochemical Parasitology, 2009, 166, 153-158.	1.1	14
143	Expression of Tim-1 and Tim-3 in Plasmodium berghei ANKA infection. Parasitology Research, 2013, 112, 2713-2719.	1.6	14
144	Plasmodium falciparum: A Rapid DNA Fingerprinting Method Using Microsatellite Sequences withinvarClusters. Experimental Parasitology, 1997, 86, 235-236.	1.2	13

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145	Human Malaria Parasites: Are We Ready for a New Species?. Journal of Infectious Diseases, 2010, 201, 1453-1454.	4.0	13
146	Identification and characterisation of functional expressed sequence tags-derived simple sequence repeat (eSSR) markers for genetic linkage mapping of Schistosoma mansoni juvenile resistance and susceptibility loci in Biomphalaria glabrata. International Journal for Parasitology, 2013, 43, 669-677.	3.1	13
147	UTR introns, antisense RNA and differentially spliced transcripts between Plasmodium yoelii subspecies. Malaria Journal, 2016, 15, 30.	2.3	13
148	Plasmodium yoelii Erythrocyte-Binding-like Protein Modulates Host Cell Membrane Structure, Immunity, and Disease Severity. MBio, 2020, $11$ , .	4.1	13
149	Molecular characterization of Plasmodium falciparum S-adenosylmethionine synthetase. Biochemical Journal, 1999, 344, 571.	3.7	11
150	Genetic Diversity and Lack of Artemisinin Selection Signature on the Plasmodium falciparum ATP6 in the Greater Mekong Subregion. PLoS ONE, 2013, 8, e59192.	2.5	11
151	Regulation of Plasmodium yoelii Oocyst Development by Strain- and Stage-Specific Small-Subunit rRNA. MBio, 2015, 6, e00117.	4.1	11
152	Activation of cGAS TING by Lethal Malaria N67C Dictates Immunity and Mortality through Induction of CD11b <sup>+</sup> Ly6C <sup>hi</sup> Proinflammatory Monocytes. Advanced Science, 2022, 9, .	11.2	11
153	Isolation of Trichinella-Specific Antigens for Diagnosis by Gradient Monoclonal Antibody Affinity Chromatography. Journal of Parasitology, 1990, 76, 842.	0.7	10
154	Large-scale Genotyping and Genetic Mapping in Plasmodium Parasites. Korean Journal of Parasitology, 2009, 47, 83.	1.3	10
155	Monoclonal Antibodies to Porcine Tumor Necrosis Factor Alpha: Development of an Enzyme-Linked Immunosorbent Assay. Journal of Immunoassay, 1992, 13, 253-272.	0.3	9
156	Use of magnetically purified Plasmodium falciparum parasites improves the accuracy of erythrocyte invasion assays. Experimental Parasitology, 2010, 126, 278-280.	1.2	9
157	Macrophage migration inhibitory factor homolog from Plasmodium yoelii modulates monocyte recruitment and activation in spleen during infection. Parasitology Research, 2012, 110, 1755-1763.	1.6	9
158	Generation and functional characterisation of Plasmodium yoelii csp deletion mutants using a microhomology-based CRISPR/Cas9 method. International Journal for Parasitology, 2019, 49, 705-714.	3.1	9
159	Genetic diversity and population history of Plasmodium falciparum and Plasmodium vivax. Parassitologia, 2006, 48, 561-6.	0.5	9
160	Optimized protocols for improving the likelihood of cloning recombinant progeny from Plasmodium yoelii genetic crosses. Experimental Parasitology, 2013, 133, 44-50.	1.2	8
161	Genome-wide polymorphisms and development of a microarray platform to detect genetic variations in Plasmodium yoelii. Molecular and Biochemical Parasitology, 2014, 194, 9-15.	1.1	8
162	Monitoring the Prevalence of Leucocytozoon sabrazesi in Southern China and Testing Tricyclic Compounds against Gametocytes. PLoS ONE, 2016, 11, e0161869.	2.5	8

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163	Tracing the geographic origins of Plasmodium falciparummalaria parasites. Pathogens and Global Health, 2014, 108, 261-262.	2.3	7
164	Genome sequence, transcriptome, and annotation of rodent malaria parasite Plasmodium yoelii nigeriensis N67. BMC Genomics, 2021, 22, 303.	2.8	7
165	Protocol for Production of a Genetic Cross of the Rodent Malaria Parasites. Journal of Visualized Experiments, 2011, , .	0.3	6
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