

# Xin-zhuan Su

## List of Publications by Year in descending order

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179  
papers

17,581  
citations

14655

66  
h-index

15266

126  
g-index

182  
all docs

182  
docs citations

182  
times ranked

12233  
citing authors

#	ARTICLE	IF	CITATIONS
1	Activation of cGAS- $\text{STING}$ by Lethal Malaria N67C Dictates Immunity and Mortality through Induction of CD11b <sup>+</sup> Ly6C <sup>hi</sup> Proinflammatory Monocytes. <i>Advanced Science</i> , 2022, 9, .	11.2	11
2	An open dataset of <i>Plasmodium falciparum</i> genome variation in 7,000 worldwide samples. <i>Wellcome Open Research</i> , 2021, 6, 42.	1.8	97
3	Genome sequence, transcriptome, and annotation of rodent malaria parasite <i>Plasmodium yoelii nigeriensis</i> N67. <i>BMC Genomics</i> , 2021, 22, 303.	2.8	7
4	An open dataset of <i>Plasmodium falciparum</i> genome variation in 7,000 worldwide samples. <i>Wellcome Open Research</i> , 2021, 6, 42.	1.8	51
5	Zoonotic Transmission and Host Switches of Malaria Parasites. <i>Zoonoses</i> , 2021, 1, .	1.1	6
6	Melaleuca alternifolia (tea tree) oil and its monoterpene constituents in treating protozoan and helminthic infections. <i>Biomedicine and Pharmacotherapy</i> , 2020, 130, 110624.	5.6	38
7	Type I Interferons and Malaria: A Double-Edge Sword Against a Complex Parasitic Disease. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 594621.	3.9	29
8	Host-Malaria Parasite Interactions and Impacts on Mutual Evolution. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 587933.	3.9	41
9	RTP4 inhibits IFN-I response and enhances experimental cerebral malaria and neuropathology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 19465-19474.	7.1	31
10	The Roles of Type I Interferon in Co-infections With Parasites and Viruses, Bacteria, or Other Parasites. <i>Frontiers in Immunology</i> , 2020, 11, 1805.	4.8	4
11	The E3 ubiquitin ligase MARCH1 regulates antimalaria immunity through interferon signaling and T cell activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 16567-16578.	7.1	26
12	Artemisinin Resistance <sup>TM</sup> : Something New or Old? Something of a Misnomer?. <i>Trends in Parasitology</i> , 2020, 36, 735-744.	3.3	20
13	An intracellular membrane protein <i>GEP1</i> regulates xanthurenic acid induced gametogenesis of malaria parasites. <i>Nature Communications</i> , 2020, 11, 1764.	12.8	34
14	<i>Plasmodium yoelii</i> Erythrocyte-Binding-like Protein Modulates Host Cell Membrane Structure, Immunity, and Disease Severity. <i>MBio</i> , 2020, 11, .	4.1	13
15	<i>Plasmodium</i> Genomics and Genetics: New Insights into Malaria Pathogenesis, Drug Resistance, Epidemiology, and Evolution. <i>Clinical Microbiology Reviews</i> , 2019, 32, .	13.6	65
16	Leveraging crowdsourcing to accelerate global health solutions. <i>Nature Biotechnology</i> , 2019, 37, 848-850.	17.5	36
17	Generation and functional characterisation of <i>Plasmodium yoelii</i> <i>csp</i> deletion mutants using a microhomology-based CRISPR/Cas9 method. <i>International Journal for Parasitology</i> , 2019, 49, 705-714.	3.1	9
18	Artemisinin and its derivatives in treating helminthic infections beyond schistosomiasis. <i>Pharmacological Research</i> , 2018, 133, 77-100.	7.1	33

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19	A Cas9 transgenic <i>Plasmodium yoelii</i> parasite for efficient gene editing. <i>Molecular and Biochemical Parasitology</i> , 2018, 222, 21-28.	1.1	16
20	Erythrocytic ferroportin reduces intracellular iron accumulation, hemolysis, and malaria risk. <i>Science</i> , 2018, 359, 1520-1523.	12.6	104
21	Inflammasome activation negatively regulates MyD88-IRF7 type I IFN signaling and anti-malaria immunity. <i>Nature Communications</i> , 2018, 9, 4964.	12.8	46
22	Artemisinin resistance phenotypes and K13 inheritance in a <i>Plasmodium falciparum</i> cross and <i>Aotus</i> model. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12513-12518.	7.1	46
23	Detection of host pathways universally inhibited after <i>Plasmodium yoelii</i> infection for immune intervention. <i>Scientific Reports</i> , 2018, 8, 15280.	3.3	15
24	ISP1-Anchored Polarization of GCÎ²/CDC50A Complex Initiates Malaria Ookinete Gliding Motility. <i>Current Biology</i> , 2018, 28, 2763-2776.e6.	3.9	54
25	Temporal changes in genetic diversity of msp-1, msp-2, and msp-3 in <i>Plasmodium falciparum</i> isolates from Grande Comore Island after introduction of ACT. <i>Malaria Journal</i> , 2018, 17, 83.	2.3	15
26	Large-scale Artemisinin+Piperaquine Mass Drug Administration With or Without Primaquine Dramatically Reduces Malaria in a Highly Endemic Region of Africa. <i>Clinical Infectious Diseases</i> , 2018, 67, 1670-1676.	5.8	39
27	The roles of galectins in parasitic infections. <i>Acta Tropica</i> , 2018, 177, 97-104.	2.0	38
28	CRISPR/Cas9 mediated sequential editing of genes critical for ookinete motility in <i>Plasmodium yoelii</i> . <i>Molecular and Biochemical Parasitology</i> , 2017, 212, 1-8.	1.1	47
29	FOSL1 Inhibits Type I Interferon Responses to Malaria and Viral Infections by Blocking TBK1 and TRAF3/TRIF Interactions. <i>MBio</i> , 2017, 8, .	4.1	38
30	A <i>Plasmodium yoelii</i> HECT-like E3 ubiquitin ligase regulates parasite growth and virulence. <i>Nature Communications</i> , 2017, 8, 223.	12.8	18
31	Reflections on the publication of artemisinin chemical structure 40 years ago. <i>Science Bulletin</i> , 2017, 62, 1171-1172.	9.0	0
32	Mechanism of splenic cell death and host mortality in a <i>Plasmodium yoelii</i> malaria model. <i>Scientific Reports</i> , 2017, 7, 10438.	3.3	19
33	Systematic CRISPR-Cas9-Mediated Modifications of <i>Plasmodium yoelii</i> ApiAP2 Genes Reveal Functional Insights into Parasite Development. <i>MBio</i> , 2017, 8, .	4.1	66
34	Artemisinin and its derivatives in treating protozoan infections beyond malaria. <i>Pharmacological Research</i> , 2017, 117, 192-217.	7.1	82
35	Increased CD40 Expression Enhances Early STING-Mediated Type I Interferon Response and Host Survival in a Rodent Malaria Model. <i>PLoS Pathogens</i> , 2016, 12, e1005930.	4.7	29
36	Monitoring the Prevalence of <i>Leucocytozoon sabraezesi</i> in Southern China and Testing Tricyclic Compounds against Gametocytes. <i>PLoS ONE</i> , 2016, 11, e0161869.	2.5	8

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37	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
38	Indels, structural variation, and recombination drive genomic diversity in <i>Plasmodium falciparum</i> . Genome Research, 2016, 26, 1288-1299.	5.5	180
39	PfCRT and PfMDR1 modulate interactions of artemisinin derivatives and ion channel blockers. Scientific Reports, 2016, 6, 25379.	3.3	15
40	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
41	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
42	Blockage of Galectin-receptor Interactions by $\beta$ -lactose Exacerbates Plasmodium berghei-induced Pulmonary Immunopathology. Scientific Reports, 2016, 6, 32024.	3.3	17
43	UTR introns, antisense RNA and differentially spliced transcripts between Plasmodium yoelii subspecies. Malaria Journal, 2016, 15, 30.	2.3	13
44	High-throughput matrix screening identifies synergistic and antagonistic antimalarial drug combinations. Scientific Reports, 2015, 5, 13891.	3.3	92
45	Polymorphisms of the artemisinin resistant marker (K13) in Plasmodium falciparum parasite populations of Grande Comore Island 10 years after artemisinin combination therapy. Parasites and Vectors, 2015, 8, 634.	2.5	29
46	Bone-Marrow-Resident NK Cells Prime Monocytes for Regulatory Function during Infection. Immunity, 2015, 42, 1130-1142.	14.3	199
47	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
48	The discovery of artemisinin and the Nobel Prize in Physiology or Medicine. Science China Life Sciences, 2015, 58, 1175-1179.	4.9	189
49	Regulation of Plasmodium yoelii Oocyst Development by Strain- and Stage-Specific Small-Subunit rRNA. MBio, 2015, 6, e00117.	4.1	11
50	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
51	The Gametocytes of Leucocytozoon sabraezesi Infect Chicken Thrombocytes, Not Other Blood Cells. PLoS ONE, 2015, 10, e0133478.	2.5	22
52	Translating Basic Research into Clinical Applications: Malaria Research at an NIH Lab. PLoS Pathogens, 2015, 11, e1005190.	4.7	0
53	Multi-Strain Infections and $\beta$ -Relapse <sup>TM</sup> of Leucocytozoon sabraezesi Gametocytes in Domestic Chickens in Southern China. PLoS ONE, 2014, 9, e94877.	2.5	6
54	Drug-Resistant Falciparum Malaria: Mechanisms, Consequences, and Challenges. , 2014, , 401-413.		2

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55	Tracing the geographic origins of <i>Plasmodium falciparum</i> malaria parasites. <i>Pathogens and Global Health</i> , 2014, 108, 261-262.	2.3	7
56	Molecular surveillance of <i>pvdhfr</i> , <i>pvdhps</i> , and <i>pvm-dr-1</i> mutations in <i>Plasmodium vivax</i> isolates from Yunnan and Anhui provinces of China. <i>Malaria Journal</i> , 2014, 13, 346.	2.3	25
57	Strain-specific innate immune signaling pathways determine malaria parasitemia dynamics and host mortality. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E511-20.	7.1	74
58	Genome-wide polymorphisms and development of a microarray platform to detect genetic variations in <i>Plasmodium yoelii</i> . <i>Molecular and Biochemical Parasitology</i> , 2014, 194, 9-15.	1.1	8
59	Genetic diversity of <i>Plasmodium vivax</i> population in Anhui province of China. <i>Malaria Journal</i> , 2014, 13, 13.	2.3	19
60	A Specific Inhibitor of PfCDPK4 Blocks Malaria Transmission: Chemical-genetic Validation. <i>Journal of Infectious Diseases</i> , 2014, 209, 275-284.	4.0	83
61	Efficient Editing of Malaria Parasite Genome Using the CRISPR/Cas9 System. <i>MBio</i> , 2014, 5, e01414-14.	4.1	119
62	Molecular and epidemiological characterization of <i>Plasmodium vivax</i> recurrent infections in southern Mexico. <i>Parasites and Vectors</i> , 2013, 6, 109.	2.5	21
63	Identification and characterisation of functional expressed sequence tags-derived simple sequence repeat (eSSR) markers for genetic linkage mapping of <i>Schistosoma mansoni</i> juvenile resistance and susceptibility loci in <i>Biomphalaria glabrata</i> . <i>International Journal for Parasitology</i> , 2013, 43, 669-677.	3.1	13
64	Expression of Tim-1 and Tim-3 in <i>Plasmodium berghei</i> ANKA infection. <i>Parasitology Research</i> , 2013, 112, 2713-2719.	1.6	14
65	Genetic loci associated with delayed clearance of <i>Plasmodium falciparum</i> following artemisinin treatment in Southeast Asia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 240-245.	7.1	242
66	Optimized protocols for improving the likelihood of cloning recombinant progeny from <i>Plasmodium yoelii</i> genetic crosses. <i>Experimental Parasitology</i> , 2013, 133, 44-50.	1.2	8
67	Chemical genomics for studying parasite gene function and interaction. <i>Trends in Parasitology</i> , 2013, 29, 603-611.	3.3	4
68	Malaria biology and disease pathogenesis: insights for new treatments. <i>Nature Medicine</i> , 2013, 19, 156-167.	30.7	456
69	Multiple populations of artemisinin-resistant <i>Plasmodium falciparum</i> in Cambodia. <i>Nature Genetics</i> , 2013, 45, 648-655.	21.4	424
70	<i>Ex Vivo</i> Susceptibility of <i>Plasmodium falciparum</i> to Antimalarial Drugs in Western, Northern, and Eastern Cambodia, 2011-2012: Association with Molecular Markers. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 5277-5283.	3.2	34
71	A Class of Tricyclic Compounds Blocking Malaria Parasite Oocyst Development and Transmission. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 425-435.	3.2	32
72	Anti-Pf25 Human Plasma Reduces Transmission of <i>Plasmodium falciparum</i> Isolates That Have Diverse Genetic Backgrounds. <i>Infection and Immunity</i> , 2013, 81, 1984-1989.	2.2	17

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73	Genome-wide profiling of chromosome interactions in <i>Plasmodium falciparum</i> characterizes nuclear architecture and reconfigurations associated with antigenic variation. <i>Molecular Microbiology</i> , 2013, 90, 519-537.	2.5	48
74	Genetic Diversity and Lack of Artemisinin Selection Signature on the <i>Plasmodium falciparum</i> ATP6 in the Greater Mekong Subregion. <i>PLoS ONE</i> , 2013, 8, e59192.	2.5	11
75	<i>Plasmodium falciparum</i> Gametocyte Development 1 (Pfgdv1) and Gametocytogenesis Early Gene Identification and Commitment to Sexual Development. <i>PLoS Pathogens</i> , 2012, 8, e1002964.	4.7	115
76	Lack of Association of the S769N Mutation in <i>Plasmodium falciparum</i> SERCA (PfATP6) with Resistance to Artemisinins. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 2546-2552.	3.2	38
77	Mechanisms of <i>in vitro</i> resistance to dihydroartemisinin in <i>Plasmodium falciparum</i> . <i>Molecular Microbiology</i> , 2012, 86, 111-128.	2.5	83
78	Artemisinin-resistant <i>Plasmodium falciparum</i> in Pursat province, western Cambodia: a parasite clearance rate study. <i>Lancet Infectious Diseases</i> , The, 2012, 12, 851-858.	9.1	294
79	Malaria in the Greater Mekong Subregion: Heterogeneity and complexity. <i>Acta Tropica</i> , 2012, 121, 227-239.	2.0	219
80	Challenges and prospects for malaria elimination in the Greater Mekong Subregion. <i>Acta Tropica</i> , 2012, 121, 240-245.	2.0	42
81	Analysis of <i>Plasmodium falciparum</i> diversity in natural infections by deep sequencing. <i>Nature</i> , 2012, 487, 375-379.	27.8	450
82	Diversity-Oriented Synthesis Yields a Novel Lead for the Treatment of Malaria. <i>ACS Medicinal Chemistry Letters</i> , 2012, 3, 112-117.	2.8	52
83	A new malaria antigen produces partial protection against <i>Plasmodium yoelii</i> challenge. <i>Parasitology Research</i> , 2012, 110, 1337-1345.	1.6	5
84	Macrophage migration inhibitory factor homolog from <i>Plasmodium yoelii</i> modulates monocyte recruitment and activation in spleen during infection. <i>Parasitology Research</i> , 2012, 110, 1755-1763.	1.6	9
85	Peripheral blood stem cell transplant-related <i>Plasmodium falciparum</i> infection in a patient with sickle cell disease. <i>Transfusion</i> , 2012, 52, 2677-2682.	1.6	23
86	Chemical Genomic Profiling for Antimalarial Therapies, Response Signatures, and Molecular Targets. <i>Science</i> , 2011, 333, 724-729.	12.6	130
87	High recombination rates and hotspots in a <i>Plasmodium falciparum</i> genetic cross. <i>Genome Biology</i> , 2011, 12, R33.	8.8	80
88	Artemisinin: Discovery from the Chinese Herbal Garden. <i>Cell</i> , 2011, 146, 855-858.	28.9	336
89	Protocol for Production of a Genetic Cross of the Rodent Malaria Parasites. <i>Journal of Visualized Experiments</i> , 2011, .	0.3	6
90	Effect of PCR extension temperature on high-throughput sequencing. <i>Molecular and Biochemical Parasitology</i> , 2011, 176, 64-67.	1.1	19

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91	Directional gene expression and antisense transcripts in sexual and asexual stages of <i>Plasmodium falciparum</i> . <i>BMC Genomics</i> , 2011, 12, 587.	2.8	309
92	Discovery of new antimalarial chemotypes through chemical methodology and library development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 6775-6780.	7.1	42
93	Linkage maps from multiple genetic crosses and loci linked to growth-related virulent phenotype in <i>Plasmodium yoelii</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E374-E382.	7.1	45
94	Population Genetic Analysis of <i>Plasmodium falciparum</i> Parasites Using a Customized Illumina GoldenGate Genotyping Assay. <i>PLoS ONE</i> , 2011, 6, e20251.	2.5	63
95	Recent Progress in Functional Genomic Research in <i>Plasmodium falciparum</i> . <i>Current Genomics</i> , 2010, 11, 279-286.	1.6	19
96	Use of magnetically purified <i>Plasmodium falciparum</i> parasites improves the accuracy of erythrocyte invasion assays. <i>Experimental Parasitology</i> , 2010, 126, 278-280.	1.2	9
97	<i>Plasmodium falciparum</i> genome-wide scans for positive selection, recombination hot spots and resistance to antimalarial drugs. <i>Nature Genetics</i> , 2010, 42, 268-271.	21.4	178
98	Increased Tolerance to Artemisinin in <i>Plasmodium falciparum</i> Is Mediated by a Quiescence Mechanism. <i>Antimicrobial Agents and Chemotherapy</i> , 2010, 54, 1872-1877.	3.2	258
99	In Vitro Sensitivity of <i>Plasmodium falciparum</i> Clinical Isolates from the China-Myanmar Border Area to Quinine and Association with Polymorphism in the Na <sup>+</sup> /H <sup>+</sup> Exchanger. <i>Antimicrobial Agents and Chemotherapy</i> , 2010, 54, 4306-4313.	3.2	54
100	Human Malaria Parasites: Are We Ready for a New Species?. <i>Journal of Infectious Diseases</i> , 2010, 201, 1453-1454.	4.0	13
101	Lack of allele-specific efficacy of a bivalent AMA1 malaria vaccine. <i>Malaria Journal</i> , 2010, 9, 175.	2.3	61
102	Genomics and Genetics of Drug Resistance and Regulation of Malaria Parasite Development. , 2010, , 169-175.		0
103	Disruption of a <i>Plasmodium falciparum</i> Multidrug Resistance-associated Protein (PfMRP) Alters Its Fitness and Transport of Antimalarial Drugs and Glutathione. <i>Journal of Biological Chemistry</i> , 2009, 284, 7687-7696.	3.4	122
104	Discovery, mechanisms of action and combination therapy of artemisinin. <i>Expert Review of Anti-Infective Therapy</i> , 2009, 7, 999-1013.	4.4	283
105	Hundreds of microsatellites for genotyping <i>Plasmodium yoelii</i> parasites. <i>Molecular and Biochemical Parasitology</i> , 2009, 166, 153-158.	1.1	14
106	Genetic mapping of targets mediating differential chemical phenotypes in <i>Plasmodium falciparum</i> . <i>Nature Chemical Biology</i> , 2009, 5, 765-771.	8.0	59
107	Large-scale Genotyping and Genetic Mapping in <i>Plasmodium</i> Parasites. <i>Korean Journal of Parasitology</i> , 2009, 47, 83.	1.3	10
108	Drug resistance and genetic mapping in <i>Plasmodium falciparum</i> . <i>Current Genetics</i> , 2008, 54, 223-239.	1.7	56

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109	Detection of genome-wide polymorphisms in the AT-rich <i>Plasmodium falciparum</i> genome using a high-density microarray. <i>BMC Genomics</i> , 2008, 9, 398.	2.8	54
110	Diversity and evolution of the <i>rhoPh1/clag</i> multigene family of <i>Plasmodium falciparum</i> . <i>Molecular and Biochemical Parasitology</i> , 2008, 158, 11-21.	1.1	42
111	Changes in the Plasmodial Surface Anion Channel Reduce Leupeptin Uptake and Can Confer Drug Resistance in <i>Plasmodium falciparum</i> -Infected Erythrocytes. <i>Antimicrobial Agents and Chemotherapy</i> , 2008, 52, 2346-2354.	3.2	45
112	Histone Acetyltransferase Inhibitor Anacardic Acid Causes Changes in Global Gene Expression during In Vitro <i>Plasmodium falciparum</i> Development. <i>Eukaryotic Cell</i> , 2008, 7, 1200-1210.	3.4	101
113	Local Adaptation and Vector-Mediated Population Structure in <i>Plasmodium vivax</i> Malaria. <i>Molecular Biology and Evolution</i> , 2008, 25, 1245-1252.	8.9	115
114	Population structure of the genes encoding the polymorphic <i>Plasmodium falciparum</i> apical membrane antigen 1: Implications for vaccine design. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 7857-7862.	7.1	83
115	Genome-Wide Compensatory Changes Accompany Drug- Selected Mutations in the <i>Plasmodium falciparum crt</i> Gene. <i>PLoS ONE</i> , 2008, 3, e2484.	2.5	70
116	Effects of <i>Plasmodium falciparum</i> Mixed Infections on In Vitro Antimalarial Drug Tests and Genotyping. <i>American Journal of Tropical Medicine and Hygiene</i> , 2008, 79, 178-184.	1.4	42
117	Effects of <i>Plasmodium falciparum</i> mixed infections on in vitro antimalarial drug tests and genotyping. <i>American Journal of Tropical Medicine and Hygiene</i> , 2008, 79, 178-84.	1.4	33
118	PfGCN5-Mediated Histone H3 Acetylation Plays a Key Role in Gene Expression in <i>Plasmodium falciparum</i> . <i>Eukaryotic Cell</i> , 2007, 6, 1219-1227.	3.4	113
119	Genome-wide variation and identification of vaccine targets in the <i>Plasmodium falciparum</i> genome. <i>Nature Genetics</i> , 2007, 39, 126-130.	21.4	212
120	Genetic linkage and association analyses for trait mapping in <i>Plasmodium falciparum</i> . <i>Nature Reviews Genetics</i> , 2007, 8, 497-506.	16.3	80
121	Mutations in transmembrane domains 1, 4 and 9 of the <i>Plasmodium falciparum</i> chloroquine resistance transporter alter susceptibility to chloroquine, quinine and quinidine. <i>Molecular Microbiology</i> , 2007, 63, 270-282.	2.5	87
122	Mutations in transmembrane domains 1, 4 and 9 of the <i>Plasmodium falciparum</i> chloroquine resistance transporter alter susceptibility to chloroquine, quinine and quinidine. <i>Molecular Microbiology</i> , 2007, 64, 1139-1139.	2.5	5
123	cDNA sequences reveal considerable gene prediction inaccuracy in the <i>Plasmodium falciparum</i> genome. <i>BMC Genomics</i> , 2007, 8, 255.	2.8	50
124	Typing <i>Plasmodium yoelii</i> microsatellites using a simple and affordable fluorescent labeling method. <i>Molecular and Biochemical Parasitology</i> , 2007, 155, 94-102.	1.1	20
125	Structural polymorphism and diversifying selection on the pregnancy malaria vaccine candidate VAR2CSA. <i>Molecular and Biochemical Parasitology</i> , 2007, 155, 103-112.	1.1	111
126	Upregulation of expression of the reticulocyte homology gene 4 in the <i>Plasmodium falciparum</i> clone Dd2 is associated with a switch in the erythrocyte invasion pathway. <i>Molecular and Biochemical Parasitology</i> , 2006, 145, 205-215.	1.1	63



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127	Global genetic diversity and evolution of var genes associated with placental and severe childhood malaria. <i>Molecular and Biochemical Parasitology</i> , 2006, 148, 169-180.	1.1	147
128	Malaria: Therapy, Genes and Vaccines. <i>Current Molecular Medicine</i> , 2006, 6, 309-326.	1.3	21
129	CD4+ T-Cell Response to Mitochondrial Cytochrome b in Human Melanoma. <i>Cancer Research</i> , 2006, 66, 5919-5926.	0.9	18
130	Genetic diversity and population history of <i>Plasmodium falciparum</i> and <i>Plasmodium vivax</i> . <i>Parassitologia</i> , 2006, 48, 561-6.	0.5	9
131	Identification of a subtelomeric gene family expressed during the asexual to sexual stage transition in <i>Plasmodium falciparum</i> . <i>Molecular and Biochemical Parasitology</i> , 2005, 143, 90-99.	1.1	84
132	Host Switch Leads to Emergence of <i>Plasmodium vivax</i> Malaria in Humans. <i>Molecular Biology and Evolution</i> , 2005, 22, 1686-1693.	8.9	199
133	Recombination Hotspots and Population Structure in <i>Plasmodium falciparum</i> . <i>PLoS Biology</i> , 2005, 3, e335.	5.6	173
134	Disruption of a <i>Plasmodium falciparum</i> gene linked to male sexual development causes early arrest in gametocytogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 16813-16818.	7.1	73
135	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. <i>American Journal of Tropical Medicine and Hygiene</i> , 2005, 72, 410-414.	1.4	92
136	Decreased prevalence of the <i>Plasmodium falciparum</i> chloroquine resistance transporter 76T marker associated with cessation of chloroquine use against <i>P. falciparum</i> malaria in Hainan, People's Republic of China. <i>American Journal of Tropical Medicine and Hygiene</i> , 2005, 72, 410-4.	1.4	70
137	Polymorphism in the <i>Plasmodium falciparum</i> erythrocyte-binding ligand JESEBL/EBA-181 alters its receptor specificity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 2518-2523.	7.1	91
138	pfcr1Polymorphism and the Spread of Chloroquine Resistance in <i>Plasmodium falciparum</i> Populations across the Amazon Basin. <i>Journal of Infectious Diseases</i> , 2004, 190, 417-424.	4.0	73
139	Genetic mapping in the human malaria parasite <i>Plasmodium falciparum</i> . <i>Molecular Microbiology</i> , 2004, 53, 1573-1582.	2.5	36
140	Dissecting the loci of low-level quinine resistance in malaria parasites. <i>Molecular Microbiology</i> , 2004, 52, 985-997.	2.5	215
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