

Sachel Mok

List of Publications by Year in descending order

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Version: 2024-02-01

42
papers

3,317
citations

236925

25
h-index

265206

42
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47
all docs

47
docs citations

47
times ranked

3390
citing authors

#	ARTICLE	IF	CITATIONS
1	The Plasmodium falciparum ABC transporter ABCI3 confers parasite strain-dependent pleiotropic antimalarial drug resistance. Cell Chemical Biology, 2022, 29, 824-839.e6.	5.2	14
2	Comparative Analysis of Plasmodium falciparum Genotyping via SNP Detection, Microsatellite Profiling, and Whole-Genome Sequencing. Antimicrobial Agents and Chemotherapy, 2022, 66, AAC0116321.	3.2	8
3	Safety, pharmacokinetics, and antimalarial activity of the novel triaminopyrimidine ZY-19489: a first-in-human, randomised, placebo-controlled, double-blind, single ascending dose study, pilot food-effect study, and volunteer infection study. Lancet Infectious Diseases, The, 2022, 22, 879-890.	9.1	13
4	Identification and Profiling of a Novel Diazaspiro[3.4]octane Chemical Series Active against Multiple Stages of the Human Malaria Parasite <i>Plasmodium falciparum</i> and Optimization Efforts. Journal of Medicinal Chemistry, 2021, 64, 2291-2309.	6.4	11
5	Novel Antimalarial Tetrazoles and Amides Active against the Hemoglobin Degradation Pathway in <i>Plasmodium falciparum</i> . Journal of Medicinal Chemistry, 2021, 64, 2739-2761.	6.4	10
6	3-Hydroxy-propanamidines, a New Class of Orally Active Antimalarials Targeting Plasmodium falciparum. Journal of Medicinal Chemistry, 2021, 64, 3035-3047.	6.4	5
7	Repositioning and Characterization of 1-(Pyridin-4-yl)pyrrolidin-2-one Derivatives as <i>Plasmodium</i> Cytoplasmic Prolyl-tRNA Synthetase Inhibitors. ACS Infectious Diseases, 2021, 7, 1680-1689.	3.8	14
8	Potent Antimalarials with Development Potential Identified by Structure-Guided Computational Optimization of a Pyrrole-Based Dihydroorotate Dehydrogenase Inhibitor Series. Journal of Medicinal Chemistry, 2021, 64, 6085-6136.	6.4	24
9	Plasmodium falciparum K13 mutations in Africa and Asia impact artemisinin resistance and parasite fitness. ELife, 2021, 10, .	6.0	85
10	The antimalarial MMV688533 provides potential for single-dose cures with a high barrier to <i>Plasmodium falciparum</i> parasite resistance. Science Translational Medicine, 2021, 13, .	12.4	25
11	Chemoprotective antimalarials identified through quantitative high-throughput screening of Plasmodium blood and liver stage parasites. Scientific Reports, 2021, 11, 2121.	3.3	14
12	Artemisinin-resistant K13 mutations rewire Plasmodium falciparum's intra-erythrocytic metabolic program to enhance survival. Nature Communications, 2021, 12, 530.	12.8	82
13	Molecular Mechanisms of Drug Resistance in <i>Plasmodium falciparum</i> Malaria. Annual Review of Microbiology, 2020, 74, 431-454.	7.3	123
14	Inhibition of Resistance-Refractory P. falciparum Kinase PKG Delivers Prophylactic, Blood Stage, and Transmission-Blocking Antiplasmodial Activity. Cell Chemical Biology, 2020, 27, 806-816.e8.	5.2	56
15	The Antimalarial Natural Product Salinipostin A Identifies Essential $\hat{\pm}/\hat{2}$ Serine Hydrolases Involved in Lipid Metabolism in P. <i>falciparum</i> Parasites. Cell Chemical Biology, 2020, 27, 143-157.e5.	5.2	48
16	Insights into the intracellular localization, protein associations and artemisinin resistance properties of Plasmodium falciparum K13. PLoS Pathogens, 2020, 16, e1008482.	4.7	60
17	Local emergence in Amazonia of Plasmodium falciparum k13 C580Y mutants associated with in vitro artemisinin resistance. ELife, 2020, 9, .	6.0	102
18	Global Spread of Mutant PfCRT and Its Pleiotropic Impact on Plasmodium falciparum Multidrug Resistance and Fitness. MBio, 2019, 10, .	4.1	35

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19	Adaptation of <i>Plasmodium falciparum</i> to its transmission environment. <i>Nature Ecology and Evolution</i> , 2018, 2, 377-387.	7.8	65
20	The origins of malaria artemisinin resistance defined by a genetic and transcriptomic background. <i>Nature Communications</i> , 2018, 9, 5158.	12.8	41
21	Gene copy number variation in natural populations of <i>Plasmodium falciparum</i> in Eastern Africa. <i>BMC Genomics</i> , 2018, 19, 372.	2.8	12
22	Emerging Southeast Asian PfCRT mutations confer <i>Plasmodium falciparum</i> resistance to the first-line antimalarial piperazine. <i>Nature Communications</i> , 2018, 9, 3314.	12.8	183
23	Oxidative stress and protein damage responses mediate artemisinin resistance in malaria parasites. <i>PLoS Pathogens</i> , 2018, 14, e1006930.	4.7	129
24	A Variant PfCRT Isoform Can Contribute to <i>Plasmodium falciparum</i> Resistance to the First-Line Partner Drug Piperazine. <i>MBio</i> , 2017, 8, .	4.1	82
25	New insights into the <i>Plasmodium vivax</i> transcriptome using RNA-Seq. <i>Scientific Reports</i> , 2016, 6, 20498.	3.3	65
26	Integrated analysis of the <i>Plasmodium</i> species transcriptome. <i>EBioMedicine</i> , 2016, 7, 255-266.	6.1	55
27	A crucial piece in the puzzle of the artemisinin resistance mechanism in <i>Plasmodium falciparum</i> . <i>Trends in Parasitology</i> , 2015, 31, 345-346.	3.3	6
28	Targeting the Cell Stress Response of <i>Plasmodium falciparum</i> to Overcome Artemisinin Resistance. <i>PLoS Biology</i> , 2015, 13, e1002132.	5.6	254
29	<i>Plasmodium knowlesi</i> gene expression differs in ex vivo compared to in vitro blood-stage cultures. <i>Malaria Journal</i> , 2015, 14, 110.	2.3	31
30	Population transcriptomics of human malaria parasites reveals the mechanism of artemisinin resistance. <i>Science</i> , 2015, 347, 431-435.	12.6	362
31	Structural polymorphism in the promoter of <i>pfmrp2</i> confers <i>Plasmodium falciparum</i> tolerance to quinoline drugs. <i>Molecular Microbiology</i> , 2014, 91, 918-934.	2.5	28
32	Dynamic Epigenetic Regulation of Gene Expression during the Life Cycle of Malaria Parasite <i>Plasmodium falciparum</i> . <i>PLoS Pathogens</i> , 2013, 9, e1003170.	4.7	90
33	A Whole Cell Pathway Screen Reveals Seven Novel Chemosensitizers to Combat Chloroquine Resistant Malaria. <i>Scientific Reports</i> , 2013, 3, 1734.	3.3	23
34	A subset of group A-like <i>var</i> genes encodes the malaria parasite ligands for binding to human brain endothelial cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E1772-81.	7.1	183
35	Transcriptional variation in the malaria parasite <i>Plasmodium falciparum</i> . <i>Genome Research</i> , 2012, 22, 925-938.	5.5	194
36	DNA Microarray-Based Genome-Wide Analyses of <i>Plasmodium</i> Parasites. <i>Methods in Molecular Biology</i> , 2012, 923, 189-211.	0.9	21

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37	Design of a variant surface antigen-supplemented microarray chip for whole transcriptome analysis of multiple <i>Plasmodium falciparum</i> cytoadherent strains, and identification of strain-transcendent rif and stevor genes. <i>Malaria Journal</i> , 2011, 10, 180.	2.3	13
38	Artemisinin resistance in <i>Plasmodium falciparum</i> is associated with an altered temporal pattern of transcription. <i>BMC Genomics</i> , 2011, 12, 391.	2.8	135
39	Transcriptional profiling of growth perturbations of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature Biotechnology</i> , 2010, 28, 91-98.	17.5	196
40	Comparative Transcriptional and Genomic Analysis of <i>Plasmodium falciparum</i> Field Isolates. <i>PLoS Pathogens</i> , 2009, 5, e1000644.	4.7	76
41	Quantitative protein expression profiling reveals extensive post-transcriptional regulation and post-translational modifications in schizont-stage malaria parasites. <i>Genome Biology</i> , 2008, 9, R177.	9.6	107
42	The transcriptome of <i>Plasmodium vivax</i> reveals divergence and diversity of transcriptional regulation in malaria parasites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 16290-16295.	7.1	234