

Timothy J C Anderson

List of Publications by Year in descending order

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71
papers

5,690
citations

147726

31
h-index

110317

64
g-index

89
all docs

89
docs citations

89
times ranked

5329
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic analysis of a parasite invasion: Colonization of the Americas by the blood fluke <i>Schistosoma mansoni</i> . <i>Molecular Ecology</i> , 2022, 31, 2242-2263.	2.0	11
2	Snails, microbiomes, and schistosomes: a three-way interaction?. <i>Trends in Parasitology</i> , 2022, 38, 353-355.	1.5	12
3	Optimizing bulk segregant analysis of drug resistance using <i>Plasmodium falciparum</i> genetic crosses conducted in humanized mice. <i>IScience</i> , 2022, 25, 104095.	1.9	8
4	Nutrient Limitation Magnifies Fitness Costs of Antimalarial Drug Resistance Mutations. <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, e0152921.	1.4	9
5	A Malaria Parasite Cross Reveals Genetic Determinants of <i>Plasmodium falciparum</i> Growth in Different Culture Media. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, .	1.8	6
6	Schistosome Sulfotransferases: Mode of Action, Expression and Localization. <i>Pharmaceutics</i> , 2022, 14, 1416.	2.0	3
7	<i>Schistosoma mansoni</i> . <i>Trends in Parasitology</i> , 2021, 37, 176-177.	1.5	9
8	Genetic architecture of transmission stage production and virulence in schistosome parasites. <i>Virulence</i> , 2021, 12, 1508-1526.	1.8	12
9	An open dataset of <i>Plasmodium falciparum</i> genome variation in 7,000 worldwide samples. <i>Wellcome Open Research</i> , 2021, 6, 42.	0.9	97
10	The power and promise of genetic mapping from <i>Plasmodium falciparum</i> crosses utilizing human liver-chimeric mice. <i>Communications Biology</i> , 2021, 4, 734.	2.0	13
11	<i>Plasmodium falciparum</i> K13 mutations in Africa and Asia impact artemisinin resistance and parasite fitness. <i>ELife</i> , 2021, 10, .	2.8	85
12	An open dataset of <i>Plasmodium falciparum</i> genome variation in 7,000 worldwide samples. <i>Wellcome Open Research</i> , 2021, 6, 42.	0.9	51
13	Rational approach to drug discovery for human schistosomiasis. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2021, 16, 140-147.	1.4	8
14	Single-genome sequencing reveals within-host evolution of human malaria parasites. <i>Cell Host and Microbe</i> , 2021, 29, 1496-1506.e3.	5.1	11
15	Genetic analysis of praziquantel response in schistosome parasites implicates a transient receptor potential channel. <i>Science Translational Medicine</i> , 2021, 13, eabj9114.	5.8	42
16	Co-transmission of Related Malaria Parasite Lineages Shapes Within-Host Parasite Diversity. <i>Cell Host and Microbe</i> , 2020, 27, 93-103.e4.	5.1	67
17	The hemolymph of <i>Biomphalaria</i> snail vectors of schistosomiasis supports a diverse microbiome. <i>Environmental Microbiology</i> , 2020, 22, 5450-5466.	1.8	9
18	Transformative tools for parasitic flatworms. <i>Science</i> , 2020, 369, 1562-1564.	6.0	1

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19	An iterative process produces oxamniquine derivatives that kill the major species of schistosomes infecting humans. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008517.	1.3	10
20	The extended recovery ring-stage survival assay provides a superior association with patient clearance half-life and increases throughput. <i>Malaria Journal</i> , 2020, 19, 54.	0.8	15
21	Why does oxamniquine kill <i>Schistosoma mansoni</i> and not <i>S. haematobium</i> and <i>S. japonicum</i> ? <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2020, 13, 8-15.	1.4	15
22	Identity-by-descent with uncertainty characterises connectivity of <i>Plasmodium falciparum</i> populations on the Colombian-Pacific coast. <i>PLoS Genetics</i> , 2020, 16, e1009101.	1.5	19
23	Title is missing!. , 2020, 16, e1009101.		0
24	Title is missing!. , 2020, 16, e1009101.		0
25	Title is missing!. , 2020, 16, e1009101.		0
26	Title is missing!. , 2020, 16, e1009101.		0
27	Mode and Tempo of Microsatellite Length Change in a Malaria Parasite Mutation Accumulation Experiment. <i>Genome Biology and Evolution</i> , 2019, 11, 1971-1985.	1.1	25
28	Ancient Hybridization and Adaptive Introgression of an Invadysin Gene in Schistosome Parasites. <i>Molecular Biology and Evolution</i> , 2019, 36, 2127-2142.	3.5	56
29	Pairwise growth competitions identify relative fitness relationships among artemisinin resistant <i>Plasmodium falciparum</i> field isolates. <i>Malaria Journal</i> , 2019, 18, 295.	0.8	30
30	Genetic mapping of fitness determinants across the malaria parasite <i>Plasmodium falciparum</i> life cycle. <i>PLoS Genetics</i> , 2019, 15, e1008453.	1.5	33
31	Oxamniquine resistance alleles are widespread in Old World <i>Schistosoma mansoni</i> and predate drug deployment. <i>PLoS Pathogens</i> , 2019, 15, e1007881.	2.1	28
32	Striking differences in virulence, transmission and sporocyst growth dynamics between two schistosome populations. <i>Parasites and Vectors</i> , 2019, 12, 485.	1.0	13
33	Title is missing!. , 2019, 15, e1008453.		0
34	Title is missing!. , 2019, 15, e1008453.		0
35	Title is missing!. , 2019, 15, e1008453.		0
36	Design, Synthesis, and Characterization of Novel Small Molecules as Broad Range Antischistosomal Agents. <i>ACS Medicinal Chemistry Letters</i> , 2018, 9, 967-973.	1.3	17

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37	Whole genome amplification and exome sequencing of archived schistosome miracidia. <i>Parasitology</i> , 2018, 145, 1739-1747.	0.7	27
38	Genetic Crosses and Linkage Mapping in Schistosome Parasites. <i>Trends in Parasitology</i> , 2018, 34, 982-996.	1.5	29
39	Fitness Costs and the Rapid Spread of <i>kelch13</i> -C580Y Substitutions Conferring Artemisinin Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	56
40	Longitudinal genomic surveillance of <i>Plasmodium falciparum</i> malaria parasites reveals complex genomic architecture of emerging artemisinin resistance. <i>Genome Biology</i> , 2017, 18, 78.	3.8	120
41	Population Parameters Underlying an Ongoing Soft Sweep in Southeast Asian Malaria Parasites. <i>Molecular Biology and Evolution</i> , 2017, 34, 131-144.	3.5	87
42	Quantifying connectivity between local <i>Plasmodium falciparum</i> malaria parasite populations using identity by descent. <i>PLoS Genetics</i> , 2017, 13, e1007065.	1.5	98
43	Real-time PCR for sexing <i>Schistosoma mansoni</i> cercariae. <i>Molecular and Biochemical Parasitology</i> , 2016, 205, 35-38.	0.5	19
44	Independent origins of loss-of-function mutations conferring oxamniquine resistance in a Brazilian schistosome population. <i>International Journal for Parasitology</i> , 2016, 46, 417-424.	1.3	31
45	Declining Efficacy of Artemisinin Combination Therapy Against <i>P. falciparum</i> Malaria on the Thai-Myanmar Border (2003-2013): The Role of Parasite Genetic Factors. <i>Clinical Infectious Diseases</i> , 2016, 63, 784-791.	2.9	178
46	Optimal health and disease management using spatial uncertainty: a geographic characterization of emergent artemisinin-resistant <i>Plasmodium falciparum</i> distributions in Southeast Asia. <i>International Journal of Health Geographics</i> , 2016, 15, 37.	1.2	13
47	Characterization of hemolymph phenoloxidase activity in two <i>Biomphalaria</i> snail species and impact of <i>Schistosoma mansoni</i> infection. <i>Parasites and Vectors</i> , 2016, 9, 32.	1.0	53
48	Identification of Compounds with Efficacy against Malaria Parasites from Common North American Plants. <i>Journal of Natural Products</i> , 2016, 79, 490-498.	1.5	29
49	Population Structure Shapes Copy Number Variation in Malaria Parasites. <i>Molecular Biology and Evolution</i> , 2016, 33, 603-620.	3.5	45
50	<i>Plasmodium falciparum</i> genetic crosses in a humanized mouse model. <i>Nature Methods</i> , 2015, 12, 631-633.	9.0	74
51	Pooled Sequencing and Rare Variant Association Tests for Identifying the Determinants of Emerging Drug Resistance in Malaria Parasites. <i>Molecular Biology and Evolution</i> , 2015, 32, 1080-1090.	3.5	34
52	Spread of artemisinin-resistant <i>Plasmodium falciparum</i> in Myanmar: a cross-sectional survey of the K13 molecular marker. <i>Lancet Infectious Diseases</i> , The, 2015, 15, 415-421.	4.6	363
53	Structural and Functional Characterization of the Enantiomers of the Antischistosomal Drug Oxamniquine. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0004132.	1.3	20
54	Efficient linkage mapping using exome capture and extreme QTL in schistosome parasites. <i>BMC Genomics</i> , 2014, 15, 617.	1.2	45

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55	Single-cell genomics for dissection of complex malaria infections. <i>Genome Research</i> , 2014, 24, 1028-1038.	2.4	83
56	Long term persistence of clonal malaria parasite <i>Plasmodium falciparum</i> lineages in the Colombian Pacific region. <i>BMC Genetics</i> , 2013, 14, 2.	2.7	54
57	Genetic and Molecular Basis of Drug Resistance and Species-Specific Drug Action in Schistosome Parasites. <i>Science</i> , 2013, 342, 1385-1389.	6.0	137
58	Population genetic correlates of declining transmission in a human pathogen. <i>Molecular Ecology</i> , 2013, 22, 273-285.	2.0	129
59	A Systematically Improved High Quality Genome and Transcriptome of the Human Blood Fluke <i>Schistosoma mansoni</i> . <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1455.	1.3	400
60	Close kinship within multiple-genotype malaria parasite infections. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 2589-2598.	1.2	88
61	Emergence of artemisinin-resistant malaria on the western border of Thailand: a longitudinal study. <i>Lancet</i> , The, 2012, 379, 1960-1966.	6.3	768
62	A Major Genome Region Underlying Artemisinin Resistance in Malaria. <i>Science</i> , 2012, 336, 79-82.	6.0	334
63	Genomic linkage map of the human blood fluke <i>Schistosoma mansoni</i> . <i>Genome Biology</i> , 2009, 10, R71.	13.9	74
64	Adaptive Copy Number Evolution in Malaria Parasites. <i>PLoS Genetics</i> , 2008, 4, e1000243.	1.5	170
65	Combined Molecular and Clinical Assessment of <i>Plasmodium falciparum</i> Antimalarial Drug Resistance in the Lao People's Democratic Republic (Laos). <i>American Journal of Tropical Medicine and Hygiene</i> , 2007, 77, 36-43.	0.6	14
66	Recurrent Gene Amplification and Soft Selective Sweeps during Evolution of Multidrug Resistance in Malaria Parasites. <i>Molecular Biology and Evolution</i> , 2006, 24, 562-573.	3.5	138
67	The origins and spread of antimalarial drug resistance: Lessons for policy makers. <i>Acta Tropica</i> , 2005, 94, 269-280.	0.9	115
68	Molecular assessment of drug resistance in <i>Plasmodium falciparum</i> from Bahr El Gazal Province, Sudan. <i>Tropical Medicine and International Health</i> , 2003, 8, 1068-1073.	1.0	33
69	A Selective Sweep Driven by Pyrimethamine Treatment in Southeast Asian Malaria Parasites. <i>Molecular Biology and Evolution</i> , 2003, 20, 1526-1536.	3.5	291
70	Complex mutations in a high proportion of microsatellite loci from the protozoan parasite <i>Plasmodium falciparum</i> . <i>Molecular Ecology</i> , 2000, 9, 1599-1608.	2.0	71
71	Microsatellite Markers Reveal a Spectrum of Population Structures in the Malaria Parasite <i>Plasmodium falciparum</i> . <i>Molecular Biology and Evolution</i> , 2000, 17, 1467-1482.	3.5	693