Ian H Cheeseman

List of Publications by Year in descending order

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471509 610901 1,933 27 17 24 citations h-index g-index papers 37 37 37 2599 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Optimizing bulk segregant analysis of drug resistance using Plasmodium falciparum genetic crosses conducted in humanized mice. IScience, 2022, 25, 104095.	4.1	8
2	A Malaria Parasite Cross Reveals Genetic Determinants of Plasmodium falciparum Growth in Different Culture Media. Frontiers in Cellular and Infection Microbiology, 2022, 12, .	3.9	6
3	Efficiency of wholeâ€exome sequencing in old world and new world primates using human capture reagents. Journal of Medical Primatology, 2021, 50, 176-181.	0.6	5
4	The power and promise of genetic mapping from Plasmodium falciparum crosses utilizing human liver-chimeric mice. Communications Biology, 2021, 4, 734.	4.4	13
5	Single-genome sequencing reveals within-host evolution of human malaria parasites. Cell Host and Microbe, 2021, 29, 1496-1506.e3.	11.0	11
6	Single-cell genome sequencing of protozoan parasites. Trends in Parasitology, 2021, 37, 803-814.	3.3	10
7	Co-transmission of Related Malaria Parasite Lineages Shapes Within-Host Parasite Diversity. Cell Host and Microbe, 2020, 27, 93-103.e4.	11.0	67
8	Mode and Tempo of Microsatellite Length Change in a Malaria Parasite Mutation Accumulation Experiment. Genome Biology and Evolution, 2019, 11, 1971-1985.	2.5	25
9	Pairwise growth competitions identify relative fitness relationships among artemisinin resistant Plasmodium falciparum field isolates. Malaria Journal, 2019, 18, 295.	2.3	30
10	Genetic mapping of fitness determinants across the malaria parasiteÂPlasmodium falciparum life cycle. PLoS Genetics, 2019, 15, e1008453.	3 . 5	33
11	Title is missing!. , 2019, 15, e1008453.		O
12	Title is missing!. , 2019, 15, e1008453.		0
13	Title is missing!. , 2019, 15, e1008453.		O
14	Longitudinal genomic surveillance of Plasmodium falciparum malaria parasites reveals complex genomic architecture of emerging artemisinin resistance. Genome Biology, 2017, 18, 78.	8.8	120
15	Population Parameters Underlying an Ongoing Soft Sweep in Southeast Asian Malaria Parasites. Molecular Biology and Evolution, 2017, 34, 131-144.	8.9	87
16	High-Resolution Single-Cell Sequencing of Malaria Parasites. Genome Biology and Evolution, 2017, 9, 3373-3383.	2.5	41
17	Population Structure Shapes Copy Number Variation in Malaria Parasites. Molecular Biology and Evolution, 2016, 33, 603-620.	8.9	45
18	Plasmodium falciparum genetic crosses in a humanized mouse model. Nature Methods, 2015, 12, 631-633.	19.0	74

#	Article	IF	CITATION
19	Pooled Sequencing and Rare Variant Association Tests for Identifying the Determinants of Emerging Drug Resistance in Malaria Parasites. Molecular Biology and Evolution, 2015, 32, 1080-1090.	8.9	34
20	Single-cell genomics for dissection of complex malaria infections. Genome Research, 2014, 24, 1028-1038.	5. 5	83
21	Population Genomic Scan for Candidate Signatures of Balancing Selection to Guide Antigen Characterization in Malaria Parasites. PLoS Genetics, 2012, 8, e1002992.	3.5	167
22	Close kinship within multiple-genotype malaria parasite infections. Proceedings of the Royal Society B: Biological Sciences, 2012, 279, 2589-2598.	2.6	88
23	A Major Genome Region Underlying Artemisinin Resistance in Malaria. Science, 2012, 336, 79-82.	12.6	334
24	An optimized microarray platform for assaying genomic variation in Plasmodium falciparum field populations. Genome Biology, 2011, 12, R35.	9.6	26
25	Distinct Roles for FOXP3+ and FOXP3â [^] CD4+ T Cells in Regulating Cellular Immunity to Uncomplicated and Severe Plasmodium falciparum Malaria. PLoS Pathogens, 2009, 5, e1000364.	4.7	188
26	Gene copy number variation throughout the Plasmodium falciparum genome. BMC Genomics, 2009, 10, 353.	2.8	38
27	A mechanism for cross-resistance to nifurtimox and benznidazole in trypanosomes. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 5022-5027.	7.1	370