

Bronwyn Macinnis

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

5,946
citations

304743

22
h-index

642732

23
g-index

26
all docs

26
docs citations

26
times ranked

6851
citing authors

#	ARTICLE	IF	CITATIONS
1	Spread of Artemisinin Resistance in <i>Plasmodium falciparum</i> Malaria. <i>New England Journal of Medicine</i> , 2014, 371, 411-423.	27.0	1,753
2	Optimizing illumina next-generation sequencing library preparation for extremely at-biased genomes. <i>BMC Genomics</i> , 2012, 13, 1.	2.8	772
3	Genetic architecture of artemisinin-resistant <i>Plasmodium falciparum</i> . <i>Nature Genetics</i> , 2015, 47, 226-234.	21.4	515
4	Analysis of <i>Plasmodium falciparum</i> diversity in natural infections by deep sequencing. <i>Nature</i> , 2012, 487, 375-379.	27.8	450
5	Multiple populations of artemisinin-resistant <i>Plasmodium falciparum</i> in Cambodia. <i>Nature Genetics</i> , 2013, 45, 648-655.	21.4	424
6	Independent Emergence of Artemisinin Resistance Mutations Among <i>Plasmodium falciparum</i> in Southeast Asia. <i>Journal of Infectious Diseases</i> , 2015, 211, 670-679.	4.0	368
7	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
8	K13-Propeller Polymorphisms in <i>Plasmodium falciparum</i> Parasites From Sub-Saharan Africa. <i>Journal of Infectious Diseases</i> , 2015, 211, 1352-5.	4.0	203
9	Indels, structural variation, and recombination drive genomic diversity in <i>Plasmodium falciparum</i> . <i>Genome Research</i> , 2016, 26, 1288-1299.	5.5	180
10	Genomic analysis of local variation and recent evolution in <i>Plasmodium vivax</i> . <i>Nature Genetics</i> , 2016, 48, 959-964.	21.4	169
11	Population Genomic Scan for Candidate Signatures of Balancing Selection to Guide Antigen Characterization in Malaria Parasites. <i>PLoS Genetics</i> , 2012, 8, e1002992.	3.5	167
12	Genome-Wide Analysis of Selection on the Malaria Parasite <i>Plasmodium falciparum</i> in West African Populations of Differing Infection Endemicity. <i>Molecular Biology and Evolution</i> , 2014, 31, 1490-1499.	8.9	107
13	Characterization of Within-Host <i>Plasmodium falciparum</i> Diversity Using Next-Generation Sequence Data. <i>PLoS ONE</i> , 2012, 7, e32891.	2.5	102
14	An Effective Method to Purify <i>Plasmodium falciparum</i> DNA Directly from Clinical Blood Samples for Whole Genome High-Throughput Sequencing. <i>PLoS ONE</i> , 2011, 6, e22213.	2.5	68
15	Efficient Depletion of Host DNA Contamination in Malaria Clinical Sequencing. <i>Journal of Clinical Microbiology</i> , 2013, 51, 745-751.	3.9	63
16	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
17	Whole-Genome Scans Provide Evidence of Adaptive Evolution in Malawian <i>Plasmodium falciparum</i> Isolates. <i>Journal of Infectious Diseases</i> , 2014, 210, 1991-2000.	4.0	62
18	Changes in Malaria Parasite Drug Resistance in an Endemic Population Over a 25-Year Period With Resulting Genomic Evidence of Selection. <i>Journal of Infectious Diseases</i> , 2014, 209, 1126-1135.	4.0	49

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19	Genetic relatedness analysis reveals the cotransmission of genetically related <i>Plasmodium falciparum</i> parasites in Thiès, Senegal. <i>Genome Medicine</i> , 2017, 9, 5.	8.2	47
20	Drug-Resistant Genotypes and Multi-Clonality in <i>Plasmodium falciparum</i> Analysed by Direct Genome Sequencing from Peripheral Blood of Malaria Patients. <i>PLoS ONE</i> , 2011, 6, e23204.	2.5	41
21	Comparison of genomic signatures of selection on <i>Plasmodium falciparum</i> between different regions of a country with high malaria endemicity. <i>BMC Genomics</i> , 2015, 16, 527.	2.8	34
22	Optimized Whole-Genome Amplification Strategy for Extremely AT-Biased Template. <i>DNA Research</i> , 2014, 21, 661-671.	3.4	27
23	Effective Preparation of <i>Plasmodium vivax</i> Field Isolates for High-Throughput Whole Genome Sequencing. <i>PLoS ONE</i> , 2013, 8, e53160.	2.5	26
24	Potential Opportunities and Challenges of Deploying Next Generation Sequencing and CRISPR-Cas Systems to Support Diagnostics and Surveillance Towards Malaria Control and Elimination in Africa. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	3.9	6