

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	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
2	Indels, structural variation, and recombination drive genomic diversity in <i>Plasmodium falciparum</i> . <i>Genome Research</i> , 2016, 26, 1288-1299.	5.5	180
3	Genomic analysis of local variation and recent evolution in <i>Plasmodium vivax</i> . <i>Nature Genetics</i> , 2016, 48, 959-964.	21.4	169
4	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
5	Genetic architecture of artemisinin-resistant <i>Plasmodium falciparum</i> . <i>Nature Genetics</i> , 2015, 47, 226-234.	21.4	515
6	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
7	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
8	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
9	Optimized Whole-Genome Amplification Strategy for Extremely AT-Biased Template. <i>DNA Research</i> , 2014, 21, 661-671.	3.4	27
10	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
11	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
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	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
14	Multiple populations of artemisinin-resistant <i>Plasmodium falciparum</i> in Cambodia. <i>Nature Genetics</i> , 2013, 45, 648-655.	21.4	424
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	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
17	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
18	Characterization of Within-Host <i>Plasmodium falciparum</i> Diversity Using Next-Generation Sequence Data. <i>PLoS ONE</i> , 2012, 7, e32891.	2.5	102

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19	Analysis of Plasmodium falciparum diversity in natural infections by deep sequencing. Nature, 2012, 487, 375-379.	27.8	450
20	Optimizing illumina next-generation sequencing library preparation for extremely at-biased genomes. BMC Genomics, 2012, 13, 1.	2.8	772
21	An Effective Method to Purify Plasmodium falciparum DNA Directly from Clinical Blood Samples for Whole Genome High-Throughput Sequencing. PLoS ONE, 2011, 6, e22213.	2.5	68
22	Drug-Resistant Genotypes and Multi-Clonality in Plasmodium falciparum Analysed by Direct Genome Sequencing from Peripheral Blood of Malaria Patients. PLoS ONE, 2011, 6, e23204.	2.5	41
23	Population Genetic Analysis of Plasmodium falciparum Parasites Using a Customized Illumina GoldenGate Genotyping Assay. PLoS ONE, 2011, 6, e20251.	2.5	63
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. Frontiers in Cellular and Infection Microbiology, 0, 12, .	3.9	6