## Maria Isabel Veiga

List of Publications by Year in descending order

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361413 361022 38 1,448 20 35 citations h-index g-index papers 39 39 39 1755 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Chloroquine-susceptible and -resistant <i>Plasmodium falciparum</i> strains survive high chloroquine concentrations by becoming dormant but are eliminated by prolonged exposure. Journal of Antimicrobial Chemotherapy, 2022, 77, 1005-1011.	3.0	2
2	Review of Microdevices for Hemozoin-Based Malaria Detection. Biosensors, 2022, 12, 110.	4.7	14
3	Development of an Ultraviolet-C Irradiation Room in a Public Portuguese Hospital for Safe Re-Utilization of Personal Protective Respirators. International Journal of Environmental Research and Public Health, 2022, 19, 4854.	2.6	6
4	Multilayer Thin-Film Optical Filters for Reflectance-Based Malaria Diagnostics. Micromachines, 2021, 12, 890.	2.9	12
5	OmniSARS2: A Highly Sensitive and Specific RT-qPCR-Based COVID-19 Diagnostic Method Designed to Withstand SARS-CoV-2 Lineage Evolution. Biomedicines, 2021, 9, 1314.	3.2	8
6	The Future in Sensing Technologies for Malaria Surveillance: A Review of Hemozoin-Based Diagnosis. ACS Sensors, 2021, 6, 3898-3911.	7.8	14
7	Portable Device for Optical Quantification of Hemozoin in Diluted Blood Samples. IEEE Transactions on Biomedical Engineering, 2020, 67, 365-371.	4.2	12
8	Multigenic architecture of piperaquine resistance trait in Plasmodium falciparum. Lancet Infectious Diseases, The, 2020, 20, 26-27.	9.1	16
9	Expansion of a Specific Plasmodium falciparum PfMDR1 Haplotype in Southeast Asia with Increased Substrate Transport. MBio, 2020, 11, .	4.1	22
10	Rapid phenotyping towards personalized malaria medicine. Malaria Journal, 2020, 19, 68.	2.3	17
10	Rapid phenotyping towards personalized malaria medicine. Malaria Journal, 2020, 19, 68.  Mycobacterium tuberculosis associated with severe tuberculosis evades cytosolic surveillance systems and modulates IL-1β production. Nature Communications, 2020, 11, 1949.	2.3	17 52
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11	Mycobacterium tuberculosis associated with severe tuberculosis evades cytosolic surveillance systems and modulates IL- $1\hat{l}^2$ production. Nature Communications, 2020, 11, 1949.		52
11 12	Mycobacterium tuberculosis associated with severe tuberculosis evades cytosolic surveillance systems and modulates IL-1β production. Nature Communications, 2020, 11, 1949.  Investigação ao serviço da sociedade., 2020, , 310-330.  Plasmodium falciparum K13 expression associated with parasite clearance during artemisinin-based	12.8	52 O
11 12 13	Mycobacterium tuberculosis associated with severe tuberculosis evades cytosolic surveillance systems and modulates IL-1β production. Nature Communications, 2020, 11, 1949.  Investigação ao serviço da sociedade., 2020, 310-330.  Plasmodium falciparum K13 expression associated with parasite clearance during artemisinin-based combination therapy. Journal of Antimicrobial Chemotherapy, 2019, 74, 1890-1893.  Dosage of Single Low-Dose Primaquine to Stop Malaria Transmission. Journal of Infectious Diseases,	3.0	52 O 17
11 12 13	Mycobacterium tuberculosis associated with severe tuberculosis evades cytosolic surveillance systems and modulates IL-1β production. Nature Communications, 2020, 11, 1949.  Investigação ao serviço da sociedade. , 2020, , 310-330.  Plasmodium falciparum K13 expression associated with parasite clearance during artemisinin-based combination therapy. Journal of Antimicrobial Chemotherapy, 2019, 74, 1890-1893.  Dosage of Single Low-Dose Primaquine to Stop Malaria Transmission. Journal of Infectious Diseases, 2018, 217, 1849-1850. <irac composition="" of="" representation="" several="" t<="" td="" the=""><td>3.0 4.0</td><td>52 0 17</td></irac>	3.0 4.0	52 0 17
11 12 13 14	Mycobacterium tuberculosis associated with severe tuberculosis evades cytosolic surveillance systems and modulates IL-1 <sup>12</sup> production. Nature Communications, 2020, 11, 1949.  InvestigaÃSão ao serviÃSo da sociedade. , 2020, , 310-330.  Plasmodium falciparum K13 expression associated with parasite clearance during artemisinin-based combination therapy. Journal of Antimicrobial Chemotherapy, 2019, 74, 1890-1893.  Dosage of Single Low-Dose Primaquine to Stop Malaria Transmission. Journal of Infectious Diseases, 2018, 217, 1849-1850.  (i) Plasmodium falciparum (i) ÂPlasmepsin 2 Duplications, West Africa. Emerging Infectious Diseases, 2018, 24, 1591-1593.  Hexahydroquinolines are antimalarial candidates with potent blood-stage and transmission-blocking	3.0 4.0 4.3	52 0 17 0

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19	Single nucleotide polymorphisms in Plasmodium falciparum $\nu$ type H+ pyrophosphatase gene (pf $\nu$ p2) and their associations with pfcrt and pfmdr1 polymorphisms. Infection, Genetics and Evolution, 2014, 24, 111-115.	2.3	6
20	Complex Polymorphisms in the Plasmodium falciparum Multidrug Resistance Protein 2 Gene and Its Contribution to Antimalarial Response. Antimicrobial Agents and Chemotherapy, 2014, 58, 7390-7397.	3.2	25
21	<i>pfmdr1</i> Amplification Is Related to Increased Plasmodium falciparum In Vitro Sensitivity to the Bisquinoline Piperaquine. Antimicrobial Agents and Chemotherapy, 2012, 56, 3615-3619.	3.2	34
22	Novel Polymorphisms in Plasmodium falciparum ABC Transporter Genes Are Associated with Major ACT Antimalarial Drug Resistance. PLoS ONE, 2011, 6, e20212.	2.5	80
23	Prevalence of resistance associated polymorphisms in Plasmodium falciparum field isolates from southern Pakistan. Malaria Journal, 2011, 10, 18.	2.3	31
24	Drug resistance associated genetic polymorphisms in Plasmodium falciparum and Plasmodium vivax collected in Honduras, Central America. Malaria Journal, 2011, 10, 376.	2.3	32
25	Plasmodium falciparum population dynamics during the early phase of anti-malarial drug treatment in Tanzanian children with acute uncomplicated malaria. Malaria Journal, 2011, 10, 380.	2.3	25
26	PfMDR1: Mechanisms of Transport Modulation by Functional Polymorphisms. PLoS ONE, 2011, 6, e23875.	2.5	51
27	Antimalarial Exposure Delays Plasmodium falciparum Intra-Erythrocytic Cycle and Drives Drug Transporter Genes Expression. PLoS ONE, 2010, 5, e12408.	2.5	26
28	In Vivo Selection of <i>Plasmodium falciparum </i> Parasites Carrying the Chloroquine-Susceptible <i>pfcrt </i> K76 Allele after Treatment with Artemether-Lumefantrine in Africa. Journal of Infectious Diseases, 2009, 199, 750-757.	4.0	183
29	Polymorphism in PfMRP1 ( <i>Plasmodium falciparum</i> Multidrug Resistance Protein 1) Amino Acid 1466 Associated with Resistance to Sulfadoxine-Pyrimethamine Treatment. Antimicrobial Agents and Chemotherapy, 2009, 53, 2553-2556.	3.2	48
30	<i>Plasmodium falciparum</i> Multidrug Resistance Protein 1 and Artemisininâ€Based Combination Therapy in Africa. Journal of Infectious Diseases, 2009, 200, 1456-1464.	4.0	73
31	Pharmacogenomics of CYP2A6, CYP2B6, CYP2C19, CYP2D6, CYP3A4, CYP3A5 and MDR1 in Vietnam. European Journal of Clinical Pharmacology, 2009, 65, 355-363.	1.9	39
32	Diversity of the sarco/endoplasmic reticulum Ca2+-ATPase orthologue of Plasmodium falciparum (PfATP6). Infection, Genetics and Evolution, 2008, 8, 340-345.	2.3	52
33	Antimalarial resistance and DHFR/DHPS genotypes of Plasmodium falciparum three years after introduction of sulfadoxine–pyrimethamine and amodiaquine in rural Tanzania. Transactions of the Royal Society of Tropical Medicine and Hygiene, 2008, 102, 137-142.	1.8	5
34	Polymorphism of Antimalaria Drug Metabolizing, Nuclear Receptor, and Drug Transport Genes among Malaria Patients in Zanzibar, East Africa. Therapeutic Drug Monitoring, 2008, 30, 10-15.	2.0	30
35	The Vietnamese Khin Population Harbors Particular N-Acetyltransferase 2 Allele Frequencies. Clinical Chemistry, 2007, 53, 1977-1979.	3.2	5
36	Influence of Consecutiveâ€Day Blood Sampling on Polymerase Chain Reaction–Adjusted Parasitological Cure Rates in an Antimalarialâ€Drug Trial Conducted in Tanzania. Journal of Infectious Diseases, 2007, 195, 597-601.	4.0	42

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37	Multiplex PCR–RFLP methods for pfcrt, pfmdr1 and pfdhfr mutations in Plasmodium falciparum. Molecular and Cellular Probes, 2006, 20, 100-104.	2.1	49
38	Amodiaquine resistant Plasmodium falciparum malaria in vivo is associated with selection of pfcrt 76T and pfmdr1 86Y. Infection, Genetics and Evolution, 2006, 6, 309-314.	2.3	144