

Susana Campino

List of Publications by Year in descending order

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Version: 2024-02-01

135
papers

8,659
citations

71102

41
h-index

56724

83
g-index

153
all docs

153
docs citations

153
times ranked

10693
citing authors

#	ARTICLE	IF	CITATIONS
1	Optimizing illumina next-generation sequencing library preparation for extremely at-biased genomes. BMC Genomics, 2012, 13, 1.	2.8	772
2	Genetic architecture of artemisinin-resistant Plasmodium falciparum. Nature Genetics, 2015, 47, 226-234.	21.4	515
3	Analysis of Plasmodium falciparum diversity in natural infections by deep sequencing. Nature, 2012, 487, 375-379.	27.8	450
4	A transcriptional switch underlies commitment to sexual development in malaria parasites. Nature, 2014, 507, 248-252.	27.8	430
5	Multiple populations of artemisinin-resistant Plasmodium falciparum in Cambodia. Nature Genetics, 2013, 45, 648-655.	21.4	424
6	Genome-wide and fine-resolution association analysis of malaria in West Africa. Nature Genetics, 2009, 41, 657-665.	21.4	345
7	Genome-wide analysis of multi- and extensively drug-resistant Mycobacterium tuberculosis. Nature Genetics, 2018, 50, 307-316.	21.4	271
8	Integrating informatics tools and portable sequencing technology for rapid detection of resistance to anti-tuberculous drugs. Genome Medicine, 2019, 11, 41.	8.2	248
9	Genetic loci associated with delayed clearance of Plasmodium falciparum following artemisinin treatment in Southeast Asia. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 240-245.	7.1	242
10	Genomic epidemiology of artemisinin resistant malaria. Elife, 2016, 5, .	6.0	242
11	K13-Propeller Polymorphisms in Plasmodium falciparum Parasites From Sub-Saharan Africa. Journal of Infectious Diseases, 2015, 211, 1352-5.	4.0	203
12	Indels, structural variation, and recombination drive genomic diversity in Plasmodium falciparum. Genome Research, 2016, 26, 1288-1299.	5.5	180
13	Genomic analysis of local variation and recent evolution in Plasmodium vivax. Nature Genetics, 2016, 48, 959-964.	21.4	169
14	Population Genomic Scan for Candidate Signatures of Balancing Selection to Guide Antigen Characterization in Malaria Parasites. PLoS Genetics, 2012, 8, e1002992.	3.5	167
15	Identification of Common Genetic Variation That Modulates Alternative Splicing. PLoS Genetics, 2007, 3, e99.	3.5	139
16	A barcode of organellar genome polymorphisms identifies the geographic origin of Plasmodium falciparum strains. Nature Communications, 2014, 5, 4052.	12.8	130
17	Long read assemblies of geographically dispersed Plasmodium falciparum isolates reveal highly structured subtelomeres. Wellcome Open Research, 2018, 3, 52.	1.8	114
18	Allelic heterogeneity of G6PD deficiency in West Africa and severe malaria susceptibility. European Journal of Human Genetics, 2009, 17, 1080-1085.	2.8	109

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19	Characterization of Within-Host Plasmodium falciparum Diversity Using Next-Generation Sequence Data. PLoS ONE, 2012, 7, e32891.	2.5	102
20	Mycobacterium tuberculosis whole genome sequencing and protein structure modelling provides insights into anti-tuberculosis drug resistance. BMC Medicine, 2016, 14, 31.	5.5	102
21	Prevention of Diabetes in Nonobese Diabetic Mice Mediated by CD1d-Restricted Nonclassical NKT Cells. Journal of Immunology, 2004, 173, 3112-3118.	0.8	98
22	Human candidate gene polymorphisms and risk of severe malaria in children in Kilifi, Kenya: a case-control association study. Lancet Haematology, 2018, 5, e333-e345.	4.6	90
23	Using CF11 cellulose columns to inexpensively and effectively remove human DNA from Plasmodium falciparum-infected whole blood samples. Malaria Journal, 2012, 11, 41.	2.3	79
24	Robust barcoding and identification of Mycobacterium tuberculosis lineages for epidemiological and clinical studies. Genome Medicine, 2020, 12, 114.	8.2	79
25	Modest heterologous protection after Plasmodium falciparum sporozoite immunization: a double-blind randomized controlled clinical trial. BMC Medicine, 2017, 15, 168.	5.5	78
26	estMOI: estimating multiplicity of infection using parasite deep sequencing data. Bioinformatics, 2014, 30, 1292-1294.	4.1	76
27	Genome-wide screen identifies new candidate genes associated with artemisinin susceptibility in Plasmodium falciparum in Kenya. Scientific Reports, 2013, 3, 3318.	3.3	75
28	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
29	High-throughput analysis of candidate imprinted genes and allele-specific gene expression in the human term placenta. BMC Genetics, 2010, 11, 25.	2.7	64
30	Characterisation of the opposing effects of G6PD deficiency on cerebral malaria and severe malarial anaemia. ELife, 2017, 6, .	6.0	64
31	Positive selection of a CD36 nonsense variant in sub-Saharan Africa, but no association with severe malaria phenotypes. Human Molecular Genetics, 2009, 18, 2683-2692.	2.9	63
32	Population Genetic Analysis of Plasmodium falciparum Parasites Using a Customized Illumina GoldenGate Genotyping Assay. PLoS ONE, 2011, 6, e20251.	2.5	63
33	Whole-Genome Scans Provide Evidence of Adaptive Evolution in Malawian Plasmodium falciparum Isolates. Journal of Infectious Diseases, 2014, 210, 1991-2000.	4.0	62
34	Recombination in pe/ppe genes contributes to genetic variation in Mycobacterium tuberculosis lineages. BMC Genomics, 2016, 17, 151.	2.8	62
35	Rapid and iterative genome editing in the malaria parasite Plasmodium knowlesi provides new tools for P. vivax research. ELife, 2019, 8, .	6.0	61
36	Genomic analysis of a pre-elimination Malaysian Plasmodium vivax population reveals selective pressures and changing transmission dynamics. Nature Communications, 2018, 9, 2585.	12.8	59

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37	The role of the red blood cell in host defence against falciparum malaria: an expanding repertoire of evolutionary alterations. <i>British Journal of Haematology</i> , 2017, 179, 543-556.	2.5	58
38	Novel genetic polymorphisms associated with severe malaria and under selective pressure in North-eastern Tanzania. <i>PLoS Genetics</i> , 2018, 14, e1007172.	3.5	55
39	Identification of two cerebral malaria resistance loci using an inbred wild-derived mouse strain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 9919-9923.	7.1	54
40	Tumor Necrosis Factor and Lymphotoxin- α Polymorphisms and Severe Malaria in African Populations. <i>Journal of Infectious Diseases</i> , 2009, 199, 569-575.	4.0	52
41	PrimedRPA: primer design for recombinase polymerase amplification assays. <i>Bioinformatics</i> , 2019, 35, 682-684.	4.1	52
42	Machine Learning Predicts Accurately Mycobacterium tuberculosis Drug Resistance From Whole Genome Sequencing Data. <i>Frontiers in Genetics</i> , 2019, 10, 922.	2.3	51
43	Removing the bottleneck in whole genome sequencing of Mycobacterium tuberculosis for rapid drug resistance analysis: a call to action. <i>International Journal of Infectious Diseases</i> , 2017, 56, 130-135.	3.3	49
44	Mendelian and complex genetics of susceptibility and resistance to parasitic infections. <i>Seminars in Immunology</i> , 2006, 18, 411-422.	5.6	46
45	Zika might not be acting alone: Using an ecological study approach to investigate potential co-acting risk factors for an unusual pattern of microcephaly in Brazil. <i>PLoS ONE</i> , 2018, 13, e0201452.	2.5	45
46	The variability and reproducibility of whole genome sequencing technology for detecting resistance to anti-tuberculous drugs. <i>Genome Medicine</i> , 2016, 8, 132.	8.2	44
47	Susceptibility to Experimental Cerebral Malaria Induced by Plasmodium berghei ANKA in Inbred Mouse Strains Recently Derived from Wild Stock. <i>Infection and Immunity</i> , 2002, 70, 2049-2056.	2.2	42
48	Drug-Resistant Genotypes and Multi-Clonality in Plasmodium falciparum Analysed by Direct Genome Sequencing from Peripheral Blood of Malaria Patients. <i>PLoS ONE</i> , 2011, 6, e23204.	2.5	41
49	Candidate Polymorphisms and Severe Malaria in a Malian Population. <i>PLoS ONE</i> , 2012, 7, e43987.	2.5	41
50	A novel multiplex qPCR assay for detection of Plasmodium falciparum with histidine-rich protein 2 and 3 (pfhrp2 and pfhrp3) deletions in polyclonal infections. <i>EBioMedicine</i> , 2020, 55, 102757.	6.1	41
51	Global analysis of Plasmodium falciparum histidine-rich protein-2 (pfhrp2) and pfhrp3 gene deletions using whole-genome sequencing data and meta-analysis. <i>Infection, Genetics and Evolution</i> , 2018, 62, 211-219.	2.3	40
52	Candidate Human Genetic Polymorphisms and Severe Malaria in a Tanzanian Population. <i>PLoS ONE</i> , 2012, 7, e47463.	2.5	39
53	Genetic diversity of candidate loci linked to Mycobacterium tuberculosis resistance to bedaquiline, delamanid and pretomanid. <i>Scientific Reports</i> , 2021, 11, 19431.	3.3	37
54	Global genetic diversity of var2csa in Plasmodium falciparum with implications for malaria in pregnancy and vaccine development. <i>Scientific Reports</i> , 2018, 8, 15429.	3.3	35

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55	Human Candidate Polymorphisms in Sympatric Ethnic Groups Differing in Malaria Susceptibility in Mali. <i>PLoS ONE</i> , 2013, 8, e75675.	2.5	35
56	Glucose-6-phosphate dehydrogenase polymorphisms and susceptibility to mild malaria in Dogon and Fulani, Mali. <i>Malaria Journal</i> , 2014, 13, 270.	2.3	34
57	Characterizing the impact of sustained sulfadoxine/pyrimethamine use upon the <i>Plasmodium falciparum</i> population in Malawi. <i>Malaria Journal</i> , 2016, 15, 575.	2.3	34
58	<i>Mycobacterium tuberculosis</i> whole genome sequencing provides insights into the Manila strain and drug-resistance mutations in the Philippines. <i>Scientific Reports</i> , 2019, 9, 9305.	3.3	33
59	Distinctive genetic structure and selection patterns in <i>Plasmodium vivax</i> from South Asia and East Africa. <i>Nature Communications</i> , 2021, 12, 3160.	12.8	32
60	Methylation in <i>Mycobacterium tuberculosis</i> is lineage specific with associated mutations present globally. <i>Scientific Reports</i> , 2018, 8, 160.	3.3	31
61	TLR9 polymorphisms in African populations: no association with severe malaria, but evidence of cis-variants acting on gene expression. <i>Malaria Journal</i> , 2009, 8, 44.	2.3	30
62	Diabetes Protection and Restoration of Thymocyte Apoptosis in NOD Idd6 Congenic Strains. <i>Diabetes</i> , 2003, 52, 1677-1682.	0.6	29
63	Genomic variation in <i>Plasmodium vivax</i> malaria reveals regions under selective pressure. <i>PLoS ONE</i> , 2017, 12, e0177134.	2.5	29
64	Whole genome sequencing of <i>Mycobacterium tuberculosis</i> isolates and clinical outcomes of patients treated for multidrug-resistant tuberculosis in Tanzania. <i>BMC Genomics</i> , 2020, 21, 174.	2.8	28
65	A genetic association study in the Gambia using tagging polymorphisms in the major histocompatibility complex class III region implicates a HLA-B associated transcript 2 polymorphism in severe malaria susceptibility. <i>Human Genetics</i> , 2009, 125, 105-109.	3.8	27
66	Optimized Whole-Genome Amplification Strategy for Extremely AT-Biased Template. <i>DNA Research</i> , 2014, 21, 661-671.	3.4	27
67	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
68	Fc gamma Receptor α 131 Polymorphism and Malaria Susceptibility in Sympatric Ethnic Groups, Fulani and Dogon of Mali. <i>Scandinavian Journal of Immunology</i> , 2014, 79, 43-50.	2.7	26
69	Genetic determinants of anti-malarial acquired immunity in a large multi-centre study. <i>Malaria Journal</i> , 2015, 14, 333.	2.3	26
70	An integrated whole genome analysis of <i>Mycobacterium tuberculosis</i> reveals insights into relationship between its genome, transcriptome and methylome. <i>Scientific Reports</i> , 2019, 9, 5204.	3.3	26
71	Genetic diversity and risk factors for the transmission of antimicrobial resistance across human, animals and environmental compartments in East Africa: a review. <i>Antimicrobial Resistance and Infection Control</i> , 2020, 9, 127.	4.1	26
72	Using genomics to understand the origin and dispersion of multidrug and extensively drug resistant tuberculosis in Portugal. <i>Scientific Reports</i> , 2020, 10, 2600.	3.3	26

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73	Localization of a long-range cis-regulatory element of IL13 by allelic transcript ratio mapping. <i>Genome Research</i> , 2006, 17, 82-87.	5.5	25
74	Whole genome sequencing of amplified <i>Plasmodium knowlesi</i> DNA from unprocessed blood reveals genetic exchange events between Malaysian Peninsular and Borneo subpopulations. <i>Scientific Reports</i> , 2019, 9, 9873.	3.3	25
75	A comprehensive analysis of drug resistance molecular markers and <i>Plasmodium falciparum</i> genetic diversity in two malaria endemic sites in Mali. <i>Malaria Journal</i> , 2019, 18, 361.	2.3	25
76	Investigation of Host Candidate Malaria-Associated Risk/Protective SNPs in a Brazilian Amazonian Population. <i>PLoS ONE</i> , 2012, 7, e36692.	2.5	24
77	Whole genome sequencing of drug resistant <i>Mycobacterium tuberculosis</i> isolates from a high burden tuberculosis region of North West Pakistan. <i>Scientific Reports</i> , 2019, 9, 14996.	3.3	24
78	A molecular barcode to inform the geographical origin and transmission dynamics of <i>Plasmodium vivax</i> malaria. <i>PLoS Genetics</i> , 2020, 16, e1008576.	3.5	24
79	Genetic control of parasite clearance leads to resistance to <i>Plasmodium berghei</i> ANKA infection and confers immunity. <i>Genes and Immunity</i> , 2005, 6, 416-421.	4.1	23
80	PhyTB: Phylogenetic tree visualisation and sample positioning for <i>M. tuberculosis</i> . <i>BMC Bioinformatics</i> , 2015, 16, 155.	2.6	23
81	Validating Discovered Cis-Acting Regulatory Genetic Variants: Application of an Allele Specific Expression Approach to HapMap Populations. <i>PLoS ONE</i> , 2008, 3, e4105.	2.5	22
82	A reference genome and methylome for the <i>Plasmodium knowlesi</i> A1-H.1 line. <i>International Journal for Parasitology</i> , 2018, 48, 191-196.	3.1	20
83	A Poisson hierarchical modelling approach to detecting copy number variation in sequence coverage data. <i>BMC Genomics</i> , 2013, 14, 128.	2.8	19
84	Selective whole genome amplification of <i>Plasmodium malariae</i> DNA from clinical samples reveals insights into population structure. <i>Scientific Reports</i> , 2020, 10, 10832.	3.3	19
85	Genomic variation in two gametocyte non-producing <i>Plasmodium falciparum</i> clonal lines. <i>Malaria Journal</i> , 2016, 15, 229.	2.3	18
86	Analysis of nuclear and organellar genomes of <i>Plasmodium knowlesi</i> in humans reveals ancient population structure and recent recombination among host-specific subpopulations. <i>PLoS Genetics</i> , 2017, 13, e1007008.	3.5	18
87	Artemisinin resistance-associated markers in <i>Plasmodium falciparum</i> parasites from the China-Myanmar border: predicted structural stability of K13 propeller variants detected in a low-prevalence area. <i>PLoS ONE</i> , 2019, 14, e0213686.	2.5	18
88	An integrated in silico immuno-genetic analytical platform provides insights into COVID-19 serological and vaccine targets. <i>Genome Medicine</i> , 2021, 13, 4.	8.2	16
89	Whole-genome sequencing resolves a polyclonal outbreak by extended-spectrum beta-lactam and carbapenem-resistant <i>Klebsiella pneumoniae</i> in a Portuguese tertiary-care hospital. <i>Microbial Genomics</i> , 2019, 7, .	2.0	16
90	G6PD deficiency alleles in a malaria-endemic region in the Western Brazilian Amazon. <i>Malaria Journal</i> , 2017, 16, 253.	2.3	15

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91	A forward genetic screen reveals a primary role for Plasmodium falciparum Reticulocyte Binding Protein Homologue 2a and 2b in determining alternative erythrocyte invasion pathways. PLoS Pathogens, 2018, 14, e1007436.	4.7	15
92	Association of Malaria Infection During Pregnancy With Head Circumference of Newborns in the Brazilian Amazon. JAMA Network Open, 2019, 2, e193300.	5.9	15
93	Surveillance of Aedes aegypti populations in the city of Praia, Cape Verde: Zika virus infection, insecticide resistance and genetic diversity. Parasites and Vectors, 2020, 13, 481.	2.5	15
94	Differences in the frequency of genetic variants associated with iron imbalance among global populations. PLoS ONE, 2020, 15, e0235141.	2.5	15
95	Adverse pregnancy outcomes are associated with Plasmodium vivax malaria in a prospective cohort of women from the Brazilian Amazon. PLoS Neglected Tropical Diseases, 2021, 15, e0009390.	3.0	15
96	Using deep learning to identify recent positive selection in malaria parasite sequence data. Malaria Journal, 2021, 20, 270.	2.3	15
97	Genetic diversity of the Plasmodium falciparum GTP-cyclohydrolase 1, dihydrofolate reductase and dihydropteroate synthetase genes reveals new insights into sulfadoxine-pyrimethamine antimalarial drug resistance. PLoS Genetics, 2020, 16, e1009268.	3.5	15
98	Further Evidence Supporting a Role for Gs Signal Transduction in Severe Malaria Pathogenesis. PLoS ONE, 2010, 5, e10017.	2.5	14
99	Malaria Host Candidate Genes Validated by Association With Current, Recent, and Historical Measures of Transmission Intensity. Journal of Infectious Diseases, 2017, 216, 45-54.	4.0	13
100	Genomic Epidemiology of Carbapenemase Producing Klebsiella pneumoniae Strains at a Northern Portuguese Hospital Enables the Detection of a Misidentified Klebsiella variicola KPC-3 Producing Strain. Microorganisms, 2020, 8, 1986.	3.6	13
101	Association of the GNAS locus with severe malaria. Human Genetics, 2008, 124, 499-506.	3.8	12
102	Genetic diversity of next generation antimalarial targets: A baseline for drug resistance surveillance programmes. International Journal for Parasitology: Drugs and Drug Resistance, 2017, 7, 174-180.	3.4	12
103	Failure of rapid diagnostic tests in Plasmodium falciparum malaria cases among travelers to the UK and Ireland: Identification and characterisation of the parasites. International Journal of Infectious Diseases, 2021, 108, 137-144.	3.3	12
104	An In-Solution Hybridisation Method for the Isolation of Pathogen DNA from Human DNA-rich Clinical Samples for Analysis by NGS. The Open Genomics Journal, 2012, 5, 18-29.	0.5	12
105	Lack of Association of Interferon Regulatory Factor 1 with Severe Malaria in Affected Child-Parental Trio Studies across Three African Populations. PLoS ONE, 2009, 4, e4206.	2.5	11
106	Characterizing the genomic variation and population dynamics of Plasmodium falciparum malaria parasites in and around Lake Victoria, Kenya. Scientific Reports, 2021, 11, 19809.	3.3	11
107	Robust detection of point mutations involved in multidrug-resistant Mycobacterium tuberculosis in the presence of co-occurrent resistance markers. PLoS Computational Biology, 2020, 16, e1008518.	3.2	11
108	Methylation analysis of Klebsiella pneumoniae from Portuguese hospitals. Scientific Reports, 2021, 11, 6491.	3.3	10

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109	The primate malaria parasites <i>Plasmodium malariae</i> , <i>Plasmodium brasilianum</i> and <i>Plasmodium ovale</i> spp.: genomic insights into distribution, dispersal and host transitions. <i>Malaria Journal</i> , 2022, 21, 138.	2.3	10
110	SnoopCGH: software for visualizing comparative genomic hybridization data. <i>Bioinformatics</i> , 2009, 25, 2732-2733.	4.1	9
111	Bead-based assays to simultaneously detect multiple human inherited blood disorders associated with malaria. <i>Malaria Journal</i> , 2019, 18, 14.	2.3	9
112	Artemether-lumefantrine treatment failure of uncomplicated <i>Plasmodium falciparum</i> malaria in travellers coming from Angola and Mozambique. <i>International Journal of Infectious Diseases</i> , 2021, 110, 151-154.	3.3	9
113	VarB: a variation browsing and analysis tool for variants derived from next-generation sequencing data. <i>Bioinformatics</i> , 2012, 28, 2983-2985.	4.1	8
114	An analysis of large structural variation in global <i>Plasmodium falciparum</i> isolates identifies a novel duplication of the chloroquine resistance associated gene. <i>Scientific Reports</i> , 2019, 9, 8287.	3.3	8
115	A modified decision tree approach to improve the prediction and mutation discovery for drug resistance in <i>Mycobacterium tuberculosis</i> . <i>BMC Genomics</i> , 2022, 23, 46.	2.8	8
116	Detection of simple and complex de novo mutations with multiple reference sequences. <i>Genome Research</i> , 2020, 30, 1154-1169.	5.5	7
117	Characterization of rifampicin-resistant <i>Mycobacterium tuberculosis</i> in Khyber Pakhtunkhwa, Pakistan. <i>Scientific Reports</i> , 2021, 11, 14194.	3.3	7
118	Characterisation of drug-resistant <i>Mycobacterium tuberculosis</i> mutations and transmission in Pakistan. <i>Scientific Reports</i> , 2022, 12, 7703.	3.3	7
119	Unique Genetic Variation Revealed by a Microsatellite Polymorphism Survey in Ten Wild-Derived Inbred Strains. <i>Genomics</i> , 2002, 79, 618-620.	2.9	6
120	SV-Pop: population-based structural variant analysis and visualization. <i>BMC Bioinformatics</i> , 2019, 20, 136.	2.6	6
121	Drug resistance profile and clonality of <i>Plasmodium falciparum</i> parasites in Cape Verde: the 2017 malaria outbreak. <i>Malaria Journal</i> , 2021, 20, 172.	2.3	6
122	Flavivirus integrations in <i>Aedes aegypti</i> are limited and highly conserved across samples from different geographic regions unlike integrations in <i>Aedes albopictus</i> . <i>Parasites and Vectors</i> , 2021, 14, 332.	2.5	6
123	Whole genome sequencing reveals large deletions and other loss of function mutations in <i>Mycobacterium tuberculosis</i> drug resistance genes. <i>Microbial Genomics</i> , 2021, 7, .	2.0	6
124	A phylogenomic approach for the analysis of colistin resistance-associated genes in <i>Klebsiella pneumoniae</i> , its mutational diversity and implications for phenotypic resistance. <i>International Journal of Antimicrobial Agents</i> , 2022, 59, 106581.	2.5	5
125	Association of common TMPRSS6 and TF gene variants with hepcidin and iron status in healthy rural Gambians. <i>Scientific Reports</i> , 2021, 11, 8075.	3.3	4
126	A recall-by-genotype study on polymorphisms in the TMPRSS6 gene and oral iron absorption: a study protocol. <i>F1000Research</i> , 0, 8, 701.	1.6	4

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127	How has mass drug administration with dihydroartemisinin-piperazine impacted molecular markers of drug resistance? A systematic review. <i>Malaria Journal</i> , 2022, 21, .	2.3	4
128	Whole-genome sequencing as a tool for studying the microevolution of drug-resistant serial <i>Mycobacterium tuberculosis</i> isolates. <i>Tuberculosis</i> , 2021, 131, 102137.	1.9	3
129	<i>Klebsiella pneumoniae</i> and Colistin Susceptibility Testing: Performance Evaluation for Broth Microdilution, Agar Dilution and Minimum Inhibitory Concentration Test Strips and Impact of the "Skipped Well" Phenomenon. <i>Diagnostics</i> , 2021, 11, 2352.	2.6	3
130	COVID-profiler: a webserver for the analysis of SARS-CoV-2 sequencing data. <i>BMC Bioinformatics</i> , 2022, 23, 137.	2.6	3
131	De Novo Assembly of <i>Plasmodium knowlesi</i> Genomes From Clinical Samples Explains the Counterintuitive Intrachromosomal Organization of Variant <i>SICAvar</i> and <i>kir</i> Multiple Gene Family Members. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	3
132	Common Variants in the <i>TMPRSS6</i> Gene Alter Hepcidin but not Plasma Iron in Response to Oral Iron in Healthy Gambian Adults: A Recall-by-Genotype Study. <i>Current Developments in Nutrition</i> , 2021, 5, nza014.	0.3	2
133	Sero-epidemiological study of arbovirus infection following the 2015–2016 Zika virus outbreak in Cabo Verde. <i>Scientific Reports</i> , 2022, 12, .	3.3	2
134	<i>G6PD</i> Polymorphisms and Hemolysis After Antimalarial Treatment With Low Single-Dose Primaquine: A Pooled Analysis of Six African Clinical Trials. <i>Frontiers in Genetics</i> , 2021, 12, 645688.	2.3	1
135	Identification of Single-Nucleotide Polymorphisms in the Mitochondrial Genome and <i>Kelch 13</i> Gene of <i>Plasmodium falciparum</i> in Different Geographical Populations. <i>American Journal of Tropical Medicine and Hygiene</i> , 2021, , .	1.4	1