

Ernest Diez Benavente

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

39 papers	546 citations	14 h-index	22 g-index
45 ext. papers	824 ext. citations	5.3 avg, IF	3.36 L-index

#	Paper	IF	Citations
39	Modest heterologous protection after Plasmodium falciparum sporozoite immunization: a double-blind randomized controlled clinical trial. <i>BMC Medicine</i> , 2017 , 15, 168	11.4	56
38	Genome-scale comparison of expanded gene families in Plasmodium ovale wallikeri and Plasmodium ovale curtisi with Plasmodium malariae and with other Plasmodium species. <i>International Journal for Parasitology</i> , 2016 , 46, 685-96	4.3	43
37	Discordant bioinformatic predictions of antimicrobial resistance from whole-genome sequencing data of bacterial isolates: an inter-laboratory study. <i>Microbial Genomics</i> , 2020 , 6,	4.4	33
36	Rapid and iterative genome editing in the malaria parasite provides new tools for research. <i>ELife</i> , 2019 , 8,	8.9	32
35	Global genetic diversity of var2csa in Plasmodium falciparum with implications for malaria in pregnancy and vaccine development. <i>Scientific Reports</i> , 2018 , 8, 15429	4.9	29
34	Genomic analysis of a pre-elimination Malaysian Plasmodium vivax population reveals selective pressures and changing transmission dynamics. <i>Nature Communications</i> , 2018 , 9, 2585	17.4	29
33	Characterizing the impact of sustained sulfadoxine/pyrimethamine use upon the Plasmodium falciparum population in Malawi. <i>Malaria Journal</i> , 2016 , 15, 575	3.6	28
32	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	4.5	28
31	Machine Learning Predicts Accurately Drug Resistance From Whole Genome Sequencing Data. <i>Frontiers in Genetics</i> , 2019 , 10, 922	4.5	25
30	Know Your Heart: Rationale, design and conduct of a cross-sectional study of cardiovascular structure, function and risk factors in 4500 men and women aged 35-69 years from two Russian cities, 2015-18. <i>Wellcome Open Research</i> , 2018 , 3, 67	4.8	24
29	Know Your Heart: Rationale, design and conduct of a cross-sectional study of cardiovascular structure, function and risk factors in 4500 men and women aged 35-69 years from two Russian cities, 2015-18. <i>Wellcome Open Research</i> , 2018 , 3, 67	4.8	20
28	Genomic variation in Plasmodium vivax malaria reveals regions under selective pressure. <i>PLoS ONE</i> , 2017 , 12, e0177134	3.7	17
27	PhyTB: Phylogenetic tree visualisation and sample positioning for M. tuberculosis. <i>BMC Bioinformatics</i> , 2015 , 16, 155	3.6	16
26	Genomic variation in two gametocyte non-producing Plasmodium falciparum clonal lines. <i>Malaria Journal</i> , 2016 , 15, 229	3.6	15
25	Artemisinin resistance-associated markers in Plasmodium falciparum 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	3.7	14
24	Analysis of nuclear and organellar genomes of Plasmodium knowlesi in humans reveals ancient population structure and recent recombination among host-specific subpopulations. <i>PLoS Genetics</i> , 2017 , 13, e1007008	6	13
23	Whole genome sequencing of amplified Plasmodium knowlesi DNA from unprocessed blood reveals genetic exchange events between Malaysian Peninsular and Borneo subpopulations. <i>Scientific Reports</i> , 2019 , 9, 9873	4.9	13

22	Know Your Heart: Rationale, design and conduct of a cross-sectional study of cardiovascular structure, function and risk factors in 4500 men and women aged 35-69 years from two Russian cities, 2015-18. <i>Wellcome Open Research</i> ,3, 67	4.8	13
21	A forward genetic screen reveals a primary role for Plasmodium falciparum Reticulocyte Binding Protein Homologue 2a and 2b in determining alternative erythrocyte invasion pathways. <i>PLoS Pathogens</i> , 2018 , 14, e1007436	7.6	13
20	A reference genome and methylome for the Plasmodium knowlesi A1-H.1 line. <i>International Journal for Parasitology</i> , 2018 , 48, 191-196	4.3	12
19	Genetic diversity of next generation antimalarial targets: A baseline for drug resistance surveillance programmes. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2017 , 7, 174-180	4	10
18	VivaxGEN: An open access platform for comparative analysis of short tandem repeat genotyping data in Plasmodium vivax populations. <i>PLoS Neglected Tropical Diseases</i> , 2017 , 11, e0005465	4.8	10
17	A molecular barcode to inform the geographical origin and transmission dynamics of Plasmodium vivax malaria. <i>PLoS Genetics</i> , 2020 , 16, e1008576	6	7
16	External validation of a deep learning electrocardiogram algorithm to detect ventricular dysfunction. <i>International Journal of Cardiology</i> , 2021 , 329, 130-135	3.2	7
15	An analysis of large structural variation in global Plasmodium falciparum isolates identifies a novel duplication of the chloroquine resistance associated gene. <i>Scientific Reports</i> , 2019 , 9, 8287	4.9	6
14	Selective whole genome amplification of Plasmodium malariae DNA from clinical samples reveals insights into population structure. <i>Scientific Reports</i> , 2020 , 10, 10832	4.9	5
13	Distinctive genetic structure and selection patterns in Plasmodium vivax from South Asia and East Africa. <i>Nature Communications</i> , 2021 , 12, 3160	17.4	5
12	Using deep learning to identify recent positive selection in malaria parasite sequence data. <i>Malaria Journal</i> , 2021 , 20, 270	3.6	4
11	Genetic diversity of the Plasmodium falciparum GTP-cyclohydrolase 1, dihydrofolate reductase and dihydropteroate synthetase genes reveals new insights into sulfadoxine-pyrimethamine antimalarial drug resistance. <i>PLoS Genetics</i> , 2020 , 16, e1009268	6	3
10	Drug resistance profile and clonality of Plasmodium falciparum parasites in Cape Verde: the 2017 malaria outbreak. <i>Malaria Journal</i> , 2021 , 20, 172	3.6	3
9	An inter-laboratory study to investigate the impact of the bioinformatics component on microbiome analysis using mock communities. <i>Scientific Reports</i> , 2021 , 11, 10590	4.9	3
8	Failure of rapid diagnostic tests in Plasmodium falciparum malaria cases among travelers to the UK and Ireland: Identification and characterisation of the parasites. <i>International Journal of Infectious Diseases</i> , 2021 , 108, 137-144	10.5	3
7	Studying accelerated cardiovascular ageing in Russian adults through a novel deep-learning ECG biomarker. <i>Wellcome Open Research</i> ,6, 12	4.8	3
6	Rapid and iterative genome editing in the zoonotic malaria parasite Plasmodium knowlesi: New tools for P. vivax research		1
5	Flavivirus integrations in Aedes aegypti are limited and highly conserved across samples from different geographic regions unlike integrations in Aedes albopictus. <i>Parasites and Vectors</i> , 2021 , 14, 332	4	1

4	Artemether-lumefantrine treatment failure of uncomplicated Plasmodium falciparum malaria in travellers coming from Angola and Mozambique. <i>International Journal of Infectious Diseases</i> , 2021 , 110, 151-154	10.5	1
3	The antimalarial efficacy and mechanism of resistance of the novel chemotype DDD01034957. <i>Scientific Reports</i> , 2021 , 11, 1888	4.9	0
2	Skin microbiome alters attractiveness to Anopheles mosquitoes.. <i>BMC Microbiology</i> , 2022 , 22, 98	4.5	0
1	Plasma Testosterone Levels and Atherosclerotic Plaque Gene Expression in Men With Advanced Atherosclerosis. <i>Frontiers in Cardiovascular Medicine</i> , 2021 , 8, 693351	5.4	