

Ernest Diez Benavente

List of Publications by Year in Descending Order

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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	Skin microbiome alters attractiveness to <i>Anopheles</i> mosquitoes.. <i>BMC Microbiology</i> , 2022 , 22, 98	4.5	0
38	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	3.6	3
37	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
36	Distinctive genetic structure and selection patterns in <i>Plasmodium vivax</i> from South Asia and East Africa. <i>Nature Communications</i> , 2021 , 12, 3160	17.4	5
35	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
34	Using deep learning to identify recent positive selection in malaria parasite sequence data. <i>Malaria Journal</i> , 2021 , 20, 270	3.6	4
33	Plasma Testosterone Levels and Atherosclerotic Plaque Gene Expression in Men With Advanced Atherosclerosis. <i>Frontiers in Cardiovascular Medicine</i> , 2021 , 8, 693351	5.4	
32	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	4	1
31	Failure of rapid diagnostic tests in <i>Plasmodium falciparum</i> 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
30	The antimalarial efficacy and mechanism of resistance of the novel chemotype DDD01034957. <i>Scientific Reports</i> , 2021 , 11, 1888	4.9	0
29	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	10.5	1
28	A molecular barcode to inform the geographical origin and transmission dynamics of <i>Plasmodium vivax</i> malaria. <i>PLoS Genetics</i> , 2020 , 16, e1008576	6	7
27	Genetic diversity of the <i>Plasmodium falciparum</i> 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
26	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
25	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	4.9	5
24	Machine Learning Predicts Accurately Drug Resistance From Whole Genome Sequencing Data. <i>Frontiers in Genetics</i> , 2019 , 10, 922	4.5	25
23	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	3.7	14

22	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	4.9	13
21	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	4.9	6
20	Rapid and iterative genome editing in the malaria parasite provides new tools for research. <i>ELife</i> , 2019 , 8,	8.9	32
19	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	4.3	12
18	Global analysis of <i>Plasmodium falciparum</i> histidine-rich protein-2 (pfrp2) and pfrp3 gene deletions using whole-genome sequencing data and meta-analysis. <i>Infection, Genetics and Evolution</i> , 2018 , 62, 211-219	4.5	28
17	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
16	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
15	A forward genetic screen reveals a primary role for <i>Plasmodium falciparum</i> Reticulocyte Binding Protein Homologue 2a and 2b in determining alternative erythrocyte invasion pathways. <i>PLoS Pathogens</i> , 2018 , 14, e1007436	7.6	13
14	Global genetic diversity of var2csa in <i>Plasmodium falciparum</i> with implications for malaria in pregnancy and vaccine development. <i>Scientific Reports</i> , 2018 , 8, 15429	4.9	29
13	Genomic analysis of a pre-elimination Malaysian <i>Plasmodium vivax</i> population reveals selective pressures and changing transmission dynamics. <i>Nature Communications</i> , 2018 , 9, 2585	17.4	29
12	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
11	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	6	13
10	Modest heterologous protection after <i>Plasmodium falciparum</i> sporozoite immunization: a double-blind randomized controlled clinical trial. <i>BMC Medicine</i> , 2017 , 15, 168	11.4	56
9	VivaxGEN: An open access platform for comparative analysis of short tandem repeat genotyping data in <i>Plasmodium vivax</i> populations. <i>PLoS Neglected Tropical Diseases</i> , 2017 , 11, e0005465	4.8	10
8	Genomic variation in <i>Plasmodium vivax</i> malaria reveals regions under selective pressure. <i>PLoS ONE</i> , 2017 , 12, e0177134	3.7	17
7	Genome-scale comparison of expanded gene families in <i>Plasmodium ovale wallikeri</i> and <i>Plasmodium ovale curtisi</i> with <i>Plasmodium malariae</i> and with other <i>Plasmodium</i> species. <i>International Journal for Parasitology</i> , 2016 , 46, 685-96	4.3	43
6	Characterizing the impact of sustained sulfadoxine/pyrimethamine use upon the <i>Plasmodium falciparum</i> population in Malawi. <i>Malaria Journal</i> , 2016 , 15, 575	3.6	28
5	Genomic variation in two gametocyte non-producing <i>Plasmodium falciparum</i> clonal lines. <i>Malaria Journal</i> , 2016 , 15, 229	3.6	15

4	PhyTB: Phylogenetic tree visualisation and sample positioning for M. tuberculosis. <i>BMC Bioinformatics</i> , 2015 , 16, 155	3.6	16
3	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
2	Rapid and iterative genome editing in the zoonotic malaria parasite <i>Plasmodium knowlesi</i> : New tools for <i>P. vivax</i> research		1
1	Studying accelerated cardiovascular ageing in Russian adults through a novel deep-learning ECG biomarker. <i>Wellcome Open Research</i> , 6, 12	4.8	3