

# Roberto Amato

## List of Publications by Year in descending order

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Version: 2024-02-01

45  
papers

5,283  
citations

218677

26  
h-index

361022

35  
g-index

56  
all docs

56  
docs citations

56  
times ranked

5184  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Genetic architecture of artemisinin-resistant <i>Plasmodium falciparum</i> . <i>Nature Genetics</i> , 2015, 47, 226-234.	21.4	515
3	Dihydroartemisinin-piperazine resistance in <i>Plasmodium falciparum</i> malaria in Cambodia: a multisite prospective cohort study. <i>Lancet Infectious Diseases</i> , The, 2016, 16, 357-365.	9.1	381
4	Genetic markers associated with dihydroartemisinin-piperazine failure in <i>Plasmodium falciparum</i> malaria in Cambodia: a genotype-phenotype association study. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 164-173.	9.1	301
5	Determinants of dihydroartemisinin-piperazine treatment failure in <i>Plasmodium falciparum</i> malaria in Cambodia, Thailand, and Vietnam: a prospective clinical, pharmacological, and genetic study. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 952-961.	9.1	252
6	Evolution and expansion of multidrug-resistant malaria in southeast Asia: a genomic epidemiology study. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 943-951.	9.1	219
7	Triple artemisinin-based combination therapies versus artemisinin-based combination therapies for uncomplicated <i>Plasmodium falciparum</i> malaria: a multicentre, open-label, randomised clinical trial. <i>Lancet</i> , The, 2020, 395, 1345-1360.	13.7	182
8	Genomic analysis of local variation and recent evolution in <i>Plasmodium vivax</i> . <i>Nature Genetics</i> , 2016, 48, 959-964.	21.4	169
9	FLASH: a next-generation CRISPR diagnostic for multiplexed detection of antimicrobial resistance sequences. <i>Nucleic Acids Research</i> , 2019, 47, e83-e83.	14.5	168
10	Origins of the current outbreak of multidrug-resistant malaria in southeast Asia: a retrospective genetic study. <i>Lancet Infectious Diseases</i> , The, 2018, 18, 337-345.	9.1	161
11	Major subpopulations of <i>Plasmodium falciparum</i> in sub-Saharan Africa. <i>Science</i> , 2019, 365, 813-816.	12.6	105
12	An open dataset of <i>Plasmodium falciparum</i> genome variation in 7,000 worldwide samples. <i>Wellcome Open Research</i> , 2021, 6, 42.	1.8	97
13	THE REAL McCOIL: A method for the concurrent estimation of the complexity of infection and SNP allele frequency for malaria parasites. <i>PLoS Computational Biology</i> , 2017, 13, e1005348.	3.2	93
14	Emergence of artemisinin-resistant <i>Plasmodium falciparum</i> with kelch13 C580Y mutations on the island of New Guinea. <i>PLoS Pathogens</i> , 2020, 16, e1009133.	4.7	81
15	Estimating Geographical Variation in the Risk of Zoonotic <i>Plasmodium knowlesi</i> Infection in Countries Eliminating Malaria. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004915.	3.0	76
16	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.	12.8	59
17	Genetic surveillance in the Greater Mekong subregion and South Asia to support malaria control and elimination. <i>ELife</i> , 2021, 10, .	6.0	53
18	The origins and relatedness structure of mixed infections vary with local prevalence of <i>P. falciparum</i> malaria. <i>ELife</i> , 2019, 8, .	6.0	52

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19	An open dataset of Plasmodium falciparum genome variation in 7,000 worldwide samples. Wellcome Open Research, 2021, 6, 42.	1.8	51
20	Genomic Analysis of Plasmodium vivax in Southern Ethiopia Reveals Selective Pressures in Multiple Parasite Mechanisms. Journal of Infectious Diseases, 2019, 220, 1738-1749.	4.0	50
21	Genome-Wide Scan for Signatures of Human Population Differentiation and Their Relationship with Natural Selection, Functional Pathways and Diseases. PLoS ONE, 2009, 4, e7927.	2.5	36
22	Malaria protection due to sickle haemoglobin depends on parasite genotype. Nature, 2022, 602, 106-111.	27.8	36
23	Consistent signatures of selection from genomic analysis of pairs of temporal and spatial Plasmodium falciparum populations from The Gambia. Scientific Reports, 2018, 8, 9687.	3.3	33
24	Schizophrenia and vitamin D related genes could have been subject to latitude-driven adaptation. BMC Evolutionary Biology, 2010, 10, 351.	3.2	32
25	Estimating the Ages of Selection Signals from Different Epochs in Human History. Molecular Biology and Evolution, 2016, 33, 657-669.	8.9	32
26	Molecular markers for artemisinin and partner drug resistance in natural Plasmodium falciparum populations following increased insecticide treated net coverage along the slope of mount Cameroon: cross-sectional study. Infectious Diseases of Poverty, 2017, 6, 136.	3.7	32
27	A novel approach to simulate gene-environment interactions in complex diseases. BMC Bioinformatics, 2010, 11, 8.	2.6	31
28	A single nucleotide polymorphism in the Plasmodium falciparum atg18 gene associates with artemisinin resistance and confers enhanced parasite survival under nutrient deprivation. Malaria Journal, 2018, 17, 391.	2.3	30
29	Genomic Analysis Reveals a Common Breakpoint in Amplifications of the Plasmodium vivax Multidrug Resistance 1 Locus in Thailand. Journal of Infectious Diseases, 2016, 214, 1235-1242.	4.0	29
30	A Genome Wide Association Study of Plasmodium falciparum Susceptibility to 22 Antimalarial Drugs in Kenya. PLoS ONE, 2014, 9, e96486.	2.5	27
31	A network-based approach to dissect the cilia/centrosome complex interactome. BMC Genomics, 2014, 15, 658.	2.8	19
32	Development of copy number assays for detection and surveillance of piperaquine resistance associated plasmepsin 2/3 copy number variation in Plasmodium falciparum. Malaria Journal, 2020, 19, 181.	2.3	18
33	An open dataset of Plasmodium vivax genome variation in 1,895 worldwide samples. Wellcome Open Research, 0, 7, 136.	1.8	16
34	Simulating gene-gene and gene-environment interactions in complex diseases: Gene-Environment Interaction Simulator 2. BMC Bioinformatics, 2012, 13, 132.	2.6	12
35	Spatio-temporal distribution of antimalarial drug resistant gene mutations in a Plasmodium falciparum parasite population from Kilifi, Kenya: A 25-year retrospective study. Wellcome Open Research, 0, 7, 45.	1.8	8
36	Panoptes: web-based exploration of large scale genome variation data. Bioinformatics, 2017, 33, 3243-3249.	4.1	6

#	ARTICLE	IF	CITATIONS
37	Signs of Selective Pressure on Genetic Variants Affecting Human Height. PLoS ONE, 2011, 6, e27588.	2.5	5
38	An improved combinatorial biclustering algorithm. Neural Computing and Applications, 2013, 22, 293-302.	5.6	0
39	Advances in Computational Methods for Genetic Diseases. Computational and Mathematical Methods in Medicine, 2015, 2015, 1-2.	1.3	0
40	Juggling resistance mutations. Nature Reviews Microbiology, 2018, 16, 332-332.	28.6	0
41	Novel Techniques for Microarray Data Analysis: Probabilistic Principal Surfaces and Competitive Evolution on Data. Journal of Computational and Theoretical Nanoscience, 2005, 2, 514-523.	0.4	0
42	Title is missing!. , 2020, 16, e1009133.		0
43	Title is missing!. , 2020, 16, e1009133.		0
44	Title is missing!. , 2020, 16, e1009133.		0
45	Title is missing!. , 2020, 16, e1009133.		0