

# 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	Malaria protection due to sickle haemoglobin depends on parasite genotype. <i>Nature</i> , 2022, 602, 106-111.	27.8	36
2	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
3	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	51
4	Genetic surveillance in the Greater Mekong subregion and South Asia to support malaria control and elimination. <i>ELife</i> , 2021, 10, .	6.0	53
5	Development of copy number assays for detection and surveillance of piperaquine resistance associated plasmepsin 2/3 copy number variation in <i>Plasmodium falciparum</i> . <i>Malaria Journal</i> , 2020, 19, 181.	2.3	18
6	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
7	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
8	Title is missing!. , 2020, 16, e1009133.		0
9	Title is missing!. , 2020, 16, e1009133.		0
10	Title is missing!. , 2020, 16, e1009133.		0
11	Title is missing!. , 2020, 16, e1009133.		0
12	Major subpopulations of <i>Plasmodium falciparum</i> in sub-Saharan Africa. <i>Science</i> , 2019, 365, 813-816.	12.6	105
13	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
14	Determinants of dihydroartemisinin-piperaquine 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
15	Genomic Analysis of <i>Plasmodium vivax</i> in Southern Ethiopia Reveals Selective Pressures in Multiple Parasite Mechanisms. <i>Journal of Infectious Diseases</i> , 2019, 220, 1738-1749.	4.0	50
16	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
17	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
18	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

#	ARTICLE	IF	CITATIONS
19	Juggling resistance mutations. <i>Nature Reviews Microbiology</i> , 2018, 16, 332-332.	28.6	0
20	A single nucleotide polymorphism in the <i>Plasmodium falciparum</i> atg18 gene associates with artemisinin resistance and confers enhanced parasite survival under nutrient deprivation. <i>Malaria Journal</i> , 2018, 17, 391.	2.3	30
21	Consistent signatures of selection from genomic analysis of pairs of temporal and spatial <i>Plasmodium falciparum</i> populations from The Gambia. <i>Scientific Reports</i> , 2018, 8, 9687.	3.3	33
22	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
23	Panoptes: web-based exploration of large scale genome variation data. <i>Bioinformatics</i> , 2017, 33, 3243-3249.	4.1	6
24	Genetic markers associated with dihydroartemisinin–piperaquine 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
25	Molecular markers for artemisinin and partner drug resistance in natural <i>Plasmodium falciparum</i> populations following increased insecticide treated net coverage along the slope of mount Cameroon: cross-sectional study. <i>Infectious Diseases of Poverty</i> , 2017, 6, 136.	3.7	32
26	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
27	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
28	Genomic Analysis Reveals a Common Breakpoint in Amplifications of the <i>Plasmodium vivax</i> Multidrug Resistance 1 Locus in Thailand. <i>Journal of Infectious Diseases</i> , 2016, 214, 1235-1242.	4.0	29
29	Genomic analysis of local variation and recent evolution in <i>Plasmodium vivax</i> . <i>Nature Genetics</i> , 2016, 48, 959-964.	21.4	169
30	Dihydroartemisinin–piperaquine 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
31	Estimating the Ages of Selection Signals from Different Epochs in Human History. <i>Molecular Biology and Evolution</i> , 2016, 33, 657-669.	8.9	32
32	Advances in Computational Methods for Genetic Diseases. <i>Computational and Mathematical Methods in Medicine</i> , 2015, 2015, 1-2.	1.3	0
33	Genetic architecture of artemisinin-resistant <i>Plasmodium falciparum</i> . <i>Nature Genetics</i> , 2015, 47, 226-234.	21.4	515
34	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
35	A network-based approach to dissect the cilia/centrosome complex interactome. <i>BMC Genomics</i> , 2014, 15, 658.	2.8	19
36	A Genome Wide Association Study of <i>Plasmodium falciparum</i> Susceptibility to 22 Antimalarial Drugs in Kenya. <i>PLoS ONE</i> , 2014, 9, e96486.	2.5	27

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37	An improved combinatorial biclustering algorithm. <i>Neural Computing and Applications</i> , 2013, 22, 293-302.	5.6	0
38	Simulating gene-gene and gene-environment interactions in complex diseases: Gene-Environment iNteraction Simulator 2. <i>BMC Bioinformatics</i> , 2012, 13, 132.	2.6	12
39	Signs of Selective Pressure on Genetic Variants Affecting Human Height. <i>PLoS ONE</i> , 2011, 6, e27588.	2.5	5
40	A novel approach to simulate gene-environment interactions in complex diseases. <i>BMC Bioinformatics</i> , 2010, 11, 8.	2.6	31
41	Schizophrenia and vitamin D related genes could have been subject to latitude-driven adaptation. <i>BMC Evolutionary Biology</i> , 2010, 10, 351.	3.2	32
42	Genome-Wide Scan for Signatures of Human Population Differentiation and Their Relationship with Natural Selection, Functional Pathways and Diseases. <i>PLoS ONE</i> , 2009, 4, e7927.	2.5	36
43	Novel Techniques for Microarray Data Analysis: Probabilistic Principal Surfaces and Competitive Evolution on Data. <i>Journal of Computational and Theoretical Nanoscience</i> , 2005, 2, 514-523.	0.4	0
44	Spatio-temporal distribution of antimalarial drug resistant gene mutations in a <i>Plasmodium falciparum</i> parasite population from Kilifi, Kenya: A 25-year retrospective study. <i>Wellcome Open Research</i> , 0, 7, 45.	1.8	8
45	An open dataset of <i>Plasmodium vivax</i> genome variation in 1,895 worldwide samples. <i>Wellcome Open Research</i> , 0, 7, 136.	1.8	16