

Ananias A Escalante

List of Publications by Year in descending order

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154
papers

8,756
citations

38742

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51608

86
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158
all docs

158
docs citations

158
times ranked

6464
citing authors

#	ARTICLE	IF	CITATIONS
1	The evolution of primate malaria parasites based on the gene encoding cytochrome b from the linear mitochondrial genome. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 8124-8129.	7.1	344
2	Genetic Polymorphism Among <i>Cryptosporidium parvum</i> Isolates: Evidence of Two Distinct Human Transmission Cycles. Emerging Infectious Diseases, 1997, 3, 567-573.	4.3	339
3	Two Nonrecombining Sympatric Forms of the Human Malaria Parasite <i>Plasmodium ovale</i> Occur Globally. Journal of Infectious Diseases, 2010, 201, 1544-1550.	4.0	310
4	Phylogeny of the malarial genus <i>Plasmodium</i> , derived from rRNA gene sequences.. Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 11373-11377.	7.1	280
5	The malaria parasite <i>Plasmodium vivax</i> exhibits greater genetic diversity than <i>Plasmodium falciparum</i> . Nature Genetics, 2012, 44, 1046-1050.	21.4	256
6	Association of <i>Plasmodium falciparum</i> kelch13 R561H genotypes with delayed parasite clearance in Rwanda: an open-label, single-arm, multicentre, therapeutic efficacy study. Lancet Infectious Diseases, The, 2021, 21, 1120-1128.	9.1	231
7	Genetic Polymorphism and Natural Selection in the Malaria Parasite <i>Plasmodium falciparum</i> . Genetics, 1998, 149, 189-202.	2.9	221
8	Evolution of Modern Birds Revealed by Mitogenomics: Timing the Radiation and Origin of Major Orders. Molecular Biology and Evolution, 2011, 28, 1927-1942.	8.9	211
9	Wild Primate Populations in Emerging Infectious Disease Research: The Missing Link?. Emerging Infectious Diseases, 1998, 4, 149-158.	4.3	207
10	Evolutionary origin of <i>Plasmodium</i> and other Apicomplexa based on rRNA genes.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 5793-5797.	7.1	204
11	A monkey's tale: The origin of <i>Plasmodium vivax</i> as a human malaria parasite. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 1980-1985.	7.1	202
12	Evolutionary origin of human and primate malarias: evidence from the circumsporozoite protein gene.. Molecular Biology and Evolution, 1995, 12, 616-26.	8.9	184
13	On the Diversity of Malaria Parasites in African Apes and the Origin of <i>Plasmodium falciparum</i> from Bonobos. PLoS Pathogens, 2010, 6, e1000765.	4.7	184
14	Diversity and Evolution of the Envelope Gene of Dengue Virus Type 1. Virology, 2002, 303, 110-119.	2.4	172
15	<i>Plasmodium cynomolgi</i> genome sequences provide insight into <i>Plasmodium vivax</i> and the monkey malaria clade. Nature Genetics, 2012, 44, 1051-1055.	21.4	172
16	Extreme Polymorphism in a Vaccine Antigen and Risk of Clinical Malaria: Implications for Vaccine Development. Science Translational Medicine, 2009, 1, 2ra5.	12.4	154
17	Mitochondrial DNA sequence variation among triatomine vectors of Chagas' disease.. American Journal of Tropical Medicine and Hygiene, 1999, 60, 377-386.	1.4	131
18	Antifolate Resistance in <i>Plasmodium falciparum</i> : Multiple Origins and Identification of Novel dhfr Alleles. Journal of Infectious Diseases, 2006, 194, 189-197.	4.0	122

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19	Mode and Rate of Evolution of Haemosporidian Mitochondrial Genomes: Timing the Radiation of Avian Parasites. <i>Molecular Biology and Evolution</i> , 2018, 35, 383-403.	8.9	122
20	<i>Plasmodium falciparum</i> Accompanied the Human Expansion out of Africa. <i>Current Biology</i> , 2010, 20, 1283-1289.	3.9	121
21	The genetic diversity of <i>Plasmodium vivax</i> populations. <i>Trends in Parasitology</i> , 2003, 19, 220-226.	3.3	115
22	Origin and Evolution of Sulfadoxine Resistant <i>Plasmodium falciparum</i> . <i>PLoS Pathogens</i> , 2010, 6, e1000830.	4.7	114
23	Common Origin and Fixation of <i>Plasmodium falciparum</i> dhfr and dhps Mutations Associated with Sulfadoxine-Pyrimethamine Resistance in a Low-Transmission Area in South America. <i>Antimicrobial Agents and Chemotherapy</i> , 2007, 51, 2085-2091.	3.2	111
24	The Evolutionary History of <i>Plasmodium vivax</i> as Inferred from Mitochondrial Genomes: Parasite Genetic Diversity in the Americas. <i>Molecular Biology and Evolution</i> , 2013, 30, 2050-2064.	8.9	110
25	Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-1) of <i>Plasmodium falciparum</i> . X. Asembo Bay Cohort Project. <i>Molecular and Biochemical Parasitology</i> , 2001, 113, 279-287.	1.1	108
26	The origin and age of <i>Plasmodium vivax</i> . <i>Trends in Parasitology</i> , 2006, 22, 558-563.	3.3	103
27	Assessing the effect of natural selection in malaria parasites. <i>Trends in Parasitology</i> , 2004, 20, 388-395.	3.3	99
28	Timing the origin of human malarias: the lemur puzzle. <i>BMC Evolutionary Biology</i> , 2011, 11, 299.	3.2	85
29	Malaria Molecular Epidemiology: Lessons from the International Centers of Excellence for Malaria Research Network. <i>American Journal of Tropical Medicine and Hygiene</i> , 2015, 93, 79-86.	1.4	80
30	Malaria in selected non-Amazonian countries of Latin America. <i>Acta Tropica</i> , 2012, 121, 303-314.	2.0	76
31	Human migration and the spread of malaria parasites to the New World. <i>Scientific Reports</i> , 2018, 8, 1993.	3.3	76
32	Applied Genomics: Data Mining Reveals Species-Specific Malaria Diagnostic Targets More Sensitive than 18S rRNA. <i>Journal of Clinical Microbiology</i> , 2011, 49, 2411-2418.	3.9	74
33	The Evolution of Human Populations: A Molecular Perspective. <i>Molecular Phylogenetics and Evolution</i> , 1996, 5, 188-201.	2.7	73
34	Local population structure of <i>Plasmodium</i> : impact on malaria control and elimination. <i>Malaria Journal</i> , 2012, 11, 412.	2.3	73
35	Accelerated Diversification of Nonhuman Primate Malarias in Southeast Asia: Adaptive Radiation or Geographic Speciation?. <i>Molecular Biology and Evolution</i> , 2015, 32, 422-439.	8.9	73
36	Real-Time Loop-Mediated Isothermal Amplification (RealAmp) for the Species-Specific Identification of <i>Plasmodium vivax</i> . <i>PLoS ONE</i> , 2013, 8, e54986.	2.5	68

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37	South American <i>Plasmodium falciparum</i> after the Malaria Eradication Era: Clonal Population Expansion and Survival of the Fittest Hybrids. <i>PLoS ONE</i> , 2011, 6, e23486.	2.5	66
38	Evidence of purifying selection on merozoite surface protein 8 (MSP8) and 10 (MSP10) in <i>Plasmodium</i> spp.. <i>Infection, Genetics and Evolution</i> , 2012, 12, 978-986.	2.3	65
39	Hitchhiking and Selective Sweeps of <i>Plasmodium falciparum</i> Sulfadoxine and Pyrimethamine Resistance Alleles in a Population from Central Africa. <i>Antimicrobial Agents and Chemotherapy</i> , 2008, 52, 4089-4097.	3.2	64
40	Dynamics of Malaria Drug Resistance Patterns in the Amazon Basin Region following Changes in Peruvian National Treatment Policy for Uncomplicated Malaria. <i>Antimicrobial Agents and Chemotherapy</i> , 2009, 53, 2042-2051.	3.2	64
41	A study of genetic diversity in the gene encoding the circumsporozoite protein (CSP) of <i>Plasmodium falciparum</i> from different transmission areas in XVI. Asembo Bay Cohort Project. <i>Molecular and Biochemical Parasitology</i> , 2002, 125, 83-90.	1.1	61
42	Primers targeting mitochondrial genes of avian haemosporidians: PCR detection and differential DNA amplification of parasites belonging to different genera. <i>International Journal for Parasitology</i> , 2018, 48, 657-670.	3.1	60
43	Malarial parasite diversity in chimpanzees: the value of comparative approaches to ascertain the evolution of <i>Plasmodium falciparum</i> antigens. <i>Malaria Journal</i> , 2013, 12, 328.	2.3	59
44	pfmdr1 Amplification and Fixation of pfCRT Chloroquine Resistance Alleles in <i>Plasmodium falciparum</i> in Venezuela. <i>Antimicrobial Agents and Chemotherapy</i> , 2010, 54, 1572-1579.	3.2	58
45	Pyrosequencing, a High-Throughput Method for Detecting Single Nucleotide Polymorphisms in the Dihydrofolate Reductase and Dihydropteroate Synthetase Genes of <i>Plasmodium falciparum</i> . <i>Journal of Clinical Microbiology</i> , 2006, 44, 3900-3910.	3.9	57
46	Comparative evolutionary genomics of human malaria parasites. <i>Trends in Parasitology</i> , 2008, 24, 545-550.	3.3	57
47	Molecular tools and triatomine systematics: a public health perspective. <i>Trends in Parasitology</i> , 2001, 17, 344-347.	3.3	54
48	Multiple Genetic Backgrounds of the Amplified <i>Plasmodium falciparum</i> Multidrug Resistance (<i>pfmdr1</i>) Gene and Selective Sweep of 184F Mutation in Cambodia. <i>Journal of Infectious Diseases</i> , 2010, 201, 1551-1560.	4.0	54
49	Genetic diversity in the Block 2 region of the merozoite surface protein 1 (MSP-1) of <i>Plasmodium falciparum</i> : Additional complexity and selection and convergence in fragment size polymorphism. <i>Infection, Genetics and Evolution</i> , 2006, 6, 417-424.	2.3	53
50	Evolution and phylogeny of the heterogeneous cytosolic SSU rRNA genes in the genus <i>Plasmodium</i> . <i>Molecular Phylogenetics and Evolution</i> , 2008, 47, 45-53.	2.7	53
51	Molecular evolution and intragenic recombination of the merozoite surface protein MSP-3 from the malaria parasite <i>Plasmodium vivax</i> in Thailand. <i>Parasitology</i> , 2005, 131, 25-35.	1.5	52
52	Prevalence of point mutations in the dihydrofolate reductase and dihydropteroate synthetase genes of <i>Plasmodium falciparum</i> isolates from India and Thailand: a molecular epidemiologic study. <i>Tropical Medicine and International Health</i> , 2000, 5, 737-743.	2.3	51
53	Prognostic indicators of chronic chagasic cardiopathy. <i>International Journal of Cardiology</i> , 1991, 30, 195-202.	1.7	50
54	Brief communication. The Rift Valley complex as a barrier to gene flow for <i>Anopheles gambiae</i> in Kenya: the mtDNA perspective. <i>Journal of Heredity</i> , 2000, 91, 165-168.	2.4	50

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55	Genetic diversity of vaccine candidate antigens in <i>Plasmodium falciparum</i> isolates from the Amazon basin of Peru. <i>Malaria Journal</i> , 2008, 7, 93.	2.3	49
56	Whole Genome Sequencing of Field Isolates Reveals Extensive Genetic Diversity in <i>Plasmodium vivax</i> from Colombia. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0004252.	3.0	49
57	Leucocytozoon Diversity and Possible Vectors in the Neotropical highlands of Colombia. <i>Protist</i> , 2016, 167, 185-204.	1.5	49
58	Genetic diversity and population structure of genes encoding vaccine candidate antigens of <i>Plasmodium vivax</i> . <i>Malaria Journal</i> , 2012, 11, 68.	2.3	46
59	Multiplicity of Infection and Disease Severity in <i>Plasmodium vivax</i> . <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004355.	3.0	46
60	Recent independent evolution of <i>msh2</i> polymorphism in <i>Plasmodium vivax</i> and related simian malaria parasites. <i>Molecular and Biochemical Parasitology</i> , 2007, 156, 74-79.	1.1	45
61	The spatial and temporal patterns of <i>falciparum</i> and <i>vivax</i> malaria in Peru: 1994-2006. <i>Malaria Journal</i> , 2009, 8, 142.	2.3	45
62	Differences in selective pressure on <i>dhps</i> and <i>dhfr</i> drug resistant mutations in western Kenya. <i>Malaria Journal</i> , 2012, 11, 77.	2.3	45
63	Phylogeographic Evidence for 2 Genetically Distinct Zoonotic <i>Plasmodium knowlesi</i> Parasites, Malaysia. <i>Emerging Infectious Diseases</i> , 2016, 22, 1371-1380.	4.3	45
64	Decline in Sulfadoxine-Pyrimethamine-Resistant Alleles after Change in Drug Policy in the Amazon Region of Peru. <i>Antimicrobial Agents and Chemotherapy</i> , 2008, 52, 739-741.	3.2	44
65	The origin and diversification of the merozoite surface protein 3 (<i>msh3</i>) multi-gene family in <i>Plasmodium vivax</i> and related parasites. <i>Molecular Phylogenetics and Evolution</i> , 2014, 78, 172-184.	2.7	44
66	Genome-Wide Patterns of Genetic Polymorphism and Signatures of Selection in <i>Plasmodium vivax</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 106-119.	2.5	44
67	A comparative study of the genetic diversity of the 42kDa fragment of the merozoite surface protein 1 in <i>Plasmodium falciparum</i> and <i>P. vivax</i> . <i>Infection, Genetics and Evolution</i> , 2007, 7, 180-187.	2.3	43
68	The dynamics of mutations associated with anti-malarial drug resistance in <i>Plasmodium falciparum</i> . <i>Trends in Parasitology</i> , 2009, 25, 557-563.	3.3	42
69	Genomics, Population Genetics and Evolutionary History of <i>Plasmodium vivax</i> . <i>Advances in Parasitology</i> , 2013, 81, 203-222.	3.2	42
70	Evidence for intragenic recombination in <i>Plasmodium falciparum</i> : identification of a novel allele family in block 2 of merozoite surface protein-1: Asembo Bay Area Cohort Project XIV. <i>Molecular and Biochemical Parasitology</i> , 2002, 125, 163-171.	1.1	41
71	Tracking Origins and Spread of Sulfadoxine-Resistant <i>Plasmodium falciparum dhps</i> Alleles in Thailand. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 155-164.	3.2	40
72	Haemosporidian infection in captive masked bobwhite quail (<i>Colinus virginianus ridgwayi</i>), an endangered subspecies of the northern bobwhite quail. <i>Veterinary Parasitology</i> , 2011, 182, 113-120.	1.8	39

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73	The Origin of Malarial Parasites in Orangutans. PLoS ONE, 2012, 7, e34990.	2.5	38
74	Genetic diversity of Plasmodium vivax Duffy Binding Protein II (PvDBPII) under unstable transmission and low intensity malaria in Sri Lanka. Infection, Genetics and Evolution, 2011, 11, 1327-1339.	2.3	37
75	Characterizing the malaria rural-to-urban transmission interface: The importance of reactive case detection. PLoS Neglected Tropical Diseases, 2017, 11, e0005780.	3.0	37
76	Description and molecular characterization of Haemoproteus macrovacuolatus n. sp. (Haemosporida,) Tj ETQq0 0 0 rgBT /Overlock 10 T (Dendrocygna autumnalis) from South America. Parasitology Research, 2014, 113, 2991-3000.	1.6	35
77	Phylogenetic study of the genus Plasmodium based on the secondary structure-based alignment of the small subunit ribosomal RNA. Molecular and Biochemical Parasitology, 1997, 90, 317-321.	1.1	34
78	Malaria in Southern Venezuela: The hottest hotspot in Latin America. PLoS Neglected Tropical Diseases, 2021, 15, e0008211.	3.0	33
79	Population dynamics of rhesus macaques and associated foamy virus in Bangladesh. Emerging Microbes and Infections, 2013, 2, 1-14.	6.5	32
80	Malaria Molecular Epidemiology: An Evolutionary Genetics Perspective. Microbiology Spectrum, 2019, 7, .	3.0	31
81	Limited differentiation among Plasmodium vivax populations from the northwest and to the south Pacific Coast of Colombia: A malaria corridor?. PLoS Neglected Tropical Diseases, 2019, 13, e0007310.	3.0	31
82	Genetic Distance in Housekeeping Genes Between Plasmodium falciparum and Plasmodium reichenowi and Within P. falciparum. Journal of Molecular Evolution, 2004, 59, 687-694.	1.8	29
83	Genetic diversity and recombination at the C-terminal fragment of the merozoite surface protein-1 of Plasmodium vivax (PvMSP-1) in Sri Lanka. Infection, Genetics and Evolution, 2011, 11, 145-156.	2.3	29
84	Description of Leucocytozoon quynzae sp. nov. (Haemosporida, Leucocytozoidae) from hummingbirds, with remarks on distribution and possible vectors of leucocytozoids in South America. Parasitology Research, 2014, 113, 457-468.	1.6	29
85	A new pathogen spillover from domestic to wild animals: <i>Plasmodium juxtannucleare</i> infects free-living passerines in Brazil. Parasitology, 2018, 145, 1949-1958.	1.5	29
86	Evidence for negative selection on the gene encoding rhoptry-associated protein 1 (RAP-1) in Plasmodium spp.. Infection, Genetics and Evolution, 2010, 10, 655-661.	2.3	28
87	Polymorphism in the gene encoding the Pfs48/45 antigen of Plasmodium falciparum. XI. Asembo Bay Cohort Project. Molecular and Biochemical Parasitology, 2002, 119, 17-22.	1.1	27
88	Evaluation of the genetic diversity of domain II of Plasmodium vivax Apical Membrane Antigen 1 (PvAMA-1) and the ensuing strain-specific immune responses in patients from Sri Lanka. Vaccine, 2011, 29, 7491-7504.	3.8	25
89	Persistence of Sulfadoxine-Pyrimethamine Resistance Despite Reduction of Drug Pressure in Malawi. Journal of Infectious Diseases, 2015, 212, 694-701.	4.0	25
90	Antigenic Diversity of the Plasmodium vivax Circumsporozoite Protein in Parasite Isolates of Western Colombia. American Journal of Tropical Medicine and Hygiene, 2011, 84, 51-57.	1.4	24

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91	Identification of <i>Plasmodium</i> (<i>Haemamoeba</i>) <i>lutzi</i> (Lucena, 1939) from <i>Turdus fuscater</i> (Great Thrush) in Colombia. <i>Journal of Parasitology</i> , 2013, 99, 662-668.	0.7	24
92	Population genetic structure of the <i>Plasmodium vivax</i> circumsporozoite protein (Pvcsp) in Sri Lanka. <i>Gene</i> , 2013, 518, 381-387.	2.2	24
93	<i>Haemoproteus erythrogravidus</i> n. sp. (Haemosporida, Haemoproteidae): Description and molecular characterization of a widespread blood parasite of birds in South America. <i>Acta Tropica</i> , 2016, 159, 83-94.	2.0	24
94	Malaria in Venezuela: changes in the complexity of infection reflects the increment in transmission intensity. <i>Malaria Journal</i> , 2020, 19, 176.	2.3	24
95	PHYLOGEOGRAPHY, POPULATION STRUCTURE, AND IMPLICATIONS FOR CONSERVATION OF WHITE-TAILED DEER (<i>ODOCOILEUS VIRGINIANUS</i>) IN VENEZUELA. <i>Journal of Mammalogy</i> , 2003, 84, 1300-1315.	1.3	23
96	<i>Leucocytozoon pterotenus</i> sp. nov. (Haemosporida, Leucocytozoidae): description of the morphologically unique species from the Grallariidae birds, with remarks on the distribution of <i>Leucocytozoon</i> parasites in the Neotropics. <i>Parasitology Research</i> , 2015, 114, 1031-1044.	1.6	23
97	Disentangling <i>Leucocytozoon</i> parasite diversity in the neotropics: Descriptions of two new species and shortcomings of molecular diagnostics for leucocytozoids. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2019, 9, 159-173.	1.5	23
98	Effect of albendazole in experimental toxocariasis of mice. <i>Annals of Tropical Medicine and Parasitology</i> , 1989, 83, 621-624.	1.6	22
99	Merozoite surface protein-3 alpha as a genetic marker for epidemiologic studies in <i>Plasmodium vivax</i> : a cautionary note. <i>Malaria Journal</i> , 2013, 12, 288.	2.3	22
100	Population Genetics, Evolutionary Genomics, and Genome-Wide Studies of Malaria: A View Across the International Centers of Excellence for Malaria Research. <i>American Journal of Tropical Medicine and Hygiene</i> , 2015, 93, 87-98.	1.4	22
101	Profiles of low complexity regions in Apicomplexa. <i>BMC Evolutionary Biology</i> , 2016, 16, 47.	3.2	21
102	Malaria in pregnancy: a passive surveillance study of pregnant women in low transmission areas of Colombia, Latin America. <i>Malaria Journal</i> , 2016, 15, 66.	2.3	20
103	Phylogenetic analysis of the genus <i>Plasmodium</i> based on the gene encoding adenylosuccinate lyase. <i>Infection, Genetics and Evolution</i> , 2002, 1, 297-301.	2.3	19
104	<i>Plasmodium vivax</i> populations revisited: mitochondrial genomes of temperate strains in Asia suggest ancient population expansion. <i>BMC Evolutionary Biology</i> , 2012, 12, 22.	3.2	19
105	A Likelihood Approach to Estimate the Number of Co-Infections. <i>PLoS ONE</i> , 2014, 9, e97899.	2.5	19
106	Longitudinal analysis of <i>Plasmodium falciparum</i> genetic variation in Turbo, Colombia: implications for malaria control and elimination. <i>Malaria Journal</i> , 2015, 14, 363.	2.3	19
107	Integrating environmental and neighborhood factors in MaxEnt modeling to predict species distributions: A case study of <i>Aedes albopictus</i> in southeastern Pennsylvania. <i>PLoS ONE</i> , 2019, 14, e0223821.	2.5	19
108	Evolution of the Transmission-Blocking Vaccine Candidates Pvs28 and Pvs25 in <i>Plasmodium vivax</i> : Geographic Differentiation and Evidence of Positive Selection. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004786.	3.0	19

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109	The evolution and diversity of a low complexity vaccine candidate, merozoite surface protein 9 (MSP-9), in <i>Plasmodium vivax</i> and closely related species. <i>Infection, Genetics and Evolution</i> , 2013, 20, 239-248.	2.3	18
110	The geography of malaria genetics in the Democratic Republic of Congo: A complex and fragmented landscape. <i>Social Science and Medicine</i> , 2015, 133, 233-241.	3.8	18
111	Historical Shifts in Brazilian <i>P. falciparum</i> Population Structure and Drug Resistance Alleles. <i>PLoS ONE</i> , 2013, 8, e58984.	2.5	17
112	A Population Genetic Model for the Initial Spread of Partially Resistant Malaria Parasites under Anti-Malarial Combination Therapy and Weak Intra-host Competition. <i>PLoS ONE</i> , 2014, 9, e101601.	2.5	16
113	Chronic <i>Plasmodium brasilianum</i> infections in wild Peruvian tamarins. <i>PLoS ONE</i> , 2017, 12, e0184504.	2.5	16
114	The impact of imported malaria by gold miners in Roraima: characterizing the spatial dynamics of autochthonous and imported malaria in an urban region of Boa Vista. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2020, 115, e200043.	1.6	16
115	Fitness components and natural selection: why are there different patterns on the emergence of drug resistance in <i>Plasmodium falciparum</i> and <i>Plasmodium vivax</i> ?. <i>Malaria Journal</i> , 2013, 12, 15.	2.3	15
116	Genetic variation and recurrent parasitaemia in Peruvian <i>Plasmodium vivax</i> populations. <i>Malaria Journal</i> , 2014, 13, 67.	2.3	15
117	Microsatellite analysis reveals connectivity among geographically distant transmission zones of <i>Plasmodium vivax</i> in the Peruvian Amazon: A critical barrier to regional malaria elimination. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007876.	3.0	15
118	Evolution and Genetic Diversity of the <i>k13</i> Gene Associated with Artemisinin Delayed Parasite Clearance in <i>Plasmodium falciparum</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	15
119	Why <i>Plasmodium vivax</i> and <i>Plasmodium falciparum</i> are so different? A tale of two clades and their species diversities. <i>Malaria Journal</i> , 2022, 21, 139.	2.3	15
120	Malaria evolution in South Asia: Knowledge for control and elimination. <i>Acta Tropica</i> , 2012, 121, 256-266.	2.0	14
121	Changes in the frequencies of <i>Plasmodium falciparum</i> dhps and dhfr drug-resistant mutations in children from Western Kenya from 2005 to 2018: the rise of Pfdhps S436H. <i>Malaria Journal</i> , 2020, 19, 378.	2.3	14
122	Molecular Evolution of PvMSP3 α Block II in <i>Plasmodium vivax</i> from Diverse Geographic Origins. <i>PLoS ONE</i> , 2015, 10, e0135396.	2.5	13
123	Prospective Study of <i>Plasmodium vivax</i> Malaria Recurrence after Radical Treatment with a Chloroquine-Primaquine Standard Regimen in Turbo, Colombia. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 4610-4619.	3.2	13
124	Assessing the Effect of Selection at the Amino Acid Level in Malaria Antigen Sequences Through Bayesian Generalized Linear Models. <i>Journal of the American Statistical Association</i> , 2008, 103, 1496-1507.	3.1	12
125	Polymorphism of the Pv200L Fragment of Merozoite Surface Protein-1 of <i>Plasmodium vivax</i> in Clinical Isolates from the Pacific Coast of Colombia. <i>American Journal of Tropical Medicine and Hygiene</i> , 2011, 84, 64-70.	1.4	12
126	Limited genetic variation in the <i>Plasmodium falciparum</i> heme detoxification protein (HDP). <i>Infection, Genetics and Evolution</i> , 2009, 9, 286-289.	2.3	11

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127	Evolution of the merozoite surface protein 7 (msp7) family in <i>Plasmodium vivax</i> and <i>P. falciparum</i> : A comparative approach. <i>Infection, Genetics and Evolution</i> , 2017, 50, 7-19.	2.3	11
128	<i>Plasmodium</i> parasites in reptiles from the Colombia Orinoco-Amazon basin: a re-description of <i>Plasmodium kentropyxi</i> Lainson R, Landau I, Paperna I, 2001 and <i>Plasmodium carmelinoi</i> Lainson R, Franco CM, da Matta R, 2010. <i>Parasitology Research</i> , 2018, 117, 1357-1370.	1.6	11
129	Genetic backgrounds of the <i>Plasmodium falciparum</i> chloroquine resistant transporter (pfcr) alleles in Pakistan. <i>Infection, Genetics and Evolution</i> , 2012, 12, 278-281.	2.3	10
130	A phylogenetic study of <i>Haemocystidium</i> parasites and other Haemosporida using complete mitochondrial genome sequences. <i>Infection, Genetics and Evolution</i> , 2020, 85, 104576.	2.3	9
131	The apicoplast of <i>Haemoproteus columbae</i> : A comparative study of this organelle genome in Haemosporida. <i>Molecular Phylogenetics and Evolution</i> , 2021, 161, 107185.	2.7	8
132	Blood parasites infecting the Hoatzin (<i>Opisthocomus hoazin</i>), a unique neotropical folivorous bird. <i>PeerJ</i> , 2019, 7, e6361.	2.0	8
133	Morphological differences between Venezuelan and African microfilariae of <i>Onchocerca volvulus</i> . <i>Journal of Helminthology</i> , 1988, 62, 345-351.	1.0	7
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