

# Ananias A Escalante

## List of Publications by Year in descending order

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154  
papers

8,756  
citations

38742

50  
h-index

51608

86  
g-index

158  
all docs

158  
docs citations

158  
times ranked

6464  
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolutionary Insights into the Microneme-Secreted, Chitinase-Containing High-Molecular-Weight Protein Complexes Involved in <i>Plasmodium</i> Invasion of the Mosquito Midgut. <i>Infection and Immunity</i> , 2022, 90, IA10031421.	2.2	5
2	Complement component 3 mutations alter the longitudinal risk of pediatric malaria and severe malarial anemia. <i>Experimental Biology and Medicine</i> , 2022, 247, 672-682.	2.4	3
3	Larval habitats, species composition and distribution of malaria vectors in regions with autochthonous and imported malaria in Roraima state, Brazil. <i>Malaria Journal</i> , 2022, 21, 13.	2.3	2
4	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
5	The evolution of primate malaria parasites: A study on the origin and diversification of <i>Plasmodium</i> in lemurs. <i>Molecular Phylogenetics and Evolution</i> , 2022, 174, 107551.	2.7	3
6	Complexity of malaria transmission dynamics in the Brazilian Atlantic Forest. <i>Current Research in Parasitology and Vector-borne Diseases</i> , 2021, 1, 100032.	1.9	5
7	<i>Plasmodium ouropretensis</i> , n. sp., a new case of non-erythrocytic species within lizard malaria parasites. <i>Parasitology</i> , 2021, 148, 1467-1474.	1.5	1
8	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
9	Association of <i>Plasmodium falciparum</i> kelch13 R561H genotypes with delayed parasite clearance in Rwanda: an open-label, single-arm, multicentre, therapeutic efficacy study. <i>Lancet Infectious Diseases</i> , 2021, 21, 1120-1128.	9.1	231
10	The clinical-epidemiological profile of malaria patients from Southern Venezuela, a critical hotspot in Latin America. <i>Malaria Journal</i> , 2021, 20, 375.	2.3	1
11	Negligible evidence for detrimental effects of <i>Leucocytozoon</i> infections among Emperor Geese ( <i>Anser</i> ) Tj ETQq1 1 0.784314 rgBT /Over Parasites and Wildlife, 2021, 16, 103-112.	1.5	2
12	Malaria in Southern Venezuela: The hottest hotspot in Latin America. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0008211.	3.0	33
13	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
14	The endangered California Condor ( <i>Gymnogyps californianus</i> ) population is exposed to local haemosporidian parasites. <i>Scientific Reports</i> , 2020, 10, 17947.	3.3	4
15	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
16	Cophylogenetic Patterns and Speciation in Avian Haemosporidians. , 2020, , 401-427.		2
17	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
18	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

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19	Malaria Molecular Epidemiology: An Evolutionary Genetics Perspective. Microbiology Spectrum, 2019, 7, .	3.0	31
20	Integrating environmental and neighborhood factors in MaxEnt modeling to predict species distributions: A case study of Aedes albopictus in southeastern Pennsylvania. PLoS ONE, 2019, 14, e0223821.	2.5	19
21	Microsatellite analysis reveals connectivity among geographically distant transmission zones of Plasmodium vivax in the Peruvian Amazon: A critical barrier to regional malaria elimination. PLoS Neglected Tropical Diseases, 2019, 13, e0007876.	3.0	15
22	Haemocystidium spp., a species complex infecting ancient aquatic turtles of the family Podocnemididae: First report of these parasites in Podocnemis vogli from the Orinoquia. International Journal for Parasitology: Parasites and Wildlife, 2019, 10, 299-309.	1.5	7
23	Disentangling Leucocytozoon parasite diversity in the neotropics: Descriptions of two new species and shortcomings of molecular diagnostics for leucocytozooids. International Journal for Parasitology: Parasites and Wildlife, 2019, 9, 159-173.	1.5	23
24	Evolution and Genetic Diversity of the <i>k13</i> Gene Associated with Artemisinin Delayed Parasite Clearance in Plasmodium falciparum. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	15
25	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
26	Blood parasites infecting the Hoatzin ( <i>Opisthocomus hoazin</i> ), a unique neotropical folivorous bird. PeerJ, 2019, 7, e6361.	2.0	8
27	Title is missing!. , 2019, 13, e0007876.		0
28	Title is missing!. , 2019, 13, e0007876.		0
29	Title is missing!. , 2019, 13, e0007876.		0
30	Title is missing!. , 2019, 13, e0007876.		0
31	Plasmodium parasites in reptiles from the Colombia Orinoco-Amazon basin: a re-description of Plasmodium kentropyxi Lainson R, Landau I, Paperna I, 2001 and Plasmodium carmelinoi Lainson R, Franco CM, da Matta R, 2010. Parasitology Research, 2018, 117, 1357-1370.	1.6	11
32	Primers targeting mitochondrial genes of avian haemosporidians: PCR detection and differential DNA amplification of parasites belonging to different genera. International Journal for Parasitology, 2018, 48, 657-670.	3.1	60
33	Mode and Rate of Evolution of Haemosporidian Mitochondrial Genomes: Timing the Radiation of Avian Parasites. Molecular Biology and Evolution, 2018, 35, 383-403.	8.9	122
34	Human migration and the spread of malaria parasites to the New World. Scientific Reports, 2018, 8, 1993.	3.3	76
35	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
36	Evolution of the merozoite surface protein 7 (msp7) family in Plasmodium vivax and P. falciparum : A comparative approach. Infection, Genetics and Evolution, 2017, 50, 7-19.	2.3	11

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37	Characterizing the malaria rural-to-urban transmission interface: The importance of reactive case detection. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005780.	3.0	37
38	Chronic <i>Plasmodium brasilianum</i> infections in wild Peruvian tamarins. <i>PLoS ONE</i> , 2017, 12, e0184504.	2.5	16
39	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
40	<i>Leucocytozoon</i> Diversity and Possible Vectors in the Neotropical highlands of Colombia. <i>Protist</i> , 2016, 167, 185-204.	1.5	49
41	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
42	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
43	Profiles of low complexity regions in Apicomplexa. <i>BMC Evolutionary Biology</i> , 2016, 16, 47.	3.2	21
44	<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
45	Multiplicity of Infection and Disease Severity in <i>Plasmodium vivax</i> . <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004355.	3.0	46
46	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
47	The effect of local variation in malaria transmission on the prevalence of sulfadoxine-pyrimethamine resistant haplotypes and selective sweep characteristics in Malawi. <i>Malaria Journal</i> , 2015, 14, 387.	2.3	5
48	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
49	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
50	Molecular Evolution of PvMSP3 Block II in <i>Plasmodium vivax</i> from Diverse Geographic Origins. <i>PLoS ONE</i> , 2015, 10, e0135396.	2.5	13
51	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
52	Accelerated Diversification of Nonhuman Primate Malaria in Southeast Asia: Adaptive Radiation or Geographic Speciation?. <i>Molecular Biology and Evolution</i> , 2015, 32, 422-439.	8.9	73
53	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
54	<i>Leucocytozoon pterotenuis</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

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55	Persistence of Sulfadoxine-Pyrimethamine Resistance Despite Reduction of Drug Pressure in Malawi. <i>Journal of Infectious Diseases</i> , 2015, 212, 694-701.	4.0	25
56	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
57	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
58	A Likelihood Approach to Estimate the Number of Co-Infections. <i>PLoS ONE</i> , 2014, 9, e97899.	2.5	19
59	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
60	Description of <i>Leucocytozoon quynzae</i> sp. nov. (Haemosporida, Leucocytozoidae) from hummingbirds, with remarks on distribution and possible vectors of leucocytozoids in South America. <i>Parasitology Research</i> , 2014, 113, 457-468.	1.6	29
61	Description and molecular characterization of <i>Haemoproteus macrovacuolatus</i> n. sp. (Haemosporida,) Tj ETQq1 1 0.784314 rgBT /Overl ( <i>Dendrocygna autumnalis</i> ) from South America. <i>Parasitology Research</i> , 2014, 113, 2991-3000.	1.6	35
62	Genetic variation and recurrent parasitaemia in Peruvian <i>Plasmodium vivax</i> populations. <i>Malaria Journal</i> , 2014, 13, 67.	2.3	15
63	The origin and diversification of the merozoite surface protein 3 (msp3) multi-gene family in <i>Plasmodium vivax</i> and related parasites. <i>Molecular Phylogenetics and Evolution</i> , 2014, 78, 172-184.	2.7	44
64	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
65	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
66	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
67	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
68	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
69	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
70	Genomics, Population Genetics and Evolutionary History of <i>Plasmodium vivax</i> . <i>Advances in Parasitology</i> , 2013, 81, 203-222.	3.2	42
71	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
72	Population dynamics of rhesus macaques and associated foamy virus in Bangladesh. <i>Emerging Microbes and Infections</i> , 2013, 2, 1-14.	6.5	32

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73	Real-Time Loop-Mediated Isothermal Amplification (RealAmp) for the Species-Specific Identification of <i>Plasmodium vivax</i> . PLoS ONE, 2013, 8, e54986.	2.5	68
74	Historical Shifts in Brazilian <i>P. falciparum</i> Population Structure and Drug Resistance Alleles. PLoS ONE, 2013, 8, e58984.	2.5	17
75	<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
76	Malaria in selected non-Amazonian countries of Latin America. Acta Tropica, 2012, 121, 303-314.	2.0	76
77	Malaria evolution in South Asia: Knowledge for control and elimination. Acta Tropica, 2012, 121, 256-266.	2.0	14
78	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
79	Local population structure of <i>Plasmodium</i> : impact on malaria control and elimination. Malaria Journal, 2012, 11, 412.	2.3	73
80	Differences in selective pressure on dhps and dhfr drug resistant mutations in western Kenya. Malaria Journal, 2012, 11, 77.	2.3	45
81	Genetic diversity and population structure of genes encoding vaccine candidate antigens of <i>Plasmodium vivax</i> . Malaria Journal, 2012, 11, 68.	2.3	46
82	The Origin of Malarial Parasites in Orangutans. PLoS ONE, 2012, 7, e34990.	2.5	38
83	Genetic backgrounds of the <i>Plasmodium falciparum</i> chloroquine resistant transporter (pfcrt) alleles in Pakistan. Infection, Genetics and Evolution, 2012, 12, 278-281.	2.3	10
84	Evidence of purifying selection on merozoite surface protein 8 (MSP8) and 10 (MSP10) in <i>Plasmodium</i> spp.. Infection, Genetics and Evolution, 2012, 12, 978-986.	2.3	65
85	<i>Plasmodium vivax</i> populations revisited: mitochondrial genomes of temperate strains in Asia suggest ancient population expansion. BMC Evolutionary Biology, 2012, 12, 22.	3.2	19
86	Evaluation of the genetic diversity of domain II of <i>Plasmodium vivax</i> 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
87	South American <i>Plasmodium falciparum</i> after the Malaria Eradication Era: Clonal Population Expansion and Survival of the Fittest Hybrids. PLoS ONE, 2011, 6, e23486.	2.5	66
88	Haemosporidian infection in captive masked bobwhite quail ( <i>Colinus virginianus ridgwayi</i> ), an endangered subspecies of the northern bobwhite quail. Veterinary Parasitology, 2011, 182, 113-120.	1.8	39
89	Timing the origin of human malarias: the lemur puzzle. BMC Evolutionary Biology, 2011, 11, 299.	3.2	85
90	Genetic diversity of <i>Plasmodium vivax</i> 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

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91	Genetic diversity and recombination at the C-terminal fragment of the merozoite surface protein-1 of <i>Plasmodium vivax</i> (PvMSP-1) in Sri Lanka. <i>Infection, Genetics and Evolution</i> , 2011, 11, 145-156.	2.3	29
92	Antigenic Diversity of the <i>Plasmodium vivax</i> Circumsporozoite Protein in Parasite Isolates of Western Colombia. <i>American Journal of Tropical Medicine and Hygiene</i> , 2011, 84, 51-57.	1.4	24
93	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
94	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
95	Evolution of Modern Birds Revealed by Mitogenomics: Timing the Radiation and Origin of Major Orders. <i>Molecular Biology and Evolution</i> , 2011, 28, 1927-1942.	8.9	211
96	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
97	<i>Plasmodium falciparum</i> Accompanied the Human Expansion out of Africa. <i>Current Biology</i> , 2010, 20, 1283-1289.	3.9	121
98	Evidence for negative selection on the gene encoding rhoptry-associated protein 1 (RAP-1) in <i>Plasmodium</i> spp.. <i>Infection, Genetics and Evolution</i> , 2010, 10, 655-661.	2.3	28
99	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> , 2010, 54, 2282-2282.	3.2	0
100	<i>pfmdr1</i> Amplification and Fixation of <i>pfprt</i> Chloroquine Resistance Alleles in <i>Plasmodium falciparum</i> in Venezuela. <i>Antimicrobial Agents and Chemotherapy</i> , 2010, 54, 1572-1579.	3.2	58
101	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
102	Two Nonrecombining Sympatric Forms of the Human Malaria Parasite <i>Plasmodium ovale</i> Occur Globally. <i>Journal of Infectious Diseases</i> , 2010, 201, 1544-1550.	4.0	310
103	Origin and Evolution of Sulfadoxine Resistant <i>Plasmodium falciparum</i> . <i>PLoS Pathogens</i> , 2010, 6, e1000830.	4.7	114
104	Characterizing molecular adaptation: a hierarchical approach to assess the selective influence of amino acid properties. <i>Bioinformatics</i> , 2010, 26, 2818-2825.	4.1	4
105	On the Diversity of Malaria Parasites in African Apes and the Origin of <i>Plasmodium falciparum</i> from Bonobos. <i>PLoS Pathogens</i> , 2010, 6, e1000765.	4.7	184
106	Extreme Polymorphism in a Vaccine Antigen and Risk of Clinical Malaria: Implications for Vaccine Development. <i>Science Translational Medicine</i> , 2009, 1, 2ra5.	12.4	154
107	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
108	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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109	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
110	The spatial and temporal patterns of falciparum and vivax malaria in Peru: 1994–2006. <i>Malaria Journal</i> , 2009, 8, 142.	2.3	45
111	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
112	Comparative evolutionary genomics of human malaria parasites. <i>Trends in Parasitology</i> , 2008, 24, 545-550.	3.3	57
113	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
114	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
115	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
116	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
117	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
118	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
119	Recent independent evolution of msp1 polymorphism in <i>Plasmodium vivax</i> and related simian malaria parasites. <i>Molecular and Biochemical Parasitology</i> , 2007, 156, 74-79.	1.1	45
120	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
121	The origin and age of <i>Plasmodium vivax</i> . <i>Trends in Parasitology</i> , 2006, 22, 558-563.	3.3	103
122	Antifolate Resistance in <i>Plasmodium falciparum</i> : Multiple Origins and Identification of Novel dhfr Alleles. <i>Journal of Infectious Diseases</i> , 2006, 194, 189-197.	4.0	122
123	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
124	Molecular evolution and intragenic recombination of the merozoite surface protein MSP-3 $\pm$ from the malaria parasite <i>Plasmodium vivax</i> in Thailand. <i>Parasitology</i> , 2005, 131, 25-35.	1.5	52
125	A monkey's tale: The origin of <i>Plasmodium vivax</i> as a human malaria parasite. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 1980-1985.	7.1	202
126	Evolutionary Biology of Malarial Parasites. , 2004, , 75-112.		1



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127	Assessing the effect of natural selection in malaria parasites. <i>Trends in Parasitology</i> , 2004, 20, 388-395.	3.3	99
128	Genetic Distance in Housekeeping Genes Between <i>Plasmodium falciparum</i> and <i>Plasmodium reichenowi</i> and Within <i>P. falciparum</i> . <i>Journal of Molecular Evolution</i> , 2004, 59, 687-694.	1.8	29
129	The genetic diversity of <i>Plasmodium vivax</i> populations. <i>Trends in Parasitology</i> , 2003, 19, 220-226.	3.3	115
130	Intrinsic chaos and external noise in population dynamics. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2003, 324, 723-732.	2.6	5
131	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
132	Polymorphism in the gene encoding the Pfs48/45 antigen of <i>Plasmodium falciparum</i> . XI. Asembo Bay Cohort Project. <i>Molecular and Biochemical Parasitology</i> , 2002, 119, 17-22.	1.1	27
133	A study of genetic diversity in the gene encoding the circumsporozoite protein (CSP) of <i>Plasmodium falciparum</i> from different transmission areas. XVI. Asembo Bay Cohort Project. <i>Molecular and Biochemical Parasitology</i> , 2002, 125, 83-90.	1.1	61
134	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
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