Christophe Paupy

List of Publications by Year
in descending order

83 papers	6,103 citations	93792 39 h-index	90395 73 g-index
99 all docs	99 docs citations	99 times ranked	6179 citing authors

#	Article	IF	Citations
1	Using haematophagous fly blood meals to study the diversity of bloodâ€borne pathogens infecting wild mammals. Molecular Ecology Resources, 2022, 22, 2915-2927.	2.2	4
2	Population genomics in the arboviral vector <i>Aedes aegypti</i> reveals the genomic architecture and evolution of endogenous viral elements. Molecular Ecology, 2021, 30, 1594-1611.	2.0	37
3	Experimental infections with Zika virus strains reveal high vector competence of Aedes albopictus and Aedes aegypti populations from Gabon (Central Africa) for the African virus lineage. Emerging Microbes and Infections, 2021, 10, 1244-1253.	3.0	1
4	Enhanced Zika virus susceptibility of globally invasive <i>Aedes aegypti</i> populations. Science, 2020, 370, 991-996.	6.0	61
5	The COVID-19 pandemic should not jeopardize dengue control. PLoS Neglected Tropical Diseases, 2020, 14, e0008716.	1.3	28
6	Exome-wide association study reveals largely distinct gene sets underlying specific resistance to dengue virus types 1 and 3 in Aedes aegypti. PLoS Genetics, 2020, 16, e1008794.	1.5	13
7	Microbial community structure reveals instability of nutritional symbiosis during the evolutionary radiation of <i>Amblyomma</i> ticks. Molecular Ecology, 2020, 29, 1016-1029.	2.0	48
8	A Systematic Review: Is Aedes albopictus an Efficient Bridge Vector for Zoonotic Arboviruses?. Pathogens, 2020, 9, 266.	1.2	62
9	Survey on Non-Human Primates and Mosquitoes Does not Provide Evidences of Spillover/Spillback between the Urban and Sylvatic Cycles of Yellow Fever and Zika Viruses Following Severe Outbreaks in Southeast Brazil. Viruses, 2020, 12, 364.	1.5	19
10	A new species in the major malaria vector complex sheds light on reticulated species evolution. Scientific Reports, 2019, 9, 14753.	1.6	56
11	A New High-Throughput Tool to Screen Mosquito-Borne Viruses in Zika Virus Endemic/Epidemic Areas. Viruses, 2019, 11, 904.	1.5	16
12	Natural <i>Wolbachia</i> infections are common in the major malaria vectors in Central Africa. Evolutionary Applications, 2019, 12, 1583-1594.	1.5	36
13	<i>Haemagogus leucocelaenus</i> and <i>Haemagogus janthinomys</i> are the primary vectors in the major yellow fever outbreak in Brazil, 2016â€“2018. Emerging Microbes and Infections, 2019, 8, 218-231.	3.0	112
14	Potential of <i>Aedes albopictus</i> as a bridge vector for enzootic pathogens at the urban-forest interface in Brazil. Emerging Microbes and Infections, 2018, 7, 1-8.	3.0	47
15	Genomes of all known members of a Plasmodium subgenus reveal paths to virulent human malaria. Nature Microbiology, 2018, 3, 687-697.	5.9	129
16	What Does the Future Hold for Yellow Fever Virus? (I). Genes, 2018, 9, 291.	1.0	34
17	Population structure of a vector of human diseases: <i>Aedes aegypti</i> in its ancestral range, Africa. Ecology and Evolution, 2018, 8, 7835-7848.	0.8	57
18	Diverse laboratory colonies of Aedes aegypti harbor the same adult midgut bacterial microbiome. Parasites and Vectors, 2018, 11, 207.	1.0	63

#	Article	IF	Citations
19	What Does the Future Hold for Yellow Fever Virus? (II). Genes, 2018, 9, 425.	1.0	32
20	Plasmodium vivax-like genome sequences shed new insights into Plasmodium vivax biology and evolution. PLoS Biology, 2018, 16, e2006035.	2.6	32
21	Diversity and role of cave-dwelling hematophagous insects in pathogen transmission in the Afrotropical region. Emerging Microbes and Infections, 2017, 6, 1-6.	3.0	11
22	Potential of Aedes aegypti and Aedes albopictus populations in the Central African Republic to transmit enzootic chikungunya virus strains. Parasites and Vectors, 2017, 10, 164.	1.0	29
23	Exploring the diversity of blood-sucking Diptera in caves of Central Africa. Scientific Reports, 2017, 7, 250.	1.6	12
24	â€œShow me which parasites you carry and I will tell you what you eatâ€, or how to infer the trophic behavior of hematophagous arthropods feeding on wildlife. Ecology and Evolution, 2017, 7, 7578-7584.	0.8	12
25	Carryover effects of larval exposure to different environmental bacteria drive adult trait variation in a mosquito vector. Science Advances, 2017, 3, e1700585.	4.7	172
26	Chapitre 11. Culicinae (DipteraÂ: Culicidae). , 2017, , 243-294.		1
27	Tracking zoonotic pathogens using blood-sucking flies as 'flying syringes'. ELife, 2017, 6, .	2.8	35
28	A molecular study of the genus Spelaeomyia (Diptera: Phlebotominae) with description of the male of Spelaeomyia moucheti. Parasites and Vectors, 2016, 9, 367.	1.0	3
29	Susceptibility profile and metabolic mechanisms involved in Aedes aegypti and Aedes albopictus resistant to DDT and deltamethrin in the Central African Republic. Parasites and Vectors, 2016, 9, 599.	1.0	51
30	Ape malaria transmission and potential for ape-to-human transfers in Africa. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 5329-5334.	3.3	59
31	Bat flies (Diptera: Nycteribiidae and Streblidae) infesting cave-dwelling bats in Gabon: diversity, dynamics and potential role in Polychromophilus melanipherus transmission. Parasites and Vectors, 2016, 9, 333.	1.0	36
32	Global genetic diversity of <i>Aedes aegypti</i>. Molecular Ecology, 2016, 25, 5377-5395.	2.0	195
33	The host specificity of ape malaria parasites can be broken in confined environments. International Journal for Parasitology, 2016, 46, 737-744.	1.3	30
34	Trapping the Tiger: Efficacy of the Novel BG-Sentinel 2 With Several Attractants and Carbon Dioxide for Collecting<i>Aedes albopictus</i>(Diptera: Culicidae) in Southern France. Journal of Medical Entomology, 2016, 53, 460-465.	0.9	30
35	Haemosporidian Parasites of Antelopes and Other Vertebrates from Gabon, Central Africa. PLoS ONE, 2016, 11, e0148958.	1.1	36
36	Autochthonous dengue outbreak in NÃ®mes, South of France, July to September 2015. Eurosurveillance, 2016, 21, .	3.9	124

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37	Genetic diversity of Plasmodium falciparum isolates from Baka Pygmies and their Bantu neighbours in the north of Gabon. Malaria Journal, 2015, 14, 395.	0.8	0
38	No Evidence for Ape Plasmodium Infections in Humans in Gabon. PLoS ONE, 2015, 10, e0126933.	1.1	27
39	Diversity of malaria parasites in great apes in Gabon. Malaria Journal, 2015, 14, 111.	0.8	42
40	Invasion of Aedes albopictus (Diptera: Culicidae) into central Africa: what consequences for emerging diseases?. Parasites and Vectors, 2015, 8, 191.	1.0	72
41	Habitat segregation and ecological character displacement in cryptic African malaria mosquitoes. Evolutionary Applications, 2015, 8, 326-345.	1.5	75
42	Widespread evidence for interspecific mating between Aedes aegypti and Aedes albopictus (Diptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.0	36
43	Autochthonous Chikungunya Transmission and Extreme Climate Events in Southern France. PLoS Neglected Tropical Diseases, 2015, 9, e0003854.	1.3	59
44	Identification of an Unclassified Paramyxovirus in Coleura afra: A Potential Case of Host Specificity. PLoS ONE, 2014, 9, e115588.	1.1	8
45	Zika Virus in Gabon (Central Africa) â€" 2007: A New Threat from Aedes albopictus?. PLoS Neglected Tropical Diseases, 2014, 8, e2681.	1.3	558
46	Evidence of Dengue Virus Transmission and Factors Associated with the Presence of Anti-Dengue Virus Antibodies in Humans in Three Major Towns in Cameroon. PLoS Neglected Tropical Diseases, 2014, 8, e2950.	1.3	50
47	Origin, acquisition and diversification of heritable bacterial endosymbionts in louse flies and bat flies. Molecular Ecology, 2014, 23, 2105-2117.	2.0	38
48	Description of Anopheles gabonensis, a new species potentially involved in rodent malaria transmission in Gabon, Central Africa. Infection, Genetics and Evolution, 2014, 28, 628-634.	1.0	11
49	Diversity, host switching and evolution of <i>Plasmodium vivax</i> infecting African great apes. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 8123-8128.	3.3	82
50	First Evidence of Simultaneous Circulation of Three Different Dengue Virus Serotypes in Africa. PLoS ONE, 2013, 8, e78030.	1.1	46
51	Temporal Patterns of Abundance of Aedes aegypti and Aedes albopictus (Diptera: Culicidae) and Mitochondrial DNA Analysis of Ae. albopictus in the Central African Republic. PLoS Neglected Tropical Diseases, 2013, 7, e2590.	1.3	79
52	Insecticide-Driven Patterns of Genetic Variation in the Dengue Vector Aedes aegypti in Martinique Island. PLoS ONE, 2013, 8, e77857.	1.1	24
53	Phlebotomus (Legeromyia) multihamatus subg. nov., sp. nov. from Gabon (Diptera: Psychodidae). Memorias Do Instituto Oswaldo Cruz, 2013, 108, 845-849.	0.8	8
54	Anopheles moucheti and Anopheles vinckei Are Candidate Vectors of Ape Plasmodium Parasites, Including Plasmodium praefalciparum in Gabon. PLoS ONE, 2013, 8, e57294.	1.1	40

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55	Clinical Forms of Chikungunya in Gabon, 2010. PLoS Neglected Tropical Diseases, 2012, 6, e1517.	1.3	56
56	A Chikungunya Outbreak Associated with the Vector <i>Aedes albopictus</i> in Remote Villages of Gabon. Vector-Borne and Zoonotic Diseases, 2012, 12, 167-169.	0.6	82
57	Recent Introduction and Rapid Dissemination of Chikungunya Virus and Dengue Virus Serotype 2 Associated With Human and Mosquito Coinfections in Gabon, Central Africa. Clinical Infectious Diseases, 2012, 55, e45-e53.	2.9	145
58	Entomological profile of yellow fever epidemics in the Central African Republic, 2006â€“2010. Parasites and Vectors, 2012, 5, 175.	1.0	19
59	Notes on the blood-feeding behavior of Aedes albopictus (Diptera: Culicidae) in Cameroon. Parasites and Vectors, 2012, 5, 57.	1.0	98
60	Genetic structure and phylogeography of Aedes aegypti, the dengue and yellow-fever mosquito vector in Bolivia. Infection, Genetics and Evolution, 2012, 12, 1260-1269.	1.0	64
61	Genetic Structure of the Tiger Mosquito, Aedes albopictus, in Cameroon (Central Africa). PLoS ONE, 2011, 6, e20257.	1.1	72
62	The invaders: Phylogeography of dengue and chikungunya viruses Aedes vectors, on the South West islands of the Indian Ocean. Infection, Genetics and Evolution, 2011, 11, 1769-1781.	1.0	66
63	Insecticide susceptibility of Aedes aegypti and Aedes albopictus in Central Africa. Parasites and Vectors, 2011, 4, 79.	1.0	114
64	Worldwide patterns of genetic differentiation imply multiple â€˜domesticationsâ€™ of<i>Aedes aegypti</i>, a major vector of human diseases. Proceedings of the Royal Society B: Biological Sciences, 2011, 278, 2446-2454.	1.2	213
65	Chikungunya outbreak in a rural area of Western Cameroon in 2006: A retrospective serological and entomological survey. BMC Research Notes, 2010, 3, 128.	0.6	65
66	Morphological and genetic variability within Aedes aegypti in Niakhar, Senegal. Infection, Genetics and Evolution, 2010, 10, 473-480.	1.0	40
67	Rift Valley Fever Virus Seroprevalence in Human Rural Populations of Gabon. PLoS Neglected Tropical Diseases, 2010, 4, e763.	1.3	45
68	Comparative Role of<i>Aedes albopictus</i>and<i>Aedes aegypti</i>in the Emergence of Dengue and Chikungunya in Central Africa. Vector-Borne and Zoonotic Diseases, 2010, 10, 259-266.	0.6	241
69	Geographic and ecological distribution of the dengue and chikungunya virus vectors Aedes aegypti and Aedes albopictus in three major Cameroonian towns. Medical and Veterinary Entomology, 2010, 24, 132-141.	0.7	74
70	Aedes albopictus, an arbovirus vector: From the darkness to the light. Microbes and Infection, 2009, 11, 1177-1185.	1.0	715
71	Geographic Distribution and Developmental Sites of <i>Aedes albopictus</i> (Diptera: Culicidae) During a Chikungunya Epidemic Event. Vector-Borne and Zoonotic Diseases, 2008, 8, 25-34.	0.6	154
72	Gene Flow Between Domestic and Sylvan Populations of <I>Aedes aegypti</I> (Diptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.9	31

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73	Gene Flow Between Domestic and Sylvan Populations of Aedes aegypti (Diptera: Culicidae) in North Cameroon. Journal of Medical Entomology, 2008, 45, 391-400.	0.9	34
74	Chikungunya Virus, Cameroon, 2006. Emerging Infectious Diseases, 2007, 13, 768-771.	2.0	121
75	Aedes albopictus as an epidemic vector of chikungunya virus: another emerging problem?. Lancet Infectious Diseases, The, 2006, 6, 463-464.	4.6	213
76	Factors influencing the population structure of Aedes aegypti from the main cities in Cambodia. Heredity, 2005, 95, 144-147.	1.2	26
77	Comparisons of Amplified Fragment Length Polymorphism (AFLP), Microsatellite, and Isoenzyme Markers: Population Genetics of<i>Aedes aegypti</i>(Diptera: Culicidae) from Phnom Penh (Cambodia). Journal of Medical Entomology, 2004, 41, 664-671.	0.9	19
78	INFLUENCE OF BREEDING SITES FEATURES ON GENETIC DIFFERENTIATION OF AEDES AEGYPTI POPULATIONS ANALYZED ON A LOCAL SCALE IN PHNOM PENH MUNICIPALITY OF CAMBODIA. American Journal of Tropical Medicine and Hygiene, 2004, 71, 73-81.	0.6	32
79	Influence of breeding sites features on genetic differentiation of Aedes aegypti populations analyzed on a local scale in Phnom Penh Municipality of Cambodia. American Journal of Tropical Medicine and Hygiene, 2004, 71, 73-81.	0.6	12
80	Variation over space and time of Aedes aegypti in Phnom Penh (Cambodia): genetic structure and oral susceptibility to a dengue virus. Genetical Research, 2003, 82, 171-182.	0.3	32
81	Population structure of Aedes albopictus from La RÃ©union Island (Indian Ocean) with respect to susceptibility to a dengue virus. Heredity, 2001, 87, 273-283.	1.2	59
82	Aedes aegypti in Tahiti and Moorea (French Polynesia): isoenzyme differentiation in the mosquito population according to human population density.. American Journal of Tropical Medicine and Hygiene, 2000, 62, 217-224.	0.6	48
83	Metabarcoding: A Powerful Yet Still Underestimated Approach for the Comprehensive Study of Vector-Borne Pathogen Transmission Cycles and Their Dynamics. , 0, , .		7