

# Anavaj Sakuntabhai

## List of Publications by Year in descending order

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Version: 2024-02-01

70  
papers

4,529  
citations

172457

29  
h-index

110387

64  
g-index

76  
all docs

76  
docs citations

76  
times ranked

8422  
citing authors

#	ARTICLE	IF	CITATIONS
1	Novel and Broadly Applicable Microsatellite Markers in Identified Chromosomes of the Philippine Dengue Mosquitoes, <i>Aedes aegypti</i> (Diptera: Culicidae). <i>Journal of Medical Entomology</i> , 2022, 59, 545-553.	1.8	4
2	SARS-CoV-2 Induces Cytokine Responses in Human Basophils. <i>Frontiers in Immunology</i> , 2022, 13, 838448.	4.8	11
3	Temperature, season, and latitude influence development-related phenotypes of Philippine <i>Aedes aegypti</i> (Linnaeus): Implications for dengue control amidst global warming. <i>Parasites and Vectors</i> , 2022, 15, 74.	2.5	7
4	Single-cell temporal analysis of natural dengue infection reveals skin-homing lymphocyte expansion one day before defervescence. <i>IScience</i> , 2022, 25, 104034.	4.1	5
5	Yearly variations of the genetic structure of <i>Aedes aegypti</i> (Linnaeus) (Diptera: Culicidae) in the Philippines (2017–2019). <i>Infection, Genetics and Evolution</i> , 2022, 102, 105296.	2.3	3
6	Viral evolution sustains a dengue outbreak of enhanced severity. <i>Emerging Microbes and Infections</i> , 2021, 10, 536-544.	6.5	6
7	Dengue Virus Serotype 2 Intrahost Diversity in Patients with Different Clinical Outcomes. <i>Viruses</i> , 2021, 13, 349.	3.3	11
8	Antibody fucosylation predicts disease severity in secondary dengue infection. <i>Science</i> , 2021, 372, 1102-1105.	12.6	67
9	Association of a single nucleotide polymorphism in the <i>ubxn6</i> gene with long-term non-progression phenotype in HIV-positive individuals. <i>Clinical Microbiology and Infection</i> , 2020, 26, 107-114.	6.0	3
10	Genetic Diversity of Collaborative Cross Mice Controls Viral Replication, Clinical Severity, and Brain Pathology Induced by Zika Virus Infection, Independently of <i>Oas1b</i> . <i>Journal of Virology</i> , 2020, 94, .	3.4	32
11	Dengue viremia kinetics in asymptomatic and symptomatic infection. <i>International Journal of Infectious Diseases</i> , 2020, 101, 90-97.	3.3	21
12	Experimental adaptation of dengue virus 1 to <i>Aedes albopictus</i> mosquitoes by in vivo selection. <i>Scientific Reports</i> , 2020, 10, 18404.	3.3	10
13	Comparison of dengue case classification schemes and evaluation of biological changes in different dengue clinical patterns in a longitudinal follow-up of hospitalized children in Cambodia. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008603.	3.0	18
14	Identification and molecular characterization of the first complete genome sequence of Human Parechovirus type 15. <i>Scientific Reports</i> , 2020, 10, 6759.	3.3	5
15	A Modified mRNA Vaccine Targeting Immunodominant NS Eitopes Protects Against Dengue Virus Infection in HLA Class I Transgenic Mice. <i>Frontiers in Immunology</i> , 2019, 10, 1424.	4.8	59
16	Transcriptome Sequencing of Peripheral Blood Mononuclear Cells from Elite Controller-Long Term Non Progressors. <i>Scientific Reports</i> , 2019, 9, 14265.	3.3	29
17	Asymptomatic Dengue Virus Infections, Cambodia, 2012–2013. <i>Emerging Infectious Diseases</i> , 2019, 25, 1354-1362.	4.3	21
18	IPCAPS: an R package for iterative pruning to capture population structure. <i>Source Code for Biology and Medicine</i> , 2019, 14, 2.	1.7	11

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19	A Blood RNA Signature Detecting Severe Disease in Young Dengue Patients at Hospital Arrival. <i>Journal of Infectious Diseases</i> , 2018, 217, 1690-1698.	4.0	27
20	Population genetics-informed meta-analysis in seven genes associated with risk to dengue fever disease. <i>Infection, Genetics and Evolution</i> , 2018, 62, 60-72.	2.3	16
21	Improved Immune Responses Against Zika Virus After Sequential Dengue and Zika Virus Infection in Humans. <i>Viruses</i> , 2018, 10, 480.	3.3	25
22	Host genetic control of mosquito-borne Flavivirus infections. <i>Mammalian Genome</i> , 2018, 29, 384-407.	2.2	13
23	Genetic Characterization of Enterovirus A71 Circulating in Africa. <i>Emerging Infectious Diseases</i> , 2018, 24, 754-757.	4.3	17
24	Host ancestry and dengue fever: from mapping of candidate genes to prediction of worldwide genetic risk. <i>Future Virology</i> , 2018, 13, 647-655.	1.8	3
25	Immune Responses to Dengue and Zika Viruses – Guidance for T Cell Vaccine Development. <i>International Journal of Environmental Research and Public Health</i> , 2018, 15, 385.	2.6	11
26	Validation of genotype imputation in Southeast Asian populations and the effect of single nucleotide polymorphism annotation on imputation outcome. <i>BMC Medical Genetics</i> , 2018, 19, 23.	2.1	6
27	Neutrophil Activation and Early Features of NET Formation Are Associated With Dengue Virus Infection in Human. <i>Frontiers in Immunology</i> , 2018, 9, 3007.	4.8	56
28	Optic neuropathy and congenital glaucoma associated with probable Zika virus infection in Venezuelan patients. <i>JMM Case Reports</i> , 2018, 5, e005145.	1.3	9
29	Non-congenital severe ocular complications of Zika virus infection. <i>JMM Case Reports</i> , 2018, 5, e005152.	1.3	9
30	Joint ancestry and association test indicate two distinct pathogenic pathways involved in classical dengue fever and dengue shock syndrome. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006202.	3.0	17
31	Proteinuria during dengue fever in children. <i>International Journal of Infectious Diseases</i> , 2017, 55, 38-44.	3.3	4
32	Autochthonous Japanese Encephalitis with Yellow Fever Coinfection in Africa. <i>New England Journal of Medicine</i> , 2017, 376, 1483-1485.	27.0	99
33	Paper-based RNA detection and multiplexed analysis for Ebola virus diagnostics. <i>Scientific Reports</i> , 2017, 7, 1347.	3.3	106
34	Paper microfluidics for nucleic acid amplification testing (NAAT) of infectious diseases. <i>Lab on A Chip</i> , 2017, 17, 2347-2371.	6.0	94
35	Genetic association study of exfoliation syndrome identifies a protective rare variant at LOXL1 and five new susceptibility loci. <i>Nature Genetics</i> , 2017, 49, 993-1004.	21.4	114
36	Increased adaptive immune responses and proper feedback regulation protect against clinical dengue. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	68

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37	OSBPL10, RXRA and lipid metabolism confer African-ancestry protection against dengue haemorrhagic fever in admixed Cubans. <i>PLoS Pathogens</i> , 2017, 13, e1006220.	4.7	51
38	Genome-wide association study identifies five new susceptibility loci for primary angle closure glaucoma. <i>Nature Genetics</i> , 2016, 48, 556-562.	21.4	147
39	Human Adaptation of Ebola Virus during the West African Outbreak. <i>Cell</i> , 2016, 167, 1079-1087.e5.	28.9	180
40	Evaluation of the performances of six commercial kits designed for dengue NS1 and anti-dengue IgM, IgG and IgA detection in urine and saliva clinical specimens. <i>BMC Infectious Diseases</i> , 2016, 16, 201.	2.9	31
41	Dengue virus sero-cross-reactivity drives antibody-dependent enhancement of infection with zika virus. <i>Nature Immunology</i> , 2016, 17, 1102-1108.	14.5	781
42	Inhibition of protein kinase C promotes dengue virus replication. <i>Virology Journal</i> , 2016, 13, 35.	3.4	25
43	A Field-Deployable Reverse Transcription Recombinase Polymerase Amplification Assay for Rapid Detection of the Chikungunya Virus. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004953.	3.0	58
44	Risk Factors for Plasmodium falciparum Gametocyte Positivity in a Longitudinal Cohort. <i>PLoS ONE</i> , 2015, 10, e0123102.	2.5	14
45	Value of Routine Dengue Diagnostic Tests in Urine and Saliva Specimens. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0004100.	3.0	77
46	Recombinase Polymerase Amplification Assay for Rapid Diagnostics of Dengue Infection. <i>PLoS ONE</i> , 2015, 10, e0129682.	2.5	120
47	Modulation of Malaria Phenotypes by Pyruvate Kinase (PKLR) Variants in a Thai Population. <i>PLoS ONE</i> , 2015, 10, e0144555.	2.5	29
48	Asymptomatic humans transmit dengue virus to mosquitoes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14688-14693.	7.1	355
49	High Anti-Dengue Virus Activity of the OAS Gene Family Is Associated With Increased Severity of Dengue. <i>Journal of Infectious Diseases</i> , 2015, 212, 2011-2020.	4.0	37
50	Filter-free exhaustive odds ratio-based genome-wide interaction approach pinpoints evidence for interaction in the HLA region in psoriasis. <i>BMC Genetics</i> , 2015, 16, 11.	2.7	2
51	The genetic control of immunity to Plasmodium infection. <i>BMC Immunology</i> , 2015, 16, 14.	2.2	12
52	Epidemiological Risk Factors Associated with High Global Frequency of Inapparent Dengue Virus Infections. <i>Frontiers in Immunology</i> , 2014, 5, 280.	4.8	144
53	Dengue Expansion in Africa—Not Recognized or Not Happening?. <i>Emerging Infectious Diseases</i> , 2014, 20, .	4.3	72
54	Asthma and atopic dermatitis are associated with increased risk of clinical Plasmodium falciparum malaria. <i>BMJ Open</i> , 2013, 3, e002835.	1.9	13

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55	High Number of Previous Plasmodium falciparum Clinical Episodes Increases Risk of Future Episodes in a Sub-Group of Individuals. PLoS ONE, 2013, 8, e55666.	2.5	10
56	Clinical and Virological Study of Dengue Cases and the Members of Their Households: The Multinational DENFRAME Project. PLoS Neglected Tropical Diseases, 2012, 6, e1482.	3.0	40
57	Impact of Mosquito Bites on Asexual Parasite Density and Gametocyte Prevalence in Asymptomatic Chronic Plasmodium falciparum Infections and Correlation with IgE and IgG Titers. Infection and Immunity, 2012, 80, 2240-2246.	2.2	25
58	Genome-wide association study identifies susceptibility loci for dengue shock syndrome at MICB and PLCE1. Nature Genetics, 2011, 43, 1139-1141.	21.4	181
59	Impact of Changing Drug Treatment and Malaria Endemicity on the Heritability of Malaria Phenotypes in a Longitudinal Family-Based Cohort Study. PLoS ONE, 2011, 6, e26364.	2.5	2
60	An Exhaustive, Non-Euclidean, Non-Parametric Data Mining Tool for Unraveling the Complexity of Biological Systems – Novel Insights into Malaria. PLoS ONE, 2011, 6, e24085.	2.5	9
61	Heritability of the Human Infectious Reservoir of Malaria Parasites. PLoS ONE, 2010, 5, e11358.	2.5	39
62	The large form of human 2â€²,5â€²-Oligoadenylate Synthetase (OAS3) exerts antiviral effect against Chikungunya virus. Virology, 2009, 384, 216-222.	2.4	90
63	Genome-wide and fine-resolution association analysis of malaria in West Africa. Nature Genetics, 2009, 41, 657-665.	21.4	345
64	Human genetic determinants of dengue virus susceptibility. Microbes and Infection, 2009, 11, 143-156.	1.9	110
65	Positively Selected <i>G6PD</i> -Mahidol Mutation Reduces <i>Plasmodium vivax</i> Density in Southeast Asians. Science, 2009, 326, 1546-1549.	12.6	150
66	Evaluation of resequencing on number of tag SNPs of 13 atherosclerosis-related genes in Thai population. Journal of Human Genetics, 2008, 53, 74-86.	2.3	9
67	Heritability of <i>P. falciparum</i> and <i>P. vivax</i> Malaria in a Karen Population in Thailand. PLoS ONE, 2008, 3, e3887.	2.5	13
68	Genetic Determination and Linkage Mapping of Plasmodium falciparum Malaria Related Traits in Senegal. PLoS ONE, 2008, 3, e2000.	2.5	49
69	Genetic study of ICAM1 in clinical malaria in Senegal. Tissue Antigens, 2005, 65, 474-480.	1.0	15
70	A variant in the CD209 promoter is associated with severity of dengue disease. Nature Genetics, 2005, 37, 507-513.	21.4	267