

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	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
2	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
3	Genome-wide and fine-resolution association analysis of malaria in West Africa. <i>Nature Genetics</i> , 2009, 41, 657-665.	21.4	345
4	A variant in the CD209 promoter is associated with severity of dengue disease. <i>Nature Genetics</i> , 2005, 37, 507-513.	21.4	267
5	Genome-wide association study identifies susceptibility loci for dengue shock syndrome at MICB and PLCE1. <i>Nature Genetics</i> , 2011, 43, 1139-1141.	21.4	181
6	Human Adaptation of Ebola Virus during the West African Outbreak. <i>Cell</i> , 2016, 167, 1079-1087.e5.	28.9	180
7	Positively Selected <i>G6PD</i> -Mahidol Mutation Reduces <i>Plasmodium vivax</i> Density in Southeast Asians. <i>Science</i> , 2009, 326, 1546-1549.	12.6	150
8	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
9	Epidemiological Risk Factors Associated with High Global Frequency of Inapparent Dengue Virus Infections. <i>Frontiers in Immunology</i> , 2014, 5, 280.	4.8	144
10	Recombinase Polymerase Amplification Assay for Rapid Diagnostics of Dengue Infection. <i>PLoS ONE</i> , 2015, 10, e0129682.	2.5	120
11	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
12	Human genetic determinants of dengue virus susceptibility. <i>Microbes and Infection</i> , 2009, 11, 143-156.	1.9	110
13	Paper-based RNA detection and multiplexed analysis for Ebola virus diagnostics. <i>Scientific Reports</i> , 2017, 7, 1347.	3.3	106
14	Autochthonous Japanese Encephalitis with Yellow Fever Coinfection in Africa. <i>New England Journal of Medicine</i> , 2017, 376, 1483-1485.	27.0	99
15	Paper microfluidics for nucleic acid amplification testing (NAAT) of infectious diseases. <i>Lab on A Chip</i> , 2017, 17, 2347-2371.	6.0	94
16	The large form of human 2 ⁵ -Oligoadenylate Synthetase (OAS3) exerts antiviral effect against Chikungunya virus. <i>Virology</i> , 2009, 384, 216-222.	2.4	90
17	Value of Routine Dengue Diagnostic Tests in Urine and Saliva Specimens. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0004100.	3.0	77
18	Dengue Expansion in Africa—Not Recognized or Not Happening?. <i>Emerging Infectious Diseases</i> , 2014, 20, .	4.3	72

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19	Increased adaptive immune responses and proper feedback regulation protect against clinical dengue. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	68
20	Antibody fucosylation predicts disease severity in secondary dengue infection. <i>Science</i> , 2021, 372, 1102-1105.	12.6	67
21	A Modified mRNA Vaccine Targeting Immunodominant NS Epitopes Protects Against Dengue Virus Infection in HLA Class I Transgenic Mice. <i>Frontiers in Immunology</i> , 2019, 10, 1424.	4.8	59
22	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
23	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
24	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
25	Genetic Determination and Linkage Mapping of Plasmodium falciparum Malaria Related Traits in Senegal. <i>PLoS ONE</i> , 2008, 3, e2000.	2.5	49
26	Clinical and Virological Study of Dengue Cases and the Members of Their Households: The Multinational DENFRAME Project. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1482.	3.0	40
27	Heritability of the Human Infectious Reservoir of Malaria Parasites. <i>PLoS ONE</i> , 2010, 5, e11358.	2.5	39
28	High Anti-“Dengue Virus Activity of the <i>OAS</i> Gene Family Is Associated With Increased Severity of Dengue. <i>Journal of Infectious Diseases</i> , 2015, 212, 2011-2020.	4.0	37
29	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
30	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
31	Modulation of Malaria Phenotypes by Pyruvate Kinase (PKLR) Variants in a Thai Population. <i>PLoS ONE</i> , 2015, 10, e0144555.	2.5	29
32	Transcriptome Sequencing of Peripheral Blood Mononuclear Cells from Elite Controller-Long Term Non Progressors. <i>Scientific Reports</i> , 2019, 9, 14265.	3.3	29
33	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
34	Impact of Mosquito Bites on Asexual Parasite Density and Gametocyte Prevalence in Asymptomatic Chronic Plasmodium falciparum Infections and Correlation with IgE and IgG Titers. <i>Infection and Immunity</i> , 2012, 80, 2240-2246.	2.2	25
35	Inhibition of protein kinase C promotes dengue virus replication. <i>Virology Journal</i> , 2016, 13, 35.	3.4	25
36	Improved Immune Responses Against Zika Virus After Sequential Dengue and Zika Virus Infection in Humans. <i>Viruses</i> , 2018, 10, 480.	3.3	25

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37	Asymptomatic Dengue Virus Infections, Cambodia, 2012–2013. <i>Emerging Infectious Diseases</i> , 2019, 25, 1354-1362.	4.3	21
38	Dengue viremia kinetics in asymptomatic and symptomatic infection. <i>International Journal of Infectious Diseases</i> , 2020, 101, 90-97.	3.3	21
39	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
40	Genetic Characterization of Enterovirus A71 Circulating in Africa. <i>Emerging Infectious Diseases</i> , 2018, 24, 754-757.	4.3	17
41	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
42	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
43	Genetic study of ICAM1 in clinical malaria in Senegal. <i>Tissue Antigens</i> , 2005, 65, 474-480.	1.0	15
44	Risk Factors for Plasmodium falciparum Gametocyte Positivity in a Longitudinal Cohort. <i>PLoS ONE</i> , 2015, 10, e0123102.	2.5	14
45	Heritability of P. falciparum and P. vivax Malaria in a Karen Population in Thailand. <i>PLoS ONE</i> , 2008, 3, e3887.	2.5	13
46	Asthma and atopic dermatitis are associated with increased risk of clinical Plasmodium falciparum malaria. <i>BMJ Open</i> , 2013, 3, e002835.	1.9	13
47	Host genetic control of mosquito-borne Flavivirus infections. <i>Mammalian Genome</i> , 2018, 29, 384-407.	2.2	13
48	The genetic control of immunity to Plasmodium infection. <i>BMC Immunology</i> , 2015, 16, 14.	2.2	12
49	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
50	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
51	Dengue Virus Serotype 2 Intrahost Diversity in Patients with Different Clinical Outcomes. <i>Viruses</i> , 2021, 13, 349.	3.3	11
52	SARS-CoV-2 Induces Cytokine Responses in Human Basophils. <i>Frontiers in Immunology</i> , 2022, 13, 838448.	4.8	11
53	Experimental adaptation of dengue virus 1 to Aedes albopictus mosquitoes by in vivo selection. <i>Scientific Reports</i> , 2020, 10, 18404.	3.3	10
54	High Number of Previous Plasmodium falciparum Clinical Episodes Increases Risk of Future Episodes in a Sub-Group of Individuals. <i>PLoS ONE</i> , 2013, 8, e55666.	2.5	10

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55	Evaluation of resequencing on number of tag SNPs of 13 atherosclerosis-related genes in Thai population. <i>Journal of Human Genetics</i> , 2008, 53, 74-86.	2.3	9
56	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
57	Non-congenital severe ocular complications of Zika virus infection. <i>JMM Case Reports</i> , 2018, 5, e005152.	1.3	9
58	An Exhaustive, Non-Euclidean, Non-Parametric Data Mining Tool for Unraveling the Complexity of Biological Systems – Novel Insights into Malaria. <i>PLoS ONE</i> , 2011, 6, e24085.	2.5	9
59	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
60	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
61	Viral evolution sustains a dengue outbreak of enhanced severity. <i>Emerging Microbes and Infections</i> , 2021, 10, 536-544.	6.5	6
62	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
63	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
64	Proteinuria during dengue fever in children. <i>International Journal of Infectious Diseases</i> , 2017, 55, 38-44.	3.3	4
65	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
66	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
67	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
68	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
69	Impact of Changing Drug Treatment and Malaria Endemicity on the Heritability of Malaria Phenotypes in a Longitudinal Family-Based Cohort Study. <i>PLoS ONE</i> , 2011, 6, e26364.	2.5	2
70	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