Hidayat Trimarsanto

List of Publications by Year in descending order

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430754 434063 1,100 48 18 citations h-index papers

g-index 50 50 50 1436 docs citations times ranked citing authors all docs

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#	Article	IF	CITATIONS
1	Implementing parasite genotyping into national surveillance frameworks: feedback from control programmes and researchers in the Asia–Pacific region. Malaria Journal, 2020, 19, 271.	0.8	31
2	Molecular surveillance over 14 years confirms reduction of Plasmodium vivax and falciparum transmission after implementation of Artemisinin-based combination therapy in Papua, Indonesia. PLoS Neglected Tropical Diseases, 2020, 14, e0008295.	1.3	9
3	Genetic diversity and neutral selection in Plasmodium vivax erythrocyte binding protein correlates with patient antigenicity. PLoS Neglected Tropical Diseases, 2020, 14, e0008202.	1.3	5
4	Title is missing!. , 2020, 14, e0008295.		0
5	Title is missing!. , 2020, 14, e0008295.		O
6	Title is missing!. , 2020, 14, e0008295.		0
7	Title is missing!. , 2020, 14, e0008295.		0
8	Title is missing!. , 2020, 14, e0008295.		0
9	Title is missing!. , 2020, 14, e0008202.		0
10	Title is missing!. , 2020, 14, e0008202.		0
11	Title is missing!. , 2020, 14, e0008202.		0
12	Title is missing!. , 2020, 14, e0008202.		0
13	Clinical features and virological confirmation of perinatal dengue infection in Jambi, Indonesia: A case report. International Journal of Infectious Diseases, 2019, 86, 197-200.	1.5	2
14	Genomic Analysis of Plasmodium vivax in Southern Ethiopia Reveals Selective Pressures in Multiple Parasite Mechanisms. Journal of Infectious Diseases, 2019, 220, 1738-1749.	1.9	50
15	Placental mitochondrial DNA copy number is associated with reduced birth weight in women with placental malaria. Placenta, 2019, 80, 1-3.	0.7	4
16	Genomic analysis of dengue virus serotype 1 (DENV-1) genotypes from Surabaya, Indonesia. Virus Genes, 2018, 54, 461-465.	0.7	3
17	Genomic analysis of a pre-elimination Malaysian Plasmodium vivax population reveals selective pressures and changing transmission dynamics. Nature Communications, 2018, 9, 2585.	5. 8	59
18	Evolutionary study and phylodynamic pattern of human influenza A/H3N2 virus in Indonesia from 2008 to 2010. PLoS ONE, 2018, 13, e0201427.	1.1	3

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19	Transcription factor 7-like 2 single nucleotide polymorphisms are associated with lipid profile in the Balinese. Molecular Biology Reports, 2018, 45, 1135-1143.	1.0	5
20	Isolation and complete genome analysis of neurotropic dengue virus serotype 3 from the cerebrospinal fluid of an encephalitis patient. PLoS Neglected Tropical Diseases, 2018, 12, e0006198.	1.3	17
21	Whole genome sequencing of Indonesian dengue virus isolates using next-generation sequencing. Indonesian Journal of Biotechnology, 2018, 23, 74.	0.1	1
22	Phylogenetic and evolutionary analyses of dengue viruses isolated in Jakarta, Indonesia. Virus Genes, 2017, 53, 778-788.	0.7	18
23	Genomic characterization of Zika virus isolated from Indonesia. Virology, 2017, 510, 248-251.	1.1	8
24	Production of recombinant dengue non-structural 1 (NS1) proteins from clinical virus isolates. Protein Expression and Purification, 2017, 129, 53-59.	0.6	4
25	Clinical and virological characteristics of dengue in Surabaya, Indonesia. PLoS ONE, 2017, 12, e0178443.	1.1	35
26	Chloroquine efficacy for Plasmodium vivax in Myanmar in populations with high genetic diversity and moderate parasite gene flow. Malaria Journal, 2017, 16, 281.	0.8	24
27	VivaxGEN: An open access platform for comparative analysis of short tandem repeat genotyping data in Plasmodium vivax populations. PLoS Neglected Tropical Diseases, 2017, 11, e0005465.	1.3	13
28	Genetic micro-epidemiology of malaria in Papua Indonesia: Extensive P. vivax diversity and a distinct subpopulation of asymptomatic P. falciparum infections. PLoS ONE, 2017, 12, e0177445.	1.1	16
29	Passively versus Actively Detected Malaria: Similar Genetic Diversity but Different Complexity of Infection. American Journal of Tropical Medicine and Hygiene, 2017, 97, 1788-1796.	0.6	16
30	Where chloroquine still works: the genetic make-up and susceptibility of Plasmodium vivax to chloroquine plus primaquine in Bhutan. Malaria Journal, 2016, 15, 277.	0.8	21
31	Primer development to obtain complete coding sequence of HA and NA genes of influenza A/H3N2 virus. BMC Research Notes, 2016, 9, 423.	0.6	4
32	Genomic analysis of local variation and recent evolution in Plasmodium vivax. Nature Genetics, 2016, 48, 959-964.	9.4	169
33	A zoonotic human infection with simian malaria, Plasmodium knowlesi, in Central Kalimantan, Indonesia. Malaria Journal, 2016, 15, 218.	0.8	35
34	A new Plasmodium vivax reference sequence with improved assembly of the subtelomeres reveals an abundance of pir genes. Wellcome Open Research, 2016, 1, 4.	0.9	118
35	Further Evidence of Increasing Diversity of Plasmodium vivax in the Republic of Korea in Recent Years. PLoS ONE, 2016, 11, e0151514.	1.1	13
36	Molecular Epidemiology of P. vivax in Iran: High Diversity and Complex Sub-Structure Using Neutral Markers, but No Evidence of Y976F Mutation at pvmdr1. PLoS ONE, 2016, 11, e0166124.	1.1	17

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37	Placental weight ratio affects placental mRNA expression of insulin-like growth factor-I and long isoform of the leptin receptor in Plasmodium falciparuminfected pregnant women. Asia Pacific Journal of Clinical Nutrition, 2016, 25, S75-S82.	0.3	1
38	Exceptional Complex Chromosomal Rearrangements in Three Generations. Case Reports in Genetics, 2015, 2015, 1-5.	0.1	0
39	Contrasting Transmission Dynamics of Co-endemic Plasmodium vivax and P. falciparum: Implications for Malaria Control and Elimination. PLoS Neglected Tropical Diseases, 2015, 9, e0003739.	1.3	63
40	Genomic analysis and growth characteristic of dengue viruses from Makassar, Indonesia. Infection, Genetics and Evolution, 2015, 32, 165-177.	1.0	67
41	Variation in Complexity of Infection and Transmission Stability between Neighbouring Populations of Plasmodium vivax in Southern Ethiopia. PLoS ONE, 2015, 10, e0140780.	1.1	33
42	Molecular surveillance of Dengue in Sukabumi, West Java province, Indonesia. Journal of Infection in Developing Countries, 2014, 8, 733-741.	0.5	22
43	Genetic diversity and population structure of Plasmodium vivax in Central China. Malaria Journal, 2014, 13, 262.	0.8	22
44	Performance of Simplexa Dengue Molecular Assay Compared to Conventional and SYBR Green RT-PCR for Detection of Dengue Infection in Indonesia. PLoS ONE, 2014, 9, e103815.	1.1	34
45	Molecular Surveillance of Dengue in Semarang, Indonesia Revealed the Circulation of an Old Genotype of Dengue Virus Serotype-1. PLoS Neglected Tropical Diseases, 2013, 7, e2354.	1.3	54
46	Performance of commercial dengue NS1 ELISA and molecular analysis of NS1 gene of dengue viruses obtained during surveillance in Indonesia. BMC Infectious Diseases, 2013, 13, 611.	1.3	36
47	Uncoupling protein 2 gene polymorphisms are associated with obesity. Cardiovascular Diabetology, 2012, 11, 41.	2.7	46
48	Association of beta3-adrenergic receptor (ADRB3) Trp64Arg gene polymorphism with obesity and metabolic syndrome in the Balinese: a pilot study. BMC Research Notes, 2011, 4, 167.	0.6	15