

Hsiao-Han Chang

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

1,471
citations

516710

16
h-index

580821

25
g-index

31
all docs

31
docs citations

31
times ranked

2276
citing authors

#	ARTICLE	IF	CITATIONS
1	The impact of the COVID-19 preventive measures on influenza transmission: molecular and epidemiological evidence. <i>International Journal of Infectious Diseases</i> , 2022, 116, 11-13.	3.3	5
2	Evaluating the Performance of Malaria Genetics for Inferring Changes in Transmission Intensity Using Transmission Modeling. <i>Molecular Biology and Evolution</i> , 2021, 38, 274-289.	8.9	17
3	Variation in human mobility and its impact on the risk of future COVID-19 outbreaks in Taiwan. <i>BMC Public Health</i> , 2021, 21, 226.	2.9	44
4	Comparison of Estimated Effectiveness of Case-Based and Population-Based Interventions on COVID-19 Containment in Taiwan. <i>JAMA Internal Medicine</i> , 2021, 181, 913-921.	5.1	37
5	Low parasite connectivity among three malaria hotspots in Thailand. <i>Scientific Reports</i> , 2021, 11, 23348.	3.3	5
6	Distinguishing gene flow between malaria parasite populations. <i>PLoS Genetics</i> , 2021, 17, e1009335.	3.5	4
7	Face mask use in the general population and optimal resource allocation during the COVID-19 pandemic. <i>Nature Communications</i> , 2020, 11, 4049.	12.8	250
8	Mapping the travel patterns of people with malaria in Bangladesh. <i>BMC Medicine</i> , 2020, 18, 45.	5.5	11
9	Influenza A Hemagglutinin Passage Bias Sites and Host Specificity Mutations. <i>Cells</i> , 2019, 8, 958.	4.1	6
10	Mapping imported malaria in Bangladesh using parasite genetic and human mobility data. <i>ELife</i> , 2019, 8, .	6.0	78
11	Mapping malaria by combining parasite genomic and epidemiologic data. <i>BMC Medicine</i> , 2018, 16, 190.	5.5	68
12	Systematic analysis of protein identity between Zika virus and other arthropod-borne viruses. <i>Bulletin of the World Health Organization</i> , 2017, 95, 517-525I.	3.3	52
13	THE REAL McCOIL: A method for the concurrent estimation of the complexity of infection and SNP allele frequency for malaria parasites. <i>PLoS Computational Biology</i> , 2017, 13, e1005348.	3.2	93
14	Variation in infection length and superinfection enhance selection efficiency in the human malaria parasite. <i>Scientific Reports</i> , 2016, 6, 26370.	3.3	13
15	Persistence of <i>Plasmodium falciparum</i> parasitemia after artemisinin combination therapy: evidence from a randomized trial in Uganda. <i>Scientific Reports</i> , 2016, 6, 26330.	3.3	34
16	Identifying the effect of patient sharing on between-hospital genetic differentiation of methicillin-resistant <i>Staphylococcus aureus</i> . <i>Genome Medicine</i> , 2016, 8, 18.	8.2	20
17	Origin and Proliferation of Multiple-Drug Resistance in Bacterial Pathogens. <i>Microbiology and Molecular Biology Reviews</i> , 2015, 79, 101-116.	6.6	183
18	Sequence tag-based analysis of microbial population dynamics. <i>Nature Methods</i> , 2015, 12, 223-226.	19.0	100

#	ARTICLE	IF	CITATIONS
19	Modeling malaria genomics reveals transmission decline and rebound in Senegal. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7067-7072.	7.1	163
20	Recurrent bottlenecks in the malaria life cycle obscure signals of positive selection. Parasitology, 2015, 142, S98-S107.	1.5	16
21	Clonal Outbreak of <i>Plasmodium falciparum</i> Infection in Eastern Panama. Journal of Infectious Diseases, 2015, 211, 1087-1096.	4.0	71
22	The Distribution of Pairwise Genetic Distances: A Tool for Investigating Disease Transmission. Genetics, 2014, 198, 1395-1404.	2.9	43
23	Malaria life cycle intensifies both natural selection and random genetic drift. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20129-20134.	7.1	67
24	Genomic Sequencing of <i>Plasmodium falciparum</i> Malaria Parasites from Senegal Reveals the Demographic History of the Population. Molecular Biology and Evolution, 2012, 29, 3427-3439.	8.9	58