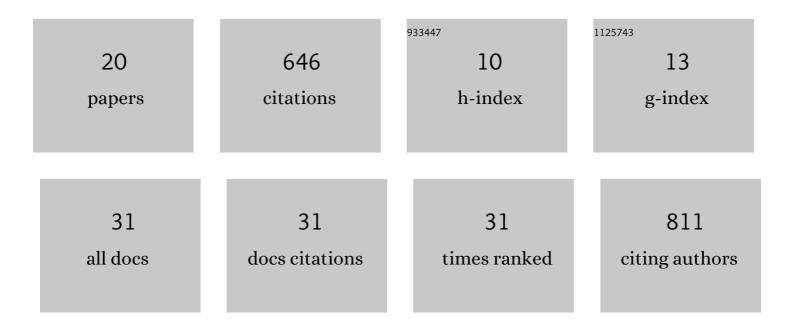
Aimee R Taylor

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3514782/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Evaluating the reliability of mobility metrics from aggregated mobile phone data as proxies for SARS-CoV-2 transmission in the USA: a population-based study. The Lancet Digital Health, 2022, 4, e27-e36.	12.3	19
2	Design and implementation of multiplexed amplicon sequencing panels to serve genomic epidemiology of infectious disease: A malaria case study. Molecular Ecology Resources, 2022, 22, 2285-2303.	4.8	18
3	Advances and opportunities in malaria population genomics. Nature Reviews Genetics, 2021, 22, 502-517.	16.3	61
4	A molecular barcode to inform the geographical origin and transmission dynamics of Plasmodium vivax malaria. PLoS Genetics, 2020, 16, e1008576.	3.5	24
5	A cautionary note on the use of unsupervised machine learning algorithms to characterise malaria parasite population structure from genetic distance matrices. PLoS Genetics, 2020, 16, e1009037.	3.5	5
6	Identity-by-descent with uncertainty characterises connectivity of Plasmodium falciparum populations on the Colombian-Pacific coast. PLoS Genetics, 2020, 16, e1009101.	3.5	19
7	Title is missing!. , 2020, 16, e1009037.		0
8	Title is missing!. , 2020, 16, e1009037.		0
9	Title is missing!. , 2020, 16, e1009037.		0
10	Title is missing!. , 2020, 16, e1009037.		0
11	Title is missing!. , 2020, 16, e1009101.		0
12	Title is missing!. , 2020, 16, e1009101.		0
13	Title is missing!. , 2020, 16, e1009101.		0
14	Title is missing!. , 2020, 16, e1009101.		0
15	Estimating Relatedness Between Malaria Parasites. Genetics, 2019, 212, 1337-1351.	2.9	47
16	A decision-theoretic approach to the evaluation of machine learning algorithms in computational drug discovery. Bioinformatics, 2019, 35, 4656-4663.	4.1	15
17	Resolving the cause of recurrent Plasmodium vivax malaria probabilistically. Nature Communications, 2019, 10, 5595.	12.8	70
18	Mapping malaria by combining parasite genomic and epidemiologic data. BMC Medicine, 2018, 16, 190.	5.5	68

#	Article	IF	CITATIONS
19	hmmIBD: software to infer pairwise identity by descent between haploid genotypes. Malaria Journal, 2018, 17, 196.	2.3	103
20	Quantifying connectivity between local Plasmodium falciparum malaria parasite populations using identity by descent. PLoS Genetics, 2017, 13, e1007065.	3.5	98