

Gerry Q Tonkin-Hill

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

30
papers

580
citations

12
h-index

24
g-index

41
ext. papers

1,157
ext. citations

9
avg, IF

4.03
L-index

#	Paper	IF	Citations
30	Genome-wide association, prediction and heritability in bacteria with application to .. <i>NAR Genomics and Bioinformatics</i> , 2022 , 4, lqac011	3.7	2
29	Genomic epidemiology of COVID-19 in care homes in the east of England. <i>ELife</i> , 2021 , 10,	8.9	8
28	Apparent nosocomial adaptation of <i>Enterococcus faecalis</i> predates the modern hospital era. <i>Nature Communications</i> , 2021 , 12, 1523	17.4	12
27	Common virulence gene expression in adult first-time infected malaria patients and severe cases. <i>ELife</i> , 2021 , 10,	8.9	3
26	Emergence and dissemination of antimicrobial resistance in <i>Escherichia coli</i> causing bloodstream infections in Norway in 2002-17: a nationwide, longitudinal, microbial population genomic study.. <i>Lancet Microbe, The</i> , 2021 , 2, e331-e341	22.2	5
25	Evolutionary analyses of the major variant surface antigen-encoding genes reveal population structure of <i>Plasmodium falciparum</i> within and between continents. <i>PLoS Genetics</i> , 2021 , 17, e1009269	6	5
24	A comprehensive and high-quality collection of genomes and their genes. <i>Microbial Genomics</i> , 2021 , 7,	4.4	12
23	Patterns of within-host genetic diversity in SARS-CoV-2. <i>ELife</i> , 2021 , 10,	8.9	26
22	Identifying targets of protective antibodies against severe malaria in Papua, Indonesia using locally expressed domains of Erythrocyte Membrane Protein 1. <i>Infection and Immunity</i> , 2021 , IAI0043521	3.7	0
21	Tentacle Transcriptomes of the Speckled Anemone (Actiniaria: Actiniidae: <i>Oulactis</i> sp.): Venom-Related Components and Their Domain Structure. <i>Marine Biotechnology</i> , 2020 , 22, 207-219	3.4	8
20	Producing polished prokaryotic pangenomes with the Panaroo pipeline. <i>Genome Biology</i> , 2020 , 21, 180	18.3	108
19	Bacterial genome-wide association study of hyper-virulent pneumococcal serotype 1 identifies genetic variation associated with neurotropism. <i>Communications Biology</i> , 2020 , 3, 559	6.7	1
18	Fast and flexible bacterial genomic epidemiology with PopPUNK. <i>Genome Research</i> , 2019 , 29, 304-316	9.7	102
17	Fast hierarchical Bayesian analysis of population structure. <i>Nucleic Acids Research</i> , 2019 , 47, 5539-5549	20.1	57
16	Genome-wide epistasis and co-selection study using mutual information. <i>Nucleic Acids Research</i> , 2019 , 47, e112	20.1	19
15	Bacterial Population Genomics 2019 , 997-1020		3
14	The inner ear proteome of fish. <i>FEBS Journal</i> , 2019 , 286, 66-81	5.7	26

13	A high parasite density environment induces transcriptional changes and cell death in Plasmodium falciparum blood stages. <i>FEBS Journal</i> , 2018 , 285, 848-870	5.7	14
12	The Plasmodium falciparum transcriptome in severe malaria reveals altered expression of genes involved in important processes including surface antigen-encoding var genes. <i>PLoS Biology</i> , 2018 , 16, e2004328	9.7	38
11	RhierBAPS: An R implementation of the population clustering algorithm hierBAPS. <i>Wellcome Open Research</i> , 2018 , 3, 93	4.8	81
10	Population genomics of virulence genes of Plasmodium falciparum in clinical isolates from Uganda. <i>Scientific Reports</i> , 2017 , 7, 11810	4.9	12
9	Stronger together. <i>Nature Reviews Microbiology</i> , 2017 , 15, 516	22.2	1
8	The Use of Imaging Mass Spectrometry to Study Peptide Toxin Distribution in Australian Sea Anemones. <i>Australian Journal of Chemistry</i> , 2017 , 70, 1235	1.2	14
7	Fast Hierarchical Bayesian Analysis of Population Structure		1
6	Producing Polished Prokaryotic Pangenomes with the Panaroo Pipeline		6
5	Genomic epidemiology of COVID-19 in care homes in the East of England		2
4	A comprehensive and high-quality collection of E. coli genomes and their genes		2
3	Gene expression profiling of malaria parasites reveals common virulence gene expression in adult first-time infected patients and severe cases		1
2	Patterns of within-host genetic diversity in SARS-CoV-2		8
1	Fast and flexible bacterial genomic epidemiology with PopPUNK		3