Gerry Q Tonkin-Hill

List of Publications by Year
in descending order

25 papers	1,719 citations

567281

15 h-index	

580821

25 g-index	

41 all docs	41 docs citations

41 times ranked	2497 citing authors

#	Article	IF	Citations
1	An accurate method for identifying recent recombinants from unaligned sequences. Bioinformatics, 2022, 38, 1823-1829.	4.1	3
2	Age-specific patterns of DBLα var diversity can explain why residents of high malaria transmission areas remain susceptible to Plasmodium falciparum blood stage infection throughout life. International Journal for Parasitology, 2022, 52, 721-731.	3.1	15
3	Genome-wide association, prediction and heritability in bacteria with application to <i>Streptococcus pneumoniae</i>. NAR Genomics and Bioinformatics, 2022, 4, lqac011.	3.2	5
4	Identifying Targets of Protective Antibodies against Severe Malaria in Papua, Indonesia, Using Locally Expressed Domains of Plasmodium falciparum Erythrocyte Membrane Protein 1. Infection and Immunity, 2022, 90, IAI0043521.	2.2	3
5	Comparative Genomics of Disease and Carriage Serotype 1 Pneumococci. Genome Biology and Evolution, 2022, 14, .	2.5	3
6	Evolutionary analyses of the major variant surface antigen-encoding genes reveal population structure of Plasmodium falciparum within and between continents. PLoS Genetics, 2021, 17, e1009269.	3.5	20
7	A comprehensive and high-quality collection of Escherichia coli genomes and their genes. Microbial Genomics, 2021, 7, .	2.0	38
8	Genomic epidemiology of COVID-19 in care homes in the east of England. ELife, 2021, 10, .	6.0	20
9	Apparent nosocomial adaptation of Enterococcus faecalis predates the modern hospital era. Nature Communications, 2021, 12, 1523.	12.8	69
10	Common virulence gene expression in adult first-time infected malaria patients and severe cases. ELife, 2021, 10, .	6.0	20
11	Emergence and dissemination of antimicrobial resistance in Escherichia coli causing bloodstream infections in Norway in 2002â€"17: a nationwide, longitudinal, microbial population genomic study. Lancet Microbe, The, 2021, 2, e331-e341.	7.3	43
12	Patterns of within-host genetic diversity in SARS-CoV-2. ELife, 2021, 10, .	6.0	110
13	Producing polished prokaryotic pangenomes with the Panaroo pipeline. Genome Biology, 2020, 21, 180.	8.8	419
14	Bacterial genome-wide association study of hyper-virulent pneumococcal serotype 1 identifies genetic variation associated with neurotropism. Communications Biology, 2020, 3, 559.	4.4	11
15	Tentacle Transcriptomes of the Speckled Anemone (Actiniaria: Actiniidae: Oulactis sp.): Venom-Related Components and Their Domain Structure. Marine Biotechnology, 2020, 22, 207-219.	2.4	19
16	Genome-wide epistasis and co-selection study using mutual information. Nucleic Acids Research, 2019, 47, e112-e112.	14.5	36
17	Fast and flexible bacterial genomic epidemiology with PopPUNK. Genome Research, 2019, 29, 304-316.	5.5	258
18	Fast hierarchical Bayesian analysis of population structure. Nucleic Acids Research, 2019, 47, 5539-5549.	14.5	173

#	Article	IF	Citations
19	The inner ear proteome of fish. FEBS Journal, 2019, 286, 66-81.	4.7	48
20	A high parasite density environment induces transcriptional changes and cell death in <i>Plasmodium falciparum</i> blood stages. FEBS Journal, 2018, 285, 848-870.	4.7	21
21	The Plasmodium falciparum transcriptome in severe malaria reveals altered expression of genes involved in important processes including surface antigenâ€"encoding var genes. PLoS Biology, 2018, 16, e2004328.	5.6	67
22	RhierBAPS: An R implementation of the population clustering algorithm hierBAPS. Wellcome Open Research, 2018, 3, 93.	1.8	198
23	Population genomics of virulence genes of Plasmodium falciparum in clinical isolates from Uganda. Scientific Reports, 2017, 7, 11810.	3.3	31
24	Stronger together. Nature Reviews Microbiology, 2017, 15, 516-516.	28.6	1
25	The Use of Imaging Mass Spectrometry to Study Peptide Toxin Distribution in Australian Sea Anemones. Australian Journal of Chemistry, 2017, 70, 1235.	0.9	20