Gerry Q Tonkin-Hill

List of Publications by Year in descending order

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CERRY O TONKIN-HILL

#	Article	IF	CITATIONS
1	Producing polished prokaryotic pangenomes with the Panaroo pipeline. Genome Biology, 2020, 21, 180.	8.8	419
2	Fast and flexible bacterial genomic epidemiology with PopPUNK. Genome Research, 2019, 29, 304-316.	5.5	258
3	RhierBAPS: An R implementation of the population clustering algorithm hierBAPS. Wellcome Open Research, 2018, 3, 93.	1.8	198
4	Fast hierarchical Bayesian analysis of population structure. Nucleic Acids Research, 2019, 47, 5539-5549.	14.5	173
5	Patterns of within-host genetic diversity in SARS-CoV-2. ELife, 2021, 10, .	6.0	110
6	Apparent nosocomial adaptation of Enterococcus faecalis predates the modern hospital era. Nature Communications, 2021, 12, 1523.	12.8	69
7	The Plasmodium falciparum transcriptome in severe malaria reveals altered expression of genes involved in important processes including surface antigen–encoding var genes. PLoS Biology, 2018, 16, e2004328.	5.6	67
8	The inner ear proteome of fish. FEBS Journal, 2019, 286, 66-81.	4.7	48
9	Emergence and dissemination of antimicrobial resistance in Escherichia coli causing bloodstream infections in Norway in 2002–17: a nationwide, longitudinal, microbial population genomic study. Lancet Microbe, The, 2021, 2, e331-e341.	7.3	43
10	A comprehensive and high-quality collection of Escherichia coli genomes and their genes. Microbial Genomics, 2021, 7, .	2.0	38
11	Genome-wide epistasis and co-selection study using mutual information. Nucleic Acids Research, 2019, 47, e112-e112.	14.5	36
12	Population genomics of virulence genes of Plasmodium falciparum in clinical isolates from Uganda. Scientific Reports, 2017, 7, 11810.	3.3	31
13	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
14	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
15	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
16	Genomic epidemiology of COVID-19 in care homes in the east of England. ELife, 2021, 10, .	6.0	20
17	Common virulence gene expression in adult first-time infected malaria patients and severe cases. ELife, 2021, 10, .	6.0	20
18	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

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19	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
20	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
21	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
22	An accurate method for identifying recent recombinants from unaligned sequences. Bioinformatics, 2022, 38, 1823-1829.	4.1	3
23	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
24	Comparative Genomics of Disease and Carriage Serotype 1 Pneumococci. Genome Biology and Evolution, 2022, 14, .	2.5	3
25	Stronger together. Nature Reviews Microbiology, 2017, 15, 516-516.	28.6	1