

# Taane G Clark

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1909755/publications.pdf>

Version: 2024-02-01

257  
papers

20,551  
citations

22099

59  
h-index

12910

131  
g-index

277  
all docs

277  
docs citations

277  
times ranked

28852  
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	13.7	4,709
2	A robust SNP barcode for typing <i>Mycobacterium tuberculosis</i> complex strains. <i>Nature Communications</i> , 2014, 5, 4812.	5.8	531
3	Targeted Restoration of the Intestinal Microbiota with a Simple, Defined Bacteriotherapy Resolves Relapsing <i>Clostridium difficile</i> Disease in Mice. <i>PLoS Pathogens</i> , 2012, 8, e1002995.	2.1	504
4	The epidemiology, pathogenesis, transmission, diagnosis, and management of multidrug-resistant, extensively drug-resistant, and incurable tuberculosis. <i>Lancet Respiratory Medicine</i> , 2017, 5, 291-360.	5.2	459
5	Analysis of <i>Plasmodium falciparum</i> diversity in natural infections by deep sequencing. <i>Nature</i> , 2012, 487, 375-379.	13.7	450
6	A transcriptional switch underlies commitment to sexual development in malaria parasites. <i>Nature</i> , 2014, 507, 248-252.	13.7	430
7	Whole genome sequencing of multiple <i>Leishmania donovani</i> clinical isolates provides insights into population structure and mechanisms of drug resistance. <i>Genome Research</i> , 2011, 21, 2143-2156.	2.4	381
8	Independent Emergence of Artemisinin Resistance Mutations Among <i>Plasmodium falciparum</i> in Southeast Asia. <i>Journal of Infectious Diseases</i> , 2015, 211, 670-679.	1.9	368
9	Quantification of the completeness of follow-up. <i>Lancet, The</i> , 2002, 359, 1309-1310.	6.3	349
10	Genome-wide and fine-resolution association analysis of malaria in West Africa. <i>Nature Genetics</i> , 2009, 41, 657-665.	9.4	345
11	Rapid determination of anti-tuberculosis drug resistance from whole-genome sequences. <i>Genome Medicine</i> , 2015, 7, 51.	3.6	323
12	Missing.... presumed at random: cost-analysis of incomplete data. <i>Health Economics (United Kingdom)</i> , 2003, 12, 377-392.	0.8	280
13	The genetic basis for smoking behavior: A systematic review and meta-analysis. <i>Nicotine and Tobacco Research</i> , 2004, 6, 583-598.	1.4	280
14	Genome-wide analysis of multi- and extensively drug-resistant <i>Mycobacterium tuberculosis</i> . <i>Nature Genetics</i> , 2018, 50, 307-316.	9.4	271
15	Personality and smoking status: A meta-analysis. <i>Nicotine and Tobacco Research</i> , 2007, 9, 405-413.	1.4	248
16	Integrating informatics tools and portable sequencing technology for rapid detection of resistance to anti-tuberculous drugs. <i>Genome Medicine</i> , 2019, 11, 41.	3.6	248
17	Genetic loci associated with delayed clearance of <i>Plasmodium falciparum</i> following artemisinin treatment in Southeast Asia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 240-245.	3.3	242
18	Randomized, placebo-controlled trial of the angiotensin-converting enzyme inhibitor, ramipril, in patients with coronary or other occlusive arterial disease. <i>Journal of the American College of Cardiology</i> , 2000, 36, 438-443.	1.2	219

#	ARTICLE	IF	CITATIONS
19	Distinct Phases of Blood Gene Expression Pattern Through Tuberculosis Treatment Reflect Modulation of the Humoral Immune Response. <i>Journal of Infectious Diseases</i> , 2013, 207, 18-29.	1.9	218
20	A genotype calling algorithm for the Illumina BeadArray platform. <i>Bioinformatics</i> , 2007, 23, 2741-2746.	1.8	209
21	Reappraisal of known malaria resistance loci in a large multicenter study. <i>Nature Genetics</i> , 2014, 46, 1197-1204.	9.4	206
22	Large-scale whole genome sequencing of <i>M. tuberculosis</i> provides insights into transmission in a high prevalence area. <i>ELife</i> , 2015, 4, .	2.8	198
23	Therapy-Related Myelodysplasia and Secondary Acute Myelogenous Leukemia After High-Dose Therapy With Autologous Hematopoietic Progenitor-Cell Support for Lymphoid Malignancies. <i>Journal of Clinical Oncology</i> , 2000, 18, 947-947.	0.8	197
24	Developing a prognostic model in the presence of missing data. <i>Journal of Clinical Epidemiology</i> , 2003, 56, 28-37.	2.4	191
25	Genome-wide significance for dense SNP and resequencing data. <i>Genetic Epidemiology</i> , 2008, 32, 179-185.	0.6	187
26	Assessing publication bias in genetic association studies: evidence from a recent meta-analysis. <i>Psychiatry Research</i> , 2004, 129, 39-44.	1.7	161
27	Recurrence due to Relapse or Reinfection With <i>Mycobacterium tuberculosis</i> : A Whole-Genome Sequencing Approach in a Large, Population-Based Cohort With a High HIV Infection Prevalence and Active Follow-up. <i>Journal of Infectious Diseases</i> , 2015, 211, 1154-1163.	1.9	149
28	A barcode of organellar genome polymorphisms identifies the geographic origin of <i>Plasmodium falciparum</i> strains. <i>Nature Communications</i> , 2014, 5, 4052.	5.8	130
29	Global expansion of <i>Mycobacterium tuberculosis</i> lineage 4 shaped by colonial migration and local adaptation. <i>Science Advances</i> , 2018, 4, eaat5869.	4.7	130
30	Use of Purified <i>Clostridium difficile</i> Spores To Facilitate Evaluation of Health Care Disinfection Regimens. <i>Applied and Environmental Microbiology</i> , 2010, 76, 6895-6900.	1.4	120
31	Admixture into and within sub-Saharan Africa. <i>ELife</i> , 2016, 5, .	2.8	120
32	Human Coronavirus NL63 Molecular Epidemiology and Evolutionary Patterns in Rural Coastal Kenya. <i>Journal of Infectious Diseases</i> , 2018, 217, 1728-1739.	1.9	116
33	Allelic heterogeneity of G6PD deficiency in West Africa and severe malaria susceptibility. <i>European Journal of Human Genetics</i> , 2009, 17, 1080-1085.	1.4	109
34	Directional Selection at the <i>pfmdr1</i> , <i>pfcr1</i> , <i>pfubp1</i> , and <i>pfap2mu</i> Loci of <i>Plasmodium falciparum</i> in Kenyan Children Treated With ACT. <i>Journal of Infectious Diseases</i> , 2014, 210, 2001-2008.	1.9	108
35	Genome-Wide Analysis of Selection on the Malaria Parasite <i>Plasmodium falciparum</i> in West African Populations of Differing Infection Endemicity. <i>Molecular Biology and Evolution</i> , 2014, 31, 1490-1499.	3.5	107
36	Outcomes, infectiousness, and transmission dynamics of patients with extensively drug-resistant tuberculosis and home-discharged patients with programmatically curable tuberculosis: a prospective cohort study. <i>Lancet Respiratory Medicine</i> , 2017, 5, 269-281.	5.2	106

#	ARTICLE	IF	CITATIONS
37	Characterization of Within-Host Plasmodium falciparum Diversity Using Next-Generation Sequence Data. PLoS ONE, 2012, 7, e32891.	1.1	102
38	Mycobacterium tuberculosis whole genome sequencing and protein structure modelling provides insights into anti-tuberculosis drug resistance. BMC Medicine, 2016, 14, 31.	2.3	102
39	A systematic survey of 13 randomized trials of non-steroidal anti-inflammatory drugs for the prevention of heterotopic bone formation after major hip surgery. Acta Orthopaedica, 2000, 71, 122-128.	1.4	99
40	Sequence-Level Population Simulations Over Large Genomic Regions. Genetics, 2007, 177, 1725-1731.	1.2	99
41	Imputation-Based Meta-Analysis of Severe Malaria in Three African Populations. PLoS Genetics, 2013, 9, e1003509.	1.5	95
42	Neuroticism Mediates the Association of the Serotonin Transporter Gene with Lifetime Major Depression. Neuropsychobiology, 2006, 53, 1-8.	0.9	94
43	The Lancet Respiratory Medicine Commission: 2019 update: epidemiology, pathogenesis, transmission, diagnosis, and management of multidrug-resistant and incurable tuberculosis. Lancet Respiratory Medicine, 2019, 7, 820-826.	5.2	92
44	Human candidate gene polymorphisms and risk of severe malaria in children in Kilifi, Kenya: a case-control association study. Lancet Haematology, 2018, 5, e333-e345.	2.2	90
45	MET and autism susceptibility: family and case-control studies. European Journal of Human Genetics, 2009, 17, 749-758.	1.4	86
46	Development and Validation of a Nomogram for Assessing Survival in Patients With COVID-19 Pneumonia. Clinical Infectious Diseases, 2021, 72, 652-660.	2.9	86
47	Primary macrophages and J774 cells respond differently to infection with Mycobacterium tuberculosis. Scientific Reports, 2017, 7, 42225.	1.6	84
48	Whole Genome Sequencing Shows a Low Proportion of Tuberculosis Disease Is Attributable to Known Close Contacts in Rural Malawi. PLoS ONE, 2015, 10, e0132840.	1.1	84
49	Immune Phenotype Predicts Risk for Posttransplantation Squamous Cell Carcinoma. Journal of the American Society of Nephrology: JASN, 2010, 21, 713-722.	3.0	82
50	SpolPred: rapid and accurate prediction of Mycobacterium tuberculosis spoligotypes from short genomic sequences. Bioinformatics, 2012, 28, 2991-2993.	1.8	80
51	PolyTB: A genomic variation map for Mycobacterium tuberculosis. Tuberculosis, 2014, 94, 346-354.	0.8	79
52	Robust barcoding and identification of Mycobacterium tuberculosis lineages for epidemiological and clinical studies. Genome Medicine, 2020, 12, 114.	3.6	79
53	Recurrence After Abdominal Surgery for Crohn's Disease. Diseases of the Colon and Rectum, 2002, 45, 377-383.	0.7	78
54	Genomic expression catalogue of a global collection of BCG vaccine strains show evidence for highly diverged metabolic and cell-wall adaptations. Scientific Reports, 2015, 5, 15443.	1.6	78

#	ARTICLE	IF	CITATIONS
55	Modest heterologous protection after <i>Plasmodium falciparum</i> sporozoite immunization: a double-blind randomized controlled clinical trial. <i>BMC Medicine</i> , 2017, 15, 168.	2.3	78
56	estMOI: estimating multiplicity of infection using parasite deep sequencing data. <i>Bioinformatics</i> , 2014, 30, 1292-1294.	1.8	76
57	Genome-wide screen identifies new candidate genes associated with artemisinin susceptibility in <i>Plasmodium falciparum</i> in Kenya. <i>Scientific Reports</i> , 2013, 3, 3318.	1.6	75
58	Elucidating Emergence and Transmission of Multidrug-Resistant Tuberculosis in Treatment Experienced Patients by Whole Genome Sequencing. <i>PLoS ONE</i> , 2013, 8, e83012.	1.1	75
59	Genome-Wide Saturation Mutagenesis of <i>Burkholderia pseudomallei</i> K96243 Predicts Essential Genes and Novel Targets for Antimicrobial Development. <i>MBio</i> , 2014, 5, e00926-13.	1.8	75
60	Population genomic structure and adaptation in the zoonotic malaria parasite <i>Plasmodium knowlesi</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13027-13032.	3.3	75
61	Detecting and Characterizing Genomic Signatures of Positive Selection in Global Populations. <i>American Journal of Human Genetics</i> , 2013, 92, 866-881.	2.6	71
62	Discordant bioinformatic predictions of antimicrobial resistance from whole-genome sequencing data of bacterial isolates: an inter-laboratory study. <i>Microbial Genomics</i> , 2020, 6, .	1.0	69
63	An Effective Method to Purify <i>Plasmodium falciparum</i> DNA Directly from Clinical Blood Samples for Whole Genome High-Throughput Sequencing. <i>PLoS ONE</i> , 2011, 6, e22213.	1.1	68
64	High-throughput analysis of candidate imprinted genes and allele-specific gene expression in the human term placenta. <i>BMC Genetics</i> , 2010, 11, 25.	2.7	64
65	Characterisation of the opposing effects of G6PD deficiency on cerebral malaria and severe malarial anaemia. <i>ELife</i> , 2017, 6, .	2.8	64
66	Understanding molecular consequences of putative drug resistant mutations in <i>Mycobacterium tuberculosis</i> . <i>Scientific Reports</i> , 2018, 8, 15356.	1.6	64
67	Positive selection of a CD36 nonsense variant in sub-Saharan Africa, but no association with severe malaria phenotypes. <i>Human Molecular Genetics</i> , 2009, 18, 2683-2692.	1.4	63
68	Contrasting Transmission Dynamics of Co-endemic <i>Plasmodium vivax</i> and <i>P. falciparum</i> : Implications for Malaria Control and Elimination. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003739.	1.3	63
69	Enrichment of Clinically Relevant Organisms in Spontaneous Preterm-Delivered Placentas and Reagent Contamination across All Clinical Groups in a Large Pregnancy Cohort in the United Kingdom. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	63
70	Population Genetic Analysis of <i>Plasmodium falciparum</i> Parasites Using a Customized Illumina GoldenGate Genotyping Assay. <i>PLoS ONE</i> , 2011, 6, e20251.	1.1	63
71	Whole-Genome Scans Provide Evidence of Adaptive Evolution in Malawian <i>Plasmodium falciparum</i> Isolates. <i>Journal of Infectious Diseases</i> , 2014, 210, 1991-2000.	1.9	62
72	Recombination in <i>pe/ppa</i> genes contributes to genetic variation in <i>Mycobacterium tuberculosis</i> lineages. <i>BMC Genomics</i> , 2016, 17, 151.	1.2	62

#	ARTICLE	IF	CITATIONS
73	Rapid and iterative genome editing in the malaria parasite <i>Plasmodium knowlesi</i> provides new tools for <i>P. vivax</i> research. <i>ELife</i> , 2019, 8, .	2.8	61
74	Genome-scale comparison of expanded gene families in <i>Plasmodium ovale wallikeri</i> and <i>Plasmodium ovale curtisi</i> with <i>Plasmodium malariae</i> and with other <i>Plasmodium</i> species. <i>International Journal for Parasitology</i> , 2016, 46, 685-696.	1.3	59
75	Genomic analysis of a pre-elimination Malaysian <i>Plasmodium vivax</i> population reveals selective pressures and changing transmission dynamics. <i>Nature Communications</i> , 2018, 9, 2585.	5.8	59
76	Whole Genome Sequencing Based Characterization of Extensively Drug-Resistant Mycobacterium tuberculosis Isolates from Pakistan. <i>PLoS ONE</i> , 2015, 10, e0117771.	1.1	59
77	Genome-wide comparisons of variation in linkage disequilibrium. <i>Genome Research</i> , 2009, 19, 1849-1860.	2.4	58
78	African Glucose-6-Phosphate Dehydrogenase Alleles Associated with Protection from Severe Malaria in Heterozygous Females in Tanzania. <i>PLoS Genetics</i> , 2015, 11, e1004960.	1.5	58
79	Genetic Diversity of <i>norA</i> , Coding for a Main Efflux Pump of <i>Staphylococcus aureus</i> . <i>Frontiers in Genetics</i> , 2018, 9, 710.	1.1	58
80	Estimating the number of coding mutations in genotypic- and phenotypic-driven N-ethyl-N-nitrosourea (ENU) screens. <i>Mammalian Genome</i> , 2006, 17, 230-238.	1.0	57
81	Identifying mixed Mycobacterium tuberculosis infections from whole genome sequence data. <i>BMC Genomics</i> , 2018, 19, 613.	1.2	57
82	Association of sub-microscopic malaria parasite carriage with transmission intensity in north-eastern Tanzania. <i>Malaria Journal</i> , 2011, 10, 370.	0.8	55
83	Novel genetic polymorphisms associated with severe malaria and under selective pressure in North-eastern Tanzania. <i>PLoS Genetics</i> , 2018, 14, e1007172.	1.5	55
84	How Myalgic Encephalomyelitis/Chronic Fatigue Syndrome (ME/CFS) Progresses: The Natural History of ME/CFS. <i>Frontiers in Neurology</i> , 2020, 11, 826.	1.1	54
85	Imputation-Based Population Genetics Analysis of <i>Plasmodium falciparum</i> Malaria Parasites. <i>PLoS Genetics</i> , 2015, 11, e1005131.	1.5	53
86	Tumor Necrosis Factor and Lymphotoxin- $\alpha$ Polymorphisms and Severe Malaria in African Populations. <i>Journal of Infectious Diseases</i> , 2009, 199, 569-575.	1.9	52
87	Unraveling Mycobacterium tuberculosis genomic diversity and evolution in Lisbon, Portugal, a highly drug resistant setting. <i>BMC Genomics</i> , 2014, 15, 991.	1.2	52
88	PrimedRPA: primer design for recombinase polymerase amplification assays. <i>Bioinformatics</i> , 2019, 35, 682-684.	1.8	52
89	Polymorphisms in leucine-rich repeat genes are associated with autism spectrum disorder susceptibility in populations of European ancestry. <i>Molecular Autism</i> , 2010, 1, 7.	2.6	51
90	Machine Learning Predicts Accurately Mycobacterium tuberculosis Drug Resistance From Whole Genome Sequencing Data. <i>Frontiers in Genetics</i> , 2019, 10, 922.	1.1	51

#	ARTICLE	IF	CITATIONS
91	Recombinations in Staphylococcal Cassette Chromosome mec Elements Compromise the Molecular Detection of Methicillin Resistance in Staphylococcus aureus. PLoS ONE, 2014, 9, e101419.	1.1	50
92	Changes in Malaria Parasite Drug Resistance in an Endemic Population Over a 25-Year Period With Resulting Genomic Evidence of Selection. Journal of Infectious Diseases, 2014, 209, 1126-1135.	1.9	49
93	Removing the bottleneck in whole genome sequencing of Mycobacterium tuberculosis for rapid drug resistance analysis: a call to action. International Journal of Infectious Diseases, 2017, 56, 130-135.	1.5	49
94	On the Usage of HWE for Identifying Genotyping Errors. Annals of Human Genetics, 2007, 71, 701-703.	0.3	47
95	Transforming Growth Factor Beta 2 and Heme Oxygenase 1 Genes Are Risk Factors for the Cerebral Malaria Syndrome in Angolan Children. PLoS ONE, 2010, 5, e11141.	1.1	47
96	Genomic Epidemiology of a Protracted Hospital Outbreak Caused by a Toxin A-Negative Clostridium difficile Sublineage PCR Ribotype 017 Strain in London, England. Journal of Clinical Microbiology, 2015, 53, 3141-3147.	1.8	46
97	Zika might not be acting alone: Using an ecological study approach to investigate potential co-acting risk factors for an unusual pattern of microcephaly in Brazil. PLoS ONE, 2018, 13, e0201452.	1.1	45
98	The variability and reproducibility of whole genome sequencing technology for detecting resistance to anti-tuberculous drugs. Genome Medicine, 2016, 8, 132.	3.6	44
99	Evidence for Host-Bacterial Co-evolution via Genome Sequence Analysis of 480 Thai Mycobacterium tuberculosis Lineage 1 Isolates. Scientific Reports, 2018, 8, 11597.	1.6	44
100	Is body mass index a risk factor for motor vehicle driver injury? A cohort study with prospective and retrospective outcomes. International Journal of Epidemiology, 2003, 32, 147-149.	0.9	43
101	No effect of low-dose aspirin for the prevention of heterotopic bone formation after total hip replacement: A randomized trial of 2,649 patients. Acta Orthopaedica, 2000, 71, 129-134.	1.4	42
102	The UK ME/CFS Biobank for biomedical research on Myalgic Encephalomyelitis/Chronic Fatigue Syndrome (ME/CFS) and Multiple Sclerosis. Open Journal of Bioresources, 2017, 4, .	1.5	42
103	Drug-Resistant Genotypes and Multi-Clonality in Plasmodium falciparum Analysed by Direct Genome Sequencing from Peripheral Blood of Malaria Patients. PLoS ONE, 2011, 6, e23204.	1.1	41
104	Candidate Polymorphisms and Severe Malaria in a Malian Population. PLoS ONE, 2012, 7, e43987.	1.1	41
105	Characterization of New Virulence Factors Involved in the Intracellular Growth and Survival of Burkholderia pseudomallei. Infection and Immunity, 2016, 84, 701-710.	1.0	41
106	Genome-wide mutagenesis and multi-drug resistance in American trypanosomes induced by the front-line drug benznidazole. Scientific Reports, 2017, 7, 14407.	1.6	41
107	Genome-wide analysis of Mycobacterium tuberculosis polymorphisms reveals lineage-specific associations with drug resistance. BMC Genomics, 2019, 20, 252.	1.2	41
108	Global analysis of Plasmodium falciparum histidine-rich protein-2 (pfhrp2) and pfhrp3 gene deletions using whole-genome sequencing data and meta-analysis. Infection, Genetics and Evolution, 2018, 62, 211-219.	1.0	40

#	ARTICLE	IF	CITATIONS
109	Know Your Heart: Rationale, design and conduct of a cross-sectional study of cardiovascular structure, function and risk factors in 4500 men and women aged 35-69 years from two Russian cities, 2015-18. Wellcome Open Research, 2018, 3, 67.	0.9	40
110	Candidate Human Genetic Polymorphisms and Severe Malaria in a Tanzanian Population. PLoS ONE, 2012, 7, e47463.	1.1	39
111	Bacterial and host determinants of cough aerosol culture positivity in patients with drug-resistant versus drug-susceptible tuberculosis. Nature Medicine, 2020, 26, 1435-1443.	15.2	38
112	Genetic diversity of candidate loci linked to Mycobacterium tuberculosis resistance to bedaquiline, delamanid and pretomanid. Scientific Reports, 2021, 11, 19431.	1.6	37
113	The genetic risk of acute seizures in African children with falciparum malaria. Epilepsia, 2013, 54, 990-1001.	2.6	36
114	Association of Cytokine and Toll-Like Receptor Gene Polymorphisms with Severe Malaria in Three Regions of Cameroon. PLoS ONE, 2013, 8, e81071.	1.1	36
115	Hand Grip Strength as a Clinical Biomarker for ME/CFS and Disease Severity. Frontiers in Neurology, 2018, 9, 992.	1.1	36
116	External validation of a deep learning electrocardiogram algorithm to detect ventricular dysfunction. International Journal of Cardiology, 2021, 329, 130-135.	0.8	36
117	Global genetic diversity of var2csa in Plasmodium falciparum with implications for malaria in pregnancy and vaccine development. Scientific Reports, 2018, 8, 15429.	1.6	35
118	A novel Ancestral Beijing sublineage of Mycobacterium tuberculosis suggests the transition site to Modern Beijing sublineages. Scientific Reports, 2019, 9, 13718.	1.6	35
119	Human Candidate Polymorphisms in Sympatric Ethnic Groups Differing in Malaria Susceptibility in Mali. PLoS ONE, 2013, 8, e75675.	1.1	35
120	Glucose-6-phosphate dehydrogenase polymorphisms and susceptibility to mild malaria in Dogon and Fulani, Mali. Malaria Journal, 2014, 13, 270.	0.8	34
121	Characterizing the impact of sustained sulfadoxine/pyrimethamine use upon the Plasmodium falciparum population in Malawi. Malaria Journal, 2016, 15, 575.	0.8	34
122	Mycobacterium tuberculosis whole genome sequencing provides insights into the Manila strain and drug-resistance mutations in the Philippines. Scientific Reports, 2019, 9, 9305.	1.6	33
123	Variation in Complexity of Infection and Transmission Stability between Neighbouring Populations of Plasmodium vivax in Southern Ethiopia. PLoS ONE, 2015, 10, e0140780.	1.1	33
124	Functional constraint and small insertions and deletions in the ENCODE regions of the human genome. Genome Biology, 2007, 8, R180.	13.9	32
125	Cathepsin-L Can Resist Lysis by Human Serum in Trypanosoma brucei brucei. PLoS Pathogens, 2014, 10, e1004130.	2.1	32
126	Knowledge, attitudes and practices regarding antimicrobial use and resistance among communities of Ilala, Kilosa and Kibaha districts of Tanzania. Antimicrobial Resistance and Infection Control, 2020, 9, 194.	1.5	32



#	ARTICLE	IF	CITATIONS
127	Distinctive genetic structure and selection patterns in Plasmodium vivax from South Asia and East Africa. Nature Communications, 2021, 12, 3160.	5.8	32
128	Methylation in Mycobacterium tuberculosis is lineage specific with associated mutations present globally. Scientific Reports, 2018, 8, 160.	1.6	31
129	Expression profile of wild-type ETV6 in childhood acute leukaemia. British Journal of Haematology, 2003, 122, 94-98.	1.2	30
130	Estimating the number of coding mutations in genotypic and phenotypic driven N-ethyl-N-nitrosourea (ENU) screens: revisited. Mammalian Genome, 2007, 18, 123-124.	1.0	30
131	TLR9 polymorphisms in African populations: no association with severe malaria, but evidence of cis-variants acting on gene expression. Malaria Journal, 2009, 8, 44.	0.8	30
132	Genomic variation in Plasmodium vivax malaria reveals regions under selective pressure. PLoS ONE, 2017, 12, e0177134.	1.1	29
133	Know Your Heart: Rationale, design and conduct of a cross-sectional study of cardiovascular structure, function and risk factors in 4500 men and women aged 35-69 years from two Russian cities, 2015-18. Wellcome Open Research, 2018, 3, 67.	0.9	29
134	Power consequences of linkage disequilibrium variation between populations. Genetic Epidemiology, 2009, 33, 128-135.	0.6	28
135	Whole genome sequencing of Mycobacterium tuberculosis isolates and clinical outcomes of patients treated for multidrug-resistant tuberculosis in Tanzania. BMC Genomics, 2020, 21, 174.	1.2	28
136	A genetic association study in the Gambia using tagging polymorphisms in the major histocompatibility complex class III region implicates a HLA-B associated transcript 2 polymorphism in severe malaria susceptibility. Human Genetics, 2009, 125, 105-109.	1.8	27
137	The Governance and Implementation of the National Action Plan on Antimicrobial Resistance in Tanzania: A Qualitative Study. Antibiotics, 2021, 10, 273.	1.5	27
138	Effective Preparation of Plasmodium vivax Field Isolates for High-Throughput Whole Genome Sequencing. PLoS ONE, 2013, 8, e53160.	1.1	26
139	Fc gamma Receptor $\gamma$ 131 Polymorphism and Malaria Susceptibility in Sympatric Ethnic Groups, Fulani and Dogon of Mali. Scandinavian Journal of Immunology, 2014, 79, 43-50.	1.3	26
140	Genetic determinants of anti-malarial acquired immunity in a large multi-centre study. Malaria Journal, 2015, 14, 333.	0.8	26
141	USP38, FREM3, SDC1, DDC, and LOC727982 Gene Polymorphisms and Differential Susceptibility to Severe Malaria in Tanzania. Journal of Infectious Diseases, 2015, 212, 1129-1139.	1.9	26
142	A multiple genome analysis of Mycobacterium tuberculosis reveals specific novel genes and mutations associated with pyrazinamide resistance. BMC Genomics, 2017, 18, 769.	1.2	26
143	An integrated whole genome analysis of Mycobacterium tuberculosis reveals insights into relationship between its genome, transcriptome and methylome. Scientific Reports, 2019, 9, 5204.	1.6	26
144	Genetic diversity and risk factors for the transmission of antimicrobial resistance across human, animals and environmental compartments in East Africa: a review. Antimicrobial Resistance and Infection Control, 2020, 9, 127.	1.5	26

#	ARTICLE	IF	CITATIONS
145	Using genomics to understand the origin and dispersion of multidrug and extensively drug resistant tuberculosis in Portugal. <i>Scientific Reports</i> , 2020, 10, 2600.	1.6	26
146	Polymorphisms in dopamine metabolic enzymes and tobacco consumption in smokers: seeking confirmation of the association in a follow-up study. <i>Pharmacogenetics and Genomics</i> , 2002, 12, 585-587.	5.7	25
147	Frequent Undetected Ward-Based Methicillin-Resistant <i>Staphylococcus aureus</i> Transmission Linked to Patient Sharing Between Hospitals. <i>Clinical Infectious Diseases</i> , 2018, 66, 840-848.	2.9	25
148	Whole genome sequencing of amplified <i>Plasmodium knowlesi</i> DNA from unprocessed blood reveals genetic exchange events between Malaysian Peninsular and Borneo subpopulations. <i>Scientific Reports</i> , 2019, 9, 9873.	1.6	25
149	Evidence of Clinical Pathology Abnormalities in People with Myalgic Encephalomyelitis/Chronic Fatigue Syndrome (ME/CFS) from an Analytic Cross-Sectional Study. <i>Diagnostics</i> , 2019, 9, 41.	1.3	25
150	A comprehensive analysis of drug resistance molecular markers and <i>Plasmodium falciparum</i> genetic diversity in two malaria endemic sites in Mali. <i>Malaria Journal</i> , 2019, 18, 361.	0.8	25
151	Investigation of Host Candidate Malaria-Associated Risk/Protective SNPs in a Brazilian Amazonian Population. <i>PLoS ONE</i> , 2012, 7, e36692.	1.1	24
152	Role of Alanine Racemase Mutations in <i>Mycobacterium tuberculosis</i> <scp>d</scp> -Cycloserine Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	24
153	Single nucleotide polymorphisms in efflux pumps genes in extensively drug resistant <i>Mycobacterium tuberculosis</i> isolates from Pakistan. <i>Tuberculosis</i> , 2017, 107, 20-30.	0.8	24
154	Whole genome sequencing of drug resistant <i>Mycobacterium tuberculosis</i> isolates from a high burden tuberculosis region of North West Pakistan. <i>Scientific Reports</i> , 2019, 9, 14996.	1.6	24
155	A molecular barcode to inform the geographical origin and transmission dynamics of <i>Plasmodium vivax</i> malaria. <i>PLoS Genetics</i> , 2020, 16, e1008576.	1.5	24
156	PlasmoView: A Web-based Resource to Visualise Global <i>Plasmodium falciparum</i> Genomic Variation. <i>Journal of Infectious Diseases</i> , 2014, 209, 1808-1815.	1.9	23
157	PhyTB: Phylogenetic tree visualisation and sample positioning for <i>M. tuberculosis</i> . <i>BMC Bioinformatics</i> , 2015, 16, 155.	1.2	23
158	Association of candidate gene polymorphisms and TGF-beta/IL-10 levels with malaria in three regions of Cameroon: a case-control study. <i>Malaria Journal</i> , 2014, 13, 236.	0.8	22
159	Genetic diversity and population structure of <i>Plasmodium vivax</i> in Central China. <i>Malaria Journal</i> , 2014, 13, 262.	0.8	22
160	Use of whole genome sequencing in surveillance of drug resistant tuberculosis. <i>Expert Review of Anti-Infective Therapy</i> , 2018, 16, 433-442.	2.0	22
161	Validating Discovered Cis-Acting Regulatory Genetic Variants: Application of an Allele Specific Expression Approach to HapMap Populations. <i>PLoS ONE</i> , 2008, 3, e4105.	1.1	22
162	Pyrazinamide resistance-conferring mutations in <i>pncA</i> and the transmission of multidrug resistant TB in Georgia. <i>BMC Infectious Diseases</i> , 2017, 17, 491.	1.3	21

#	ARTICLE	IF	CITATIONS
163	A reference genome and methylome for the Plasmodium knowlesi A1-H.1 line. International Journal for Parasitology, 2018, 48, 191-196.	1.3	20
164	Bayesian logistic regression using a perfect phylogeny. Biostatistics, 2007, 8, 32-52.	0.9	19
165	A Poisson hierarchical modelling approach to detecting copy number variation in sequence coverage data. BMC Genomics, 2013, 14, 128.	1.2	19
166	The draft genome of Mycobacterium aurum, a potential model organism for investigating drugs against Mycobacterium tuberculosis and Mycobacterium leprae. International Journal of Mycobacteriology, 2015, 4, 207-216.	0.3	19
167	Diverticulosis and nine connective tissue disorders: epidemiological support for an association. Connective Tissue Research, 2019, 60, 389-398.	1.1	19
168	Selective whole genome amplification of Plasmodium malariae DNA from clinical samples reveals insights into population structure. Scientific Reports, 2020, 10, 10832.	1.6	19
169	Genomic variation in two gametocyte non-producing Plasmodium falciparum clonal lines. Malaria Journal, 2016, 15, 229.	0.8	18
170	Analysis of nuclear and organellar genomes of Plasmodium knowlesi in humans reveals ancient population structure and recent recombination among host-specific subpopulations. PLoS Genetics, 2017, 13, e1007008.	1.5	18
171	Population-based analysis of ocular Chlamydia trachomatis in trachoma-endemic West African communities identifies genomic markers of disease severity. Genome Medicine, 2018, 10, 15.	3.6	18
172	Artemisinin resistance-associated markers in Plasmodium falciparum parasites from the China-Myanmar border: predicted structural stability of K13 propeller variants detected in a low-prevalence area. PLoS ONE, 2019, 14, e0213686.	1.1	18
173	Clonal expansion across the seas as seen through CPLP-TB database: A joint effort in cataloguing Mycobacterium tuberculosis genetic diversity in Portuguese-speaking countries. Infection, Genetics and Evolution, 2019, 72, 44-58.	1.0	18
174	Bayesian reconstruction of Mycobacterium tuberculosis transmission networks in a high incidence area over two decades in Malawi reveals associated risk factors and genomic variants. Microbial Genomics, 2020, 6, .	1.0	18
175	Combining structure and genomics to understand antimicrobial resistance. Computational and Structural Biotechnology Journal, 2020, 18, 3377-3394.	1.9	17
176	An inter-laboratory study to investigate the impact of the bioinformatics component on microbiome analysis using mock communities. Scientific Reports, 2021, 11, 10590.	1.6	17
177	Know Your Heart: Rationale, design and conduct of a cross-sectional study of cardiovascular structure, function and risk factors in 4500 men and women aged 35-69 years from two Russian cities, 2015-18. Wellcome Open Research, 0, 3, 67.	0.9	17
178	Haplotype Analyses of Haemoglobin C and Haemoglobin S and the Dynamics of the Evolutionary Response to Malaria in Kassena-Nankana District of Ghana. PLoS ONE, 2012, 7, e34565.	1.1	16
179	An integrated in silico immuno-genetic analytical platform provides insights into COVID-19 serological and vaccine targets. Genome Medicine, 2021, 13, 4.	3.6	16
180	A snapshot of translation in Mycobacterium tuberculosis during exponential growth and nutrient starvation revealed by ribosome profiling. Cell Reports, 2021, 34, 108695.	2.9	16

#	ARTICLE	IF	CITATIONS
181	Whole-genome sequencing resolves a polyclonal outbreak by extended-spectrum beta-lactam and carbapenem-resistant <i>Klebsiella pneumoniae</i> in a Portuguese tertiary-care hospital. <i>Microbial Genomics</i> , 2019, 7, .	1.0	16
182	Finding Associations in Dense Genetic Maps: A Genetic Algorithm Approach. <i>Human Heredity</i> , 2005, 60, 97-108.	0.4	15
183	G6PD deficiency alleles in a malaria-endemic region in the Western Brazilian Amazon. <i>Malaria Journal</i> , 2017, 16, 253.	0.8	15
184	A forward genetic screen reveals a primary role for <i>Plasmodium falciparum</i> Reticulocyte Binding Protein Homologue 2a and 2b in determining alternative erythrocyte invasion pathways. <i>PLoS Pathogens</i> , 2018, 14, e1007436.	2.1	15
185	Association of Malaria Infection During Pregnancy With Head Circumference of Newborns in the Brazilian Amazon. <i>JAMA Network Open</i> , 2019, 2, e193300.	2.8	15
186	Surveillance of <i>Aedes aegypti</i> populations in the city of Praia, Cape Verde: Zika virus infection, insecticide resistance and genetic diversity. <i>Parasites and Vectors</i> , 2020, 13, 481.	1.0	15
187	Differences in the frequency of genetic variants associated with iron imbalance among global populations. <i>PLoS ONE</i> , 2020, 15, e0235141.	1.1	15
188	Adverse pregnancy outcomes are associated with <i>Plasmodium vivax</i> malaria in a prospective cohort of women from the Brazilian Amazon. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009390.	1.3	15
189	Using deep learning to identify recent positive selection in malaria parasite sequence data. <i>Malaria Journal</i> , 2021, 20, 270.	0.8	15
190	Genetic diversity of the <i>Plasmodium falciparum</i> GTP-cyclohydrolase 1, dihydrofolate reductase and dihydropteroate synthetase genes reveals new insights into sulfadoxine-pyrimethamine antimalarial drug resistance. <i>PLoS Genetics</i> , 2020, 16, e1009268.	1.5	15
191	Emergence of multidrug-resistant <i>Mycobacterium tuberculosis</i> of the Beijing lineage in Portugal and Guinea-Bissau: a snapshot of moving clones by whole-genome sequencing. <i>Emerging Microbes and Infections</i> , 2020, 9, 1342-1353.	3.0	14
192	Further Evidence Supporting a Role for Gs Signal Transduction in Severe Malaria Pathogenesis. <i>PLoS ONE</i> , 2010, 5, e10017.	1.1	14
193	Multidrug-Resistant <i>Mycobacterium tuberculosis</i> of the Latin American Mediterranean Lineage, Wrongly Identified as <i>Mycobacterium pinnipedii</i> (Spoligotype International Type 863 [SIT863]), Causing Active Tuberculosis in South Brazil. <i>Journal of Clinical Microbiology</i> , 2015, 53, 3805-3811.	1.8	13
194	Malaria Host Candidate Genes Validated by Association With Current, Recent, and Historical Measures of Transmission Intensity. <i>Journal of Infectious Diseases</i> , 2017, 216, 45-54.	1.9	13
195	Genomic Epidemiology of Carbapenemase Producing <i>Klebsiella pneumoniae</i> Strains at a Northern Portuguese Hospital Enables the Detection of a Misidentified <i>Klebsiella variicola</i> KPC-3 Producing Strain. <i>Microorganisms</i> , 2020, 8, 1986.	1.6	13
196	Clusters of Drug-Resistant <i>Mycobacterium tuberculosis</i> Detected by Whole-Genome Sequence Analysis of Nationwide Sample, Thailand, 2014–2017. <i>Emerging Infectious Diseases</i> , 2021, 27, 813-822.	2.0	13
197	VivaxGEN: An open access platform for comparative analysis of short tandem repeat genotyping data in <i>Plasmodium vivax</i> populations. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005465.	1.3	13
198	Further Evidence of Increasing Diversity of <i>Plasmodium vivax</i> in the Republic of Korea in Recent Years. <i>PLoS ONE</i> , 2016, 11, e0151514.	1.1	13

#	ARTICLE	IF	CITATIONS
199	Genetic diversity of next generation antimalarial targets: A baseline for drug resistance surveillance programmes. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2017, 7, 174-180.	1.4	12
200	An In-Solution Hybridisation Method for the Isolation of Pathogen DNA from Human DNA-rich Clinical Samples for Analysis by NGS. <i>The Open Genomics Journal</i> , 2012, 5, 18-29.	0.5	12
201	Validation of a New Prognostic Index for Advanced Epithelial Ovarian Cancer: Results From Its Application to a UK-Based Cohort. <i>Journal of Clinical Oncology</i> , 2007, 25, 5669-5670.	0.8	11
202	Assessing Genuine Parents-Offspring Trios for Genetic Association Studies. <i>Human Heredity</i> , 2009, 67, 26-37.	0.4	11
203	Conjunctival fibrosis and the innate barriers to <i>Chlamydia trachomatis</i> intracellular infection: a genome wide association study. <i>Scientific Reports</i> , 2015, 5, 17447.	1.6	11
204	Lack of Association of Interferon Regulatory Factor 1 with Severe Malaria in Affected Child-Parental Trio Studies across Three African Populations. <i>PLoS ONE</i> , 2009, 4, e4206.	1.1	11
205	Genetic signatures of <i>Mycobacterium tuberculosis</i> Nonthaburi genotype revealed by whole genome analysis of isolates from tuberculous meningitis patients in Thailand. <i>PeerJ</i> , 2016, 4, e1905.	0.9	11
206	Characterizing the genomic variation and population dynamics of <i>Plasmodium falciparum</i> malaria parasites in and around Lake Victoria, Kenya. <i>Scientific Reports</i> , 2021, 11, 19809.	1.6	11
207	Robust detection of point mutations involved in multidrug-resistant <i>Mycobacterium tuberculosis</i> in the presence of co-occurrent resistance markers. <i>PLoS Computational Biology</i> , 2020, 16, e1008518.	1.5	11
208	The antimalarial efficacy and mechanism of resistance of the novel chemotype DDD01034957. <i>Scientific Reports</i> , 2021, 11, 1888.	1.6	10
209	Methylation analysis of <i>Klebsiella pneumoniae</i> from Portuguese hospitals. <i>Scientific Reports</i> , 2021, 11, 6491.	1.6	10
210	Does smoking influence survival in cancer patients through effects on respiratory and vascular disease?. <i>European Journal of Cancer Prevention</i> , 2006, 15, 87-90.	0.6	9
211	SnoopCGH: software for visualizing comparative genomic hybridization data. <i>Bioinformatics</i> , 2009, 25, 2732-2733.	1.8	9
212	Bead-based assays to simultaneously detect multiple human inherited blood disorders associated with malaria. <i>Malaria Journal</i> , 2019, 18, 14.	0.8	9
213	Practices and Challenges of Veterinary Paraprofessionals in Regards to Antimicrobial Use and Resistance in Animals in Dar Es Salaam, Tanzania. <i>Antibiotics</i> , 2021, 10, 733.	1.5	9
214	Artemether-lumefantrine treatment failure of uncomplicated <i>Plasmodium falciparum</i> malaria in travellers coming from Angola and Mozambique. <i>International Journal of Infectious Diseases</i> , 2021, 110, 151-154.	1.5	9
215	Electrochemical Detection of Single-Nucleotide Polymorphism Associated with Rifampicin Resistance in <i>Mycobacterium tuberculosis</i> Using Solid-Phase Primer Elongation with Ferrocene-Linked Redox-Labeled Nucleotides. <i>ACS Sensors</i> , 2021, 6, 4398-4407.	4.0	9
216	VarB: a variation browsing and analysis tool for variants derived from next-generation sequencing data. <i>Bioinformatics</i> , 2012, 28, 2983-2985.	1.8	8

#	ARTICLE	IF	CITATIONS
217	Turkish and Japanese Mycobacterium tuberculosis sublineages share a remote common ancestor. <i>Infection, Genetics and Evolution</i> , 2016, 45, 461-473.	1.0	8
218	An analysis of large structural variation in global Plasmodium falciparum isolates identifies a novel duplication of the chloroquine resistance associated gene. <i>Scientific Reports</i> , 2019, 9, 8287.	1.6	8
219	Studying accelerated cardiovascular ageing in Russian adults through a novel deep-learning ECG biomarker. <i>Wellcome Open Research</i> , 0, 6, 12.	0.9	8
220	A modified decision tree approach to improve the prediction and mutation discovery for drug resistance in Mycobacterium tuberculosis. <i>BMC Genomics</i> , 2022, 23, 46.	1.2	8
221	Characterization of rifampicin-resistant Mycobacterium tuberculosis in Khyber Pakhtunkhwa, Pakistan. <i>Scientific Reports</i> , 2021, 11, 14194.	1.6	7
222	Characterisation of drug-resistant Mycobacterium tuberculosis mutations and transmission in Pakistan. <i>Scientific Reports</i> , 2022, 12, 7703.	1.6	7
223	An Evolutionary Algorithm to Find Associations in Dense Genetic Maps. <i>IEEE Transactions on Evolutionary Computation</i> , 2008, 12, 297-306.	7.5	6
224	Alternate efflux pump mechanism may contribute to drug resistance in extensively drug-resistant isolates of Mycobacterium tuberculosis. <i>International Journal of Mycobacteriology</i> , 2016, 5, S97-S98.	0.3	6
225	SV-Pop: population-based structural variant analysis and visualization. <i>BMC Bioinformatics</i> , 2019, 20, 136.	1.2	6
226	Drug resistance profile and clonality of Plasmodium falciparum parasites in Cape Verde: the 2017 malaria outbreak. <i>Malaria Journal</i> , 2021, 20, 172.	0.8	6
227	Policy actors and human and animal health practitioners's perceptions of antimicrobial use and resistance in Tanzania: A qualitative study. <i>Journal of Global Antimicrobial Resistance</i> , 2021, 25, 40-47.	0.9	6
228	Flavivirus integrations in Aedes aegypti are limited and highly conserved across samples from different geographic regions unlike integrations in Aedes albopictus. <i>Parasites and Vectors</i> , 2021, 14, 332.	1.0	6
229	A Natural History of Disease Framework for Improving the Prevention, Management, and Research on Post-viral Fatigue Syndrome and Other Forms of Myalgic Encephalomyelitis/Chronic Fatigue Syndrome. <i>Frontiers in Medicine</i> , 2021, 8, 688159.	1.2	6
230	Whole genome sequencing reveals large deletions and other loss of function mutations in Mycobacterium tuberculosis drug resistance genes. <i>Microbial Genomics</i> , 2021, 7, .	1.0	6
231	Probing Differences in Gene Essentiality Between the Human and Animal Adapted Lineages of the Mycobacterium tuberculosis Complex Using TnSeq. <i>Frontiers in Veterinary Science</i> , 2021, 8, 760717.	0.9	6
232	The COVID-19 Schools Infection Survey in England: Protocol and Participation Profile for a Prospective Observational Cohort Study. <i>JMIR Research Protocols</i> , 2022, 11, e34075.	0.5	6
233	High clustering rate and genotypic drug-susceptibility screening for the newly recommended anti-tuberculosis drugs among global extensively drug-resistant Mycobacterium tuberculosis isolates. <i>Emerging Microbes and Infections</i> , 2022, 11, 1857-1866.	3.0	6
234	A Bayesian approach using covariance of single nucleotide polymorphism data to detect differences in linkage disequilibrium patterns between groups of individuals. <i>Bioinformatics</i> , 2010, 26, 1999-2003.	1.8	5

#	ARTICLE	IF	CITATIONS
235	On the Performance of Multiple Imputation Based on Chained Equations in Tackling Missing Data of the African $\alpha$ -Globin Deletion in a Malaria Association Study. <i>Annals of Human Genetics</i> , 2014, 78, 277-289.	0.3	5
236	A proportion of mutations fixed in the genomes of in vitro selected isogenic drug-resistant <i>Mycobacterium tuberculosis</i> mutants can be detected as minority variants in the parent culture. <i>FEMS Microbiology Letters</i> , 2015, 362, 1-7.	0.7	5
237	Genomic evidence supporting the clonal expansion of extensively drug-resistant tuberculosis bacteria belonging to a rare Beijing genotype. <i>Emerging Microbes and Infections</i> , 2020, 9, 2632-2641.	3.0	5
238	A phylogenomic approach for the analysis of colistin resistance-associated genes in <i>Klebsiella pneumoniae</i> , its mutational diversity and implications for phenotypic resistance. <i>International Journal of Antimicrobial Agents</i> , 2022, 59, 106581.	1.1	5
239	Framing the Drivers of Antimicrobial Resistance in Tanzania. <i>Antibiotics</i> , 2021, 10, 991.	1.5	4
240	PowerBacGWAS: a computational pipeline to perform power calculations for bacterial genome-wide association studies. <i>Communications Biology</i> , 2022, 5, 266.	2.0	4
241	How has mass drug administration with dihydroartemisinin-piperaquine impacted molecular markers of drug resistance? A systematic review. <i>Malaria Journal</i> , 2022, 21, .	0.8	4
242	SVAMP: sequence variation analysis, maps and phylogeny. <i>Bioinformatics</i> , 2014, 30, 2227-2229.	1.8	3
243	Characterization of genomic variations in SNPs of PE_PGRS genes reveals deletions and insertions in extensively drug resistant (XDR) <i>M. tuberculosis</i> strains from Pakistan. <i>International Journal of Mycobacteriology</i> , 2015, 4, 73-79.	0.3	3
244	Whole-genome sequencing as a tool for studying the microevolution of drug-resistant serial <i>Mycobacterium tuberculosis</i> isolates. <i>Tuberculosis</i> , 2021, 131, 102137.	0.8	3
245	<i>Klebsiella pneumoniae</i> and Colistin Susceptibility Testing: Performance Evaluation for Broth Microdilution, Agar Dilution and Minimum Inhibitory Concentration Test Strips and Impact of the "Skipped Well" Phenomenon. <i>Diagnostics</i> , 2021, 11, 2352.	1.3	3
246	COVID-profiler: a webserver for the analysis of SARS-CoV-2 sequencing data. <i>BMC Bioinformatics</i> , 2022, 23, 137.	1.2	3
247	De Novo Assembly of <i>Plasmodium knowlesi</i> Genomes From Clinical Samples Explains the Counterintuitive Intrachromosomal Organization of Variant SICavar and kir Multiple Gene Family Members. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
248	Reply to Collins et al. <i>Clinical Infectious Diseases</i> , 2020, 73, 558-559.	2.9	2
249	Structural and Genomic Insights Into Pyrazinamide Resistance in <i>Mycobacterium tuberculosis</i> Underlie Differences Between Ancient and Modern Lineages. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 619403.	1.6	2
250	Sero-epidemiological study of arbovirus infection following the 2015-2016 Zika virus outbreak in Cabo Verde. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
251	Whole genome sequencing-based characterization of extensively drug resistant (XDR) strains of <i>Mycobacterium tuberculosis</i> from Pakistan. <i>International Journal of Mycobacteriology</i> , 2015, 4, 11-12.	0.3	1
252	G6PD Polymorphisms and Hemolysis After Antimalarial Treatment With Low Single-Dose Primaquine: A Pooled Analysis of Six African Clinical Trials. <i>Frontiers in Genetics</i> , 2021, 12, 645688.	1.1	1

#	ARTICLE	IF	CITATIONS
253	The Effect of Missing Values for Covariates. <i>Epidemiology</i> , 2002, 13, 113.	1.2	1
254	Association of the dopamine- $\beta$ -hydroxylase gene with nicotine dependence: No evidence for mediation by personality. <i>Personality and Individual Differences</i> , 2005, 39, 1113-1122.	1.6	0
255	Ocular chlamydial genomic variants and disease severity in trachoma: a cross-sectional population-based genome-wide association study. <i>Lancet, The</i> , 2016, 387, S63.	6.3	0
256	Evolutionary Trajectories and Transmission Dynamics of Multidrug-Resistant <i>Mycobacterium tuberculosis</i> in Tibet, China. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
257	Molecular characterization of drug-resistant <i>Mycobacterium tuberculosis</i> among Filipino patients derived from the national tuberculosis prevalence survey Philippines 2016. <i>Tuberculosis</i> , 2022, , 102211.	0.8	0