

Taane G Clark

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/1909755/taane-g-clark-publications-by-year.pdf>

Version: 2024-03-20

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

251 papers	15,606 citations	56 h-index	120 g-index
277 ext. papers	18,613 ext. citations	7.3 avg, IF	5.97 L-index

#	Paper	IF	Citations
251	A modified decision tree approach to improve the prediction and mutation discovery for drug resistance in <i>Mycobacterium tuberculosis</i> .. <i>BMC Genomics</i> , 2022 , 23, 46	4.5	
250	PowerBacGWAS: a computational pipeline to perform power calculations for bacterial genome-wide association studies.. <i>Communications Biology</i> , 2022 , 5, 266	6.7	0
249	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 , 106581	14.3	1
248	COVID-profiler: a webserver for the analysis of SARS-CoV-2 sequencing data.. <i>BMC Bioinformatics</i> , 2022 , 23, 137	3.6	0
247	Characterisation of drug-resistant <i>Mycobacterium tuberculosis</i> mutations and transmission in Pakistan.. <i>Scientific Reports</i> , 2022 , 12, 7703	4.9	
246	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	2.6	
245	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	4.9	1
244	Electrochemical Detection of Single-Nucleotide Polymorphism Associated with Rifampicin Resistance in Using Solid-Phase Primer Elongation with Ferrocene-Linked Redox-Labeled Nucleotides. <i>ACS Sensors</i> , 2021 ,	9.2	1
243	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	4.9	0
242	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	2.6	0
241	Reply to Collins et al. <i>Clinical Infectious Diseases</i> , 2021 , 73, 558-559	11.6	2
240	Drug resistance profile and clonality of <i>Plasmodium falciparum</i> parasites in Cape Verde: the 2017 malaria outbreak. <i>Malaria Journal</i> , 2021 , 20, 172	3.6	3
239	Methylation analysis of <i>Klebsiella pneumoniae</i> from Portuguese hospitals. <i>Scientific Reports</i> , 2021 , 11, 6491	4.9	2
238	The Governance and Implementation of the National Action Plan on Antimicrobial Resistance in Tanzania: A Qualitative Study. <i>Antibiotics</i> , 2021 , 10,	4.9	6
237	External validation of a deep learning electrocardiogram algorithm to detect ventricular dysfunction. <i>International Journal of Cardiology</i> , 2021 , 329, 130-135	3.2	7
236	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	4.5	1
235	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	4.8	5

234	Distinctive genetic structure and selection patterns in Plasmodium vivax from South Asia and East Africa. <i>Nature Communications</i> , 2021 , 12, 3160	17.4	5
233	An inter-laboratory study to investigate the impact of the bioinformatics component on microbiome analysis using mock communities. <i>Scientific Reports</i> , 2021 , 11, 10590	4.9	3
232	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,	4.9	2
231	Using deep learning to identify recent positive selection in malaria parasite sequence data. <i>Malaria Journal</i> , 2021 , 20, 270	3.6	4
230	Policy actors and human and animal health practitioners' Perceptions of antimicrobial use and resistance in Tanzania: A qualitative study. <i>Journal of Global Antimicrobial Resistance</i> , 2021 , 25, 40-47	3.4	1
229	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	4	1
228	Characterization of rifampicin-resistant Mycobacterium tuberculosis in Khyber Pakhtunkhwa, Pakistan. <i>Scientific Reports</i> , 2021 , 11, 14194	4.9	2
227	Structural and Genomic Insights Into Pyrazinamide Resistance in Underlie Differences Between Ancient and Modern Lineages. <i>Frontiers in Molecular Biosciences</i> , 2021 , 8, 619403	5.6	1
226	Development and Validation of a Nomogram for Assessing Survival in Patients With COVID-19 Pneumonia. <i>Clinical Infectious Diseases</i> , 2021 , 72, 652-660	11.6	41
225	An integrated in silico immuno-genetic analytical platform provides insights into COVID-19 serological and vaccine targets. <i>Genome Medicine</i> , 2021 , 13, 4	14.4	11
224	The antimalarial efficacy and mechanism of resistance of the novel chemotype DDD01034957. <i>Scientific Reports</i> , 2021 , 11, 1888	4.9	0
223	A snapshot of translation in Mycobacterium tuberculosis during exponential growth and nutrient starvation revealed by ribosome profiling. <i>Cell Reports</i> , 2021 , 34, 108695	10.6	4
222	Clusters of Drug-Resistant Mycobacterium tuberculosis Detected by Whole-Genome Sequence Analysis of Nationwide Sample, Thailand, 2014-2017. <i>Emerging Infectious Diseases</i> , 2021 , 27, 813-822	10.2	4
221	Genetic diversity of candidate loci linked to Mycobacterium tuberculosis resistance to bedaquiline, delamanid and pretomanid. <i>Scientific Reports</i> , 2021 , 11, 19431	4.9	7
220	Artemether-lumefantrine treatment failure of uncomplicated Plasmodium falciparum malaria in travellers coming from Angola and Mozambique. <i>International Journal of Infectious Diseases</i> , 2021 , 110, 151-154	10.5	1
219	Probing Differences in Gene Essentiality Between the Human and Animal Adapted Lineages of the Complex Using TnSeq.. <i>Frontiers in Veterinary Science</i> , 2021 , 8, 760717	3.1	1
218	Robust barcoding and identification of Mycobacterium tuberculosis lineages for epidemiological and clinical studies. <i>Genome Medicine</i> , 2020 , 12, 114	14.4	24
217	Combining structure and genomics to understand antimicrobial resistance. <i>Computational and Structural Biotechnology Journal</i> , 2020 , 18, 3377-3394	6.8	5

216	Emergence of multidrug-resistant 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	18.9	8
215	Bacterial and host determinants of cough aerosol culture positivity in patients with drug-resistant versus drug-susceptible tuberculosis. <i>Nature Medicine</i> , 2020 , 26, 1435-1443	50.5	15
214	Differences in the frequency of genetic variants associated with iron imbalance among global populations. <i>PLoS ONE</i> , 2020 , 15, e0235141	3.7	7
213	Whole genome sequencing of Mycobacterium tuberculosis isolates and clinical outcomes of patients treated for multidrug-resistant tuberculosis in Tanzania. <i>BMC Genomics</i> , 2020 , 21, 174	4.5	12
212	Using genomics to understand the origin and dispersion of multidrug and extensively drug resistant tuberculosis in Portugal. <i>Scientific Reports</i> , 2020 , 10, 2600	4.9	10
211	A molecular barcode to inform the geographical origin and transmission dynamics of Plasmodium vivax malaria. <i>PLoS Genetics</i> , 2020 , 16, e1008576	6	7
210	Genetic diversity of the Plasmodium falciparum 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	6	3
209	Robust detection of point mutations involved in multidrug-resistant Mycobacterium tuberculosis in the presence of co-occurrent resistance markers. <i>PLoS Computational Biology</i> , 2020 , 16, e1008518	5	2
208	Discordant bioinformatic predictions of antimicrobial resistance from whole-genome sequencing data of bacterial isolates: an inter-laboratory study. <i>Microbial Genomics</i> , 2020 , 6,	4.4	33
207	Bayesian reconstruction of transmission networks in a high incidence area over two decades in Malawi reveals associated risk factors and genomic variants. <i>Microbial Genomics</i> , 2020 , 6,	4.4	5
206	Selective whole genome amplification of Plasmodium malariae DNA from clinical samples reveals insights into population structure. <i>Scientific Reports</i> , 2020 , 10, 10832	4.9	5
205	Genomic evidence supporting the clonal expansion of extensively drug-resistant tuberculosis bacteria belonging to a rare protoBeijing genotype. <i>Emerging Microbes and Infections</i> , 2020 , 9, 2632-2641	18.9	1
204	Genetic diversity and risk factors for the transmission of antimicrobial resistance across human, animals and environmental compartments in East Africa: a review. <i>Antimicrobial Resistance and Infection Control</i> , 2020 , 9, 127	6.2	9
203	How Myalgic Encephalomyelitis/Chronic Fatigue Syndrome (ME/CFS) Progresses: The Natural History of ME/CFS. <i>Frontiers in Neurology</i> , 2020 , 11, 826	4.1	21
202	Surveillance of Aedes aegypti populations in the city of Praia, Cape Verde: Zika virus infection, insecticide resistance and genetic diversity. <i>Parasites and Vectors</i> , 2020 , 13, 481	4	5
201	Knowledge, attitudes and practices regarding antimicrobial use and resistance among communities of Ilala, Kilosa and Kibaha districts of Tanzania. <i>Antimicrobial Resistance and Infection Control</i> , 2020 , 9, 194	6.2	10
200	Genomic Epidemiology of Carbapenemase Producing Strains at a Northern Portuguese Hospital Enables the Detection of a Misidentified KPC-3 Producing Strain. <i>Microorganisms</i> , 2020 , 8,	4.9	6
199	The Lancet Respiratory Medicine Commission: 2019 update: epidemiology, pathogenesis, transmission, diagnosis, and management of multidrug-resistant and incurable tuberculosis. <i>Lancet Respiratory Medicine</i> , 2019 , 7, 820-826	35.1	49

198	A novel Ancestral Beijing sublineage of <i>Mycobacterium tuberculosis</i> suggests the transition site to Modern Beijing sublineages. <i>Scientific Reports</i> , 2019 , 9, 13718	4.9	22
197	Machine Learning Predicts Accurately Drug Resistance From Whole Genome Sequencing Data. <i>Frontiers in Genetics</i> , 2019 , 10, 922	4.5	25
196	Bead-based assays to simultaneously detect multiple human inherited blood disorders associated with malaria. <i>Malaria Journal</i> , 2019 , 18, 14	3.6	3
195	Diverticulosis and nine connective tissue disorders: epidemiological support for an association. <i>Connective Tissue Research</i> , 2019 , 60, 389-398	3.3	9
194	Association of Malaria Infection During Pregnancy With Head Circumference of Newborns in the Brazilian Amazon. <i>JAMA Network Open</i> , 2019 , 2, e193300	10.4	9
193	Artemisinin resistance-associated markers in <i>Plasmodium falciparum</i> parasites from the China-Myanmar border: predicted structural stability of K13 propeller variants detected in a low-prevalence area. <i>PLoS ONE</i> , 2019 , 14, e0213686	3.7	14
192	An integrated whole genome analysis of <i>Mycobacterium tuberculosis</i> reveals insights into relationship between its genome, transcriptome and methylome. <i>Scientific Reports</i> , 2019 , 9, 5204	4.9	18
191	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,	3.8	13
190	Genome-wide analysis of <i>Mycobacterium tuberculosis</i> polymorphisms reveals lineage-specific associations with drug resistance. <i>BMC Genomics</i> , 2019 , 20, 252	4.5	24
189	PrimedRPA: primer design for recombinase polymerase amplification assays. <i>Bioinformatics</i> , 2019 , 35, 682-684	7.2	21
188	SV-Pop: population-based structural variant analysis and visualization. <i>BMC Bioinformatics</i> , 2019 , 20, 136	3.6	6
187	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	4.9	13
186	<i>Mycobacterium tuberculosis</i> whole genome sequencing provides insights into the Manila strain and drug-resistance mutations in the Philippines. <i>Scientific Reports</i> , 2019 , 9, 9305	4.9	18
185	Integrating informatics tools and portable sequencing technology for rapid detection of resistance to anti-tuberculous drugs. <i>Genome Medicine</i> , 2019 , 11, 41	14.4	95
184	An analysis of large structural variation in global <i>Plasmodium falciparum</i> isolates identifies a novel duplication of the chloroquine resistance associated gene. <i>Scientific Reports</i> , 2019 , 9, 8287	4.9	6
183	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	4.9	13
182	Rapid and iterative genome editing in the malaria parasite provides new tools for research. <i>ELife</i> , 2019 , 8,	8.9	32
181	Whole-genome sequencing resolves a polyclonal outbreak by extended-spectrum beta-lactam and carbapenem-resistant in a Portuguese tertiary-care hospital. <i>Microbial Genomics</i> , 2019 , 7,	4.4	10

180	A comprehensive analysis of drug resistance molecular markers and Plasmodium falciparum genetic diversity in two malaria endemic sites in Mali. <i>Malaria Journal</i> , 2019 , 18, 361	3.6	14
179	Clonal expansion across the seas as seen through CPLP-TB database: A joint effort in cataloguing Mycobacterium tuberculosis genetic diversity in Portuguese-speaking countries. <i>Infection, Genetics and Evolution</i> , 2019 , 72, 44-58	4.5	14
178	Frequent Undetected Ward-Based Methicillin-Resistant Staphylococcus aureus Transmission Linked to Patient Sharing Between Hospitals. <i>Clinical Infectious Diseases</i> , 2018 , 66, 840-848	11.6	19
177	Genome-wide analysis of multi- and extensively drug-resistant Mycobacterium tuberculosis. <i>Nature Genetics</i> , 2018 , 50, 307-316	36.3	160
176	Methylation in Mycobacterium tuberculosis is lineage specific with associated mutations present globally. <i>Scientific Reports</i> , 2018 , 8, 160	4.9	22
175	A reference genome and methylome for the Plasmodium knowlesi A1-H.1 line. <i>International Journal for Parasitology</i> , 2018 , 48, 191-196	4.3	12
174	Use of whole genome sequencing in surveillance of drug resistant tuberculosis. <i>Expert Review of Anti-Infective Therapy</i> , 2018 , 16, 433-442	5.5	15
173	Human Coronavirus NL63 Molecular Epidemiology and Evolutionary Patterns in Rural Coastal Kenya. <i>Journal of Infectious Diseases</i> , 2018 , 217, 1728-1739	7	87
172	Human candidate gene polymorphisms and risk of severe malaria in children in Kilifi, Kenya: a case-control association study. <i>Lancet Haematology</i> , 2018 , 5, e333-e345	14.6	38
171	Population-based analysis of ocular Chlamydia trachomatis in trachoma-endemic West African communities identifies genomic markers of disease severity. <i>Genome Medicine</i> , 2018 , 10, 15	14.4	8
170	Global analysis of Plasmodium falciparum histidine-rich protein-2 (pfhrp2) and pfhrp3 gene deletions using whole-genome sequencing data and meta-analysis. <i>Infection, Genetics and Evolution</i> , 2018 , 62, 211-219	4.5	28
169	Evidence for Host-Bacterial Co-evolution via Genome Sequence Analysis of 480 Thai Mycobacterium tuberculosis Lineage 1 Isolates. <i>Scientific Reports</i> , 2018 , 8, 11597	4.9	30
168	Identifying mixed Mycobacterium tuberculosis infections from whole genome sequence data. <i>BMC Genomics</i> , 2018 , 19, 613	4.5	38
167	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. <i>PLoS ONE</i> , 2018 , 13, e0201452	3.7	30
166	Novel genetic polymorphisms associated with severe malaria and under selective pressure in North-eastern Tanzania. <i>PLoS Genetics</i> , 2018 , 14, e1007172	6	29
165	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. <i>Wellcome Open Research</i> , 2018 , 3, 67	4.8	24
164	Genetic Diversity of , Coding for a Main Efflux Pump of. <i>Frontiers in Genetics</i> , 2018 , 9, 710	4.5	31
163	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. <i>Wellcome Open Research</i> , 2018 , 3, 67	4.8	20

162	Hand Grip Strength as a Clinical Biomarker for ME/CFS and Disease Severity. <i>Frontiers in Neurology</i> , 2018 , 9, 992	4.1	18
161	A forward genetic screen reveals a primary role for Plasmodium falciparum Reticulocyte Binding Protein Homologue 2a and 2b in determining alternative erythrocyte invasion pathways. <i>PLoS Pathogens</i> , 2018 , 14, e1007436	7.6	13
160	Understanding molecular consequences of putative drug resistant mutations in Mycobacterium tuberculosis. <i>Scientific Reports</i> , 2018 , 8, 15356	4.9	37
159	Global expansion of lineage 4 shaped by colonial migration and local adaptation. <i>Science Advances</i> , 2018 , 4, eaat5869	14.3	71
158	Global genetic diversity of var2csa in Plasmodium falciparum with implications for malaria in pregnancy and vaccine development. <i>Scientific Reports</i> , 2018 , 8, 15429	4.9	29
157	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,	4.8	43
156	Genomic analysis of a pre-elimination Malaysian Plasmodium vivax population reveals selective pressures and changing transmission dynamics. <i>Nature Communications</i> , 2018 , 9, 2585	17.4	29
155	Primary macrophages and J774 cells respond differently to infection with Mycobacterium tuberculosis. <i>Scientific Reports</i> , 2017 , 7, 42225	4.9	46
154	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	4	10
153	The epidemiology, pathogenesis, transmission, diagnosis, and management of multidrug-resistant, extensively drug-resistant, and incurable tuberculosis. <i>Lancet Respiratory Medicine</i> , 2017 ,	35.1	313
152	Removing the bottleneck in whole genome sequencing of Mycobacterium tuberculosis for rapid drug resistance analysis: a call to action. <i>International Journal of Infectious Diseases</i> , 2017 , 56, 130-135	10.5	37
151	Genome-wide mutagenesis and multi-drug resistance in American trypanosomes induced by the front-line drug benznidazole. <i>Scientific Reports</i> , 2017 , 7, 14407	4.9	31
150	Role of Alanine Racemase Mutations in Mycobacterium tuberculosis d-Cycloserine Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2017 , 61,	5.9	16
149	Analysis of nuclear and organellar genomes of Plasmodium knowlesi in humans reveals ancient population structure and recent recombination among host-specific subpopulations. <i>PLoS Genetics</i> , 2017 , 13, e1007008	6	13
148	Modest heterologous protection after Plasmodium falciparum sporozoite immunization: a double-blind randomized controlled clinical trial. <i>BMC Medicine</i> , 2017 , 15, 168	11.4	56
147	Pyrazinamide resistance-conferring mutations in pncA and the transmission of multidrug resistant TB in Georgia. <i>BMC Infectious Diseases</i> , 2017 , 17, 491	4	13
146	Characterisation of the opposing effects of G6PD deficiency on cerebral malaria and severe malarial anaemia. <i>ELife</i> , 2017 , 6,	8.9	45
145	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	7	10

144	Single nucleotide polymorphisms in efflux pumps genes in extensively drug resistant Mycobacterium tuberculosis isolates from Pakistan. <i>Tuberculosis</i> , 2017 , 107, 20-30	2.6	19
143	G6PD deficiency alleles in a malaria-endemic region in the Western Brazilian Amazon. <i>Malaria Journal</i> , 2017 , 16, 253	3.6	11
142	A multiple genome analysis of Mycobacterium tuberculosis reveals specific novel genes and mutations associated with pyrazinamide resistance. <i>BMC Genomics</i> , 2017 , 18, 769	4.5	15
141	VivaxGEN: An open access platform for comparative analysis of short tandem repeat genotyping data in Plasmodium vivax populations. <i>PLoS Neglected Tropical Diseases</i> , 2017 , 11, e0005465	4.8	10
140	Genomic variation in Plasmodium vivax malaria reveals regions under selective pressure. <i>PLoS ONE</i> , 2017 , 12, e0177134	3.7	17
139	The UK ME/CFS Biobank for biomedical research on Myalgic Encephalomyelitis/Chronic Fatigue Syndrome (ME/CFS) and Multiple Sclerosis. <i>Open Journal of Bioresources</i> , 2017 , 4,	0.9	24
138	Outcomes, infectiousness, and transmission dynamics of patients with extensively drug-resistant tuberculosis and home-discharged patients with programmatically incurable tuberculosis: a prospective cohort study. <i>Lancet Respiratory Medicine</i> , 2017 , 5, 269-281	35.1	80
137	Genome-scale comparison of expanded gene families in Plasmodium ovale wallikeri and Plasmodium ovale curtisi with Plasmodium malariae and with other Plasmodium species. <i>International Journal for Parasitology</i> , 2016 , 46, 685-96	4.3	43
136	Turkish and Japanese Mycobacterium tuberculosis sublineages share a remote common ancestor. <i>Infection, Genetics and Evolution</i> , 2016 , 45, 461-473	4.5	5
135	Characterizing the impact of sustained sulfadoxine/pyrimethamine use upon the Plasmodium falciparum population in Malawi. <i>Malaria Journal</i> , 2016 , 15, 575	3.6	28
134	Genomic variation in two gametocyte non-producing Plasmodium falciparum clonal lines. <i>Malaria Journal</i> , 2016 , 15, 229	3.6	15
133	Further Evidence of Increasing Diversity of Plasmodium vivax in the Republic of Korea in Recent Years. <i>PLoS ONE</i> , 2016 , 11, e0151514	3.7	13
132	Genetic signatures of Mycobacterium tuberculosis Nonthaburi genotype revealed by whole genome analysis of isolates from tuberculous meningitis patients in Thailand. <i>PeerJ</i> , 2016 , 4, e1905	3.1	8
131	Admixture into and within sub-Saharan Africa. <i>ELife</i> , 2016 , 5,	8.9	77
130	The variability and reproducibility of whole genome sequencing technology for detecting resistance to anti-tuberculous drugs. <i>Genome Medicine</i> , 2016 , 8, 132	14.4	31
129	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 Suppl 1, S97-S98	0.9	6
128	Mycobacterium tuberculosis whole genome sequencing and protein structure modelling provides insights into anti-tuberculosis drug resistance. <i>BMC Medicine</i> , 2016 , 14, 31	11.4	77
127	Recombination in pe/ppe genes contributes to genetic variation in Mycobacterium tuberculosis lineages. <i>BMC Genomics</i> , 2016 , 17, 151	4.5	43

126	A proportion of mutations fixed in the genomes of in vitro selected isogenic drug-resistant Mycobacterium tuberculosis mutants can be detected as minority variants in the parent culture. <i>FEMS Microbiology Letters</i> , 2015 , 362, 1-7	2.9	5
125	Contrasting Transmission Dynamics of Co-endemic Plasmodium vivax and P. falciparum: Implications for Malaria Control and Elimination. <i>PLoS Neglected Tropical Diseases</i> , 2015 , 9, e0003739	4.8	50
124	The draft genome of Mycobacterium aurum, a potential model organism for investigating drugs against Mycobacterium tuberculosis and Mycobacterium leprae. <i>International Journal of Mycobacteriology</i> , 2015 , 4, 207-16	0.9	14
123	Recurrence due to relapse or reinfection with Mycobacterium tuberculosis: 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, 1154-63	7	116
122	Imputation-based population genetics analysis of Plasmodium falciparum malaria parasites. <i>PLoS Genetics</i> , 2015 , 11, e1005131	6	28
121	African glucose-6-phosphate dehydrogenase alleles associated with protection from severe malaria in heterozygous females in Tanzania. <i>PLoS Genetics</i> , 2015 , 11, e1004960	6	43
120	Characterization of genomic variations in SNPs of PE_PGRS genes reveals deletions and insertions in extensively drug resistant (XDR) M. tuberculosis strains from Pakistan. <i>International Journal of Mycobacteriology</i> , 2015 , 4, 73-9	0.9	2
119	Multidrug-Resistant Mycobacterium tuberculosis of the Latin American Mediterranean Lineage, Wrongly Identified as Mycobacterium pinnipedii (Spoligotype International Type 863 [SIT863]), Causing Active Tuberculosis in South Brazil. <i>Journal of Clinical Microbiology</i> , 2015 , 53, 3805-11	9.7	11
118	Genomic Epidemiology of a Protracted Hospital Outbreak Caused by a Toxin A-Negative Clostridium difficile Sublineage PCR Ribotype 017 Strain in London, England. <i>Journal of Clinical Microbiology</i> , 2015 , 53, 3141-7	9.7	37
117	Independent emergence of artemisinin resistance mutations among Plasmodium falciparum in Southeast Asia. <i>Journal of Infectious Diseases</i> , 2015 , 211, 670-9	7	307
116	Characterization of New Virulence Factors Involved in the Intracellular Growth and Survival of Burkholderia pseudomallei. <i>Infection and Immunity</i> , 2015 , 84, 701-10	3.7	25
115	Conjunctival fibrosis and the innate barriers to Chlamydia trachomatis intracellular infection: a genome wide association study. <i>Scientific Reports</i> , 2015 , 5, 17447	4.9	9
114	Genomic expression catalogue of a global collection of BCG vaccine strains show evidence for highly diverged metabolic and cell-wall adaptations. <i>Scientific Reports</i> , 2015 , 5, 15443	4.9	57
113	Genetic determinants of anti-malarial acquired immunity in a large multi-centre study. <i>Malaria Journal</i> , 2015 , 14, 333	3.6	16
112	PhyTB: Phylogenetic tree visualisation and sample positioning for M. tuberculosis. <i>BMC Bioinformatics</i> , 2015 , 16, 155	3.6	16
111	Rapid determination of anti-tuberculosis drug resistance from whole-genome sequences. <i>Genome Medicine</i> , 2015 , 7, 51	14.4	234
110	USP38, FREM3, SDC1, DDC, and LOC727982 Gene Polymorphisms and Differential Susceptibility to Severe Malaria in Tanzania. <i>Journal of Infectious Diseases</i> , 2015 , 212, 1129-39	7	19
109	Population genomic structure and adaptation in the zoonotic malaria parasite Plasmodium knowlesi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 13027-32	11.5	62

108	Whole genome sequencing based characterization of extensively drug-resistant Mycobacterium tuberculosis isolates from Pakistan. <i>PLoS ONE</i> , 2015 , 10, e0117771	3.7	41
107	Whole Genome Sequencing Shows a Low Proportion of Tuberculosis Disease Is Attributable to Known Close Contacts in Rural Malawi. <i>PLoS ONE</i> , 2015 , 10, e0132840	3.7	64
106	Variation in Complexity of Infection and Transmission Stability between Neighbouring Populations of Plasmodium vivax in Southern Ethiopia. <i>PLoS ONE</i> , 2015 , 10, e0140780	3.7	30
105	Large-scale whole genome sequencing of M. tuberculosis provides insights into transmission in a high prevalence area. <i>ELife</i> , 2015 , 4,	8.9	152
104	On the performance of multiple imputation based on chained equations in tackling missing data of the African B.7 -globin deletion in a malaria association study. <i>Annals of Human Genetics</i> , 2014 , 78, 277-89	3.2	5
103	Reappraisal of known malaria resistance loci in a large multicenter study. <i>Nature Genetics</i> , 2014 , 46, 1197-204	3.9	150
102	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	3.6	13
101	Genetic diversity and population structure of Plasmodium vivax in Central China. <i>Malaria Journal</i> , 2014 , 13, 262	3.6	18
100	Glucose-6-phosphate dehydrogenase polymorphisms and susceptibility to mild malaria in Dogon and Fulani, Mali. <i>Malaria Journal</i> , 2014 , 13, 270	3.6	28
99	A transcriptional switch underlies commitment to sexual development in malaria parasites. <i>Nature</i> , 2014 , 507, 248-52	50.4	305
98	A barcode of organellar genome polymorphisms identifies the geographic origin of Plasmodium falciparum strains. <i>Nature Communications</i> , 2014 , 5, 4052	17.4	83
97	PolyTB: a genomic variation map for Mycobacterium tuberculosis. <i>Tuberculosis</i> , 2014 , 94, 346-54	2.6	64
96	Genome-wide saturation mutagenesis of Burkholderia pseudomallei K96243 predicts essential genes and novel targets for antimicrobial development. <i>MBio</i> , 2014 , 5, e00926-13	7.8	57
95	Cathepsin-L can resist lysis by human serum in Trypanosoma brucei brucei. <i>PLoS Pathogens</i> , 2014 , 10, e1004130	7.6	25
94	Whole-genome scans provide evidence of adaptive evolution in Malawian Plasmodium falciparum isolates. <i>Journal of Infectious Diseases</i> , 2014 , 210, 1991-2000	7	36
93	SVAMP: sequence variation analysis, maps and phylogeny. <i>Bioinformatics</i> , 2014 , 30, 2227-9	7.2	3
92	A robust SNP barcode for typing Mycobacterium tuberculosis complex strains. <i>Nature Communications</i> , 2014 , 5, 4812	17.4	355
91	Fc gamma receptor IIa-H131R polymorphism and malaria susceptibility in sympatric ethnic groups, Fulani and Dogon of Mali. <i>Scandinavian Journal of Immunology</i> , 2014 , 79, 43-50	3.4	19

90	Directional selection at the pfmdr1, pfcr1, pfubp1, and pfap2mu loci of Plasmodium falciparum in Kenyan children treated with ACT. <i>Journal of Infectious Diseases</i> , 2014 , 210, 2001-8	7	81
89	PlasmoView: a web-based resource to visualise global Plasmodium falciparum genomic variation. <i>Journal of Infectious Diseases</i> , 2014 , 209, 1808-15	7	20
88	Unraveling Mycobacterium tuberculosis genomic diversity and evolution in Lisbon, Portugal, a highly drug resistant setting. <i>BMC Genomics</i> , 2014 , 15, 991	4.5	45
87	Changes in malaria parasite drug resistance in an endemic population over a 25-year period with resulting genomic evidence of selection. <i>Journal of Infectious Diseases</i> , 2014 , 209, 1126-35	7	36
86	estMOI: estimating multiplicity of infection using parasite deep sequencing data. <i>Bioinformatics</i> , 2014 , 30, 1292-4	7.2	44
85	Genome-wide analysis of selection on the malaria parasite Plasmodium falciparum in West African populations of differing infection endemicity. <i>Molecular Biology and Evolution</i> , 2014 , 31, 1490-9	8.3	82
84	Recombinations in staphylococcal cassette chromosome mec elements compromise the molecular detection of methicillin resistance in Staphylococcus aureus. <i>PLoS ONE</i> , 2014 , 9, e101419	3.7	42
83	A Poisson hierarchical modelling approach to detecting copy number variation in sequence coverage data. <i>BMC Genomics</i> , 2013 , 14, 128	4.5	16
82	Detecting and characterizing genomic signatures of positive selection in global populations. <i>American Journal of Human Genetics</i> , 2013 , 92, 866-81	11	56
81	Genetic loci associated with delayed clearance of Plasmodium falciparum following artemisinin treatment in Southeast Asia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 240-5	11.5	214
80	Imputation-based meta-analysis of severe malaria in three African populations. <i>PLoS Genetics</i> , 2013 , 9, e1003509	6	74
79	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	7	179
78	The genetic risk of acute seizures in African children with falciparum malaria. <i>Epilepsia</i> , 2013 , 54, 990-1001	6.4	27
77	Genome-wide screen identifies new candidate genes associated with artemisinin susceptibility in Plasmodium falciparum in Kenya. <i>Scientific Reports</i> , 2013 , 3, 3318	4.9	52
76	Effective preparation of Plasmodium vivax field isolates for high-throughput whole genome sequencing. <i>PLoS ONE</i> , 2013 , 8, e53160	3.7	24
75	Association of cytokine and Toll-like receptor gene polymorphisms with severe malaria in three regions of Cameroon. <i>PLoS ONE</i> , 2013 , 8, e81071	3.7	25
74	Elucidating emergence and transmission of multidrug-resistant tuberculosis in treatment experienced patients by whole genome sequencing. <i>PLoS ONE</i> , 2013 , 8, e83012	3.7	56
73	Human candidate polymorphisms in sympatric ethnic groups differing in malaria susceptibility in Mali. <i>PLoS ONE</i> , 2013 , 8, e75675	3.7	29

72	SpolPred: rapid and accurate prediction of Mycobacterium tuberculosis spoligotypes from short genomic sequences. <i>Bioinformatics</i> , 2012 , 28, 2991-3	7.2	74
71	Characterization of within-host Plasmodium falciparum diversity using next-generation sequence data. <i>PLoS ONE</i> , 2012 , 7, e32891	3.7	70
70	Haplotype analyses of haemoglobin C and haemoglobin S and the dynamics of the evolutionary response to malaria in Kassena-Nankana District of Ghana. <i>PLoS ONE</i> , 2012 , 7, e34565	3.7	13
69	Investigation of host candidate malaria-associated risk/protective SNPs in a Brazilian Amazonian population. <i>PLoS ONE</i> , 2012 , 7, e36692	3.7	18
68	Candidate polymorphisms and severe malaria in a Malian population. <i>PLoS ONE</i> , 2012 , 7, e43987	3.7	31
67	Candidate human genetic polymorphisms and severe malaria in a Tanzanian population. <i>PLoS ONE</i> , 2012 , 7, e47463	3.7	30
66	Analysis of Plasmodium falciparum diversity in natural infections by deep sequencing. <i>Nature</i> , 2012 , 487, 375-9	50.4	345
65	VarB: a variation browsing and analysis tool for variants derived from next-generation sequencing data. <i>Bioinformatics</i> , 2012 , 28, 2983-5	7.2	8
64	Targeted restoration of the intestinal microbiota with a simple, defined bacteriotherapy resolves relapsing Clostridium difficile disease in mice. <i>PLoS Pathogens</i> , 2012 , 8, e1002995	7.6	403
63	An In-Solution Hybridisation Method for the Isolation of Pathogen DNA from Human DNA-rich Clinical Samples for Analysis by NGS 2012 , 5,		8
62	An effective method to purify Plasmodium falciparum DNA directly from clinical blood samples for whole genome high-throughput sequencing. <i>PLoS ONE</i> , 2011 , 6, e22213	3.7	58
61	Drug-resistant genotypes and multi-clonality in Plasmodium falciparum analysed by direct genome sequencing from peripheral blood of malaria patients. <i>PLoS ONE</i> , 2011 , 6, e23204	3.7	38
60	Association of sub-microscopic malaria parasite carriage with transmission intensity in north-eastern Tanzania. <i>Malaria Journal</i> , 2011 , 10, 370	3.6	46
59	Whole genome sequencing of multiple Leishmania donovani clinical isolates provides insights into population structure and mechanisms of drug resistance. <i>Genome Research</i> , 2011 , 21, 2143-56	9.7	319
58	Population genetic analysis of Plasmodium falciparum parasites using a customized Illumina GoldenGate genotyping assay. <i>PLoS ONE</i> , 2011 , 6, e20251	3.7	38
57	Transforming growth factor beta 2 and heme oxygenase 1 genes are risk factors for the cerebral malaria syndrome in Angolan children. <i>PLoS ONE</i> , 2010 , 5, e11141	3.7	40
56	Immune phenotype predicts risk for posttransplantation squamous cell carcinoma. <i>Journal of the American Society of Nephrology: JASN</i> , 2010 , 21, 713-22	12.7	64
55	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	7.2	5

54	Use of purified <i>Clostridium difficile</i> spores to facilitate evaluation of health care disinfection regimens. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 6895-900	4.8	88
53	High-throughput analysis of candidate imprinted genes and allele-specific gene expression in the human term placenta. <i>BMC Genetics</i> , 2010 , 11, 25	2.6	51
52	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	6.5	47
51	Further evidence supporting a role for gs signal transduction in severe malaria pathogenesis. <i>PLoS ONE</i> , 2010 , 5, e10017	3.7	10
50	Tumor necrosis factor and lymphotoxin-alpha polymorphisms and severe malaria in African populations. <i>Journal of Infectious Diseases</i> , 2009 , 199, 569-75	7	42
49	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, 2683-92	5.6	53
48	Assessing genuine parents-offspring trios for genetic association studies. <i>Human Heredity</i> , 2009 , 67, 26-37	1.1	10
47	SnoopCGH: software for visualizing comparative genomic hybridization data. <i>Bioinformatics</i> , 2009 , 25, 2732-3	7.2	9
46	Genome-wide comparisons of variation in linkage disequilibrium. <i>Genome Research</i> , 2009 , 19, 1849-60	9.7	53
45	Power consequences of linkage disequilibrium variation between populations. <i>Genetic Epidemiology</i> , 2009 , 33, 128-35	2.6	27
44	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. <i>Human Genetics</i> , 2009 , 125, 105-9	6.3	19
43	MET and autism susceptibility: family and case-control studies. <i>European Journal of Human Genetics</i> , 2009 , 17, 749-58	5.3	66
42	Allelic heterogeneity of G6PD deficiency in West Africa and severe malaria susceptibility. <i>European Journal of Human Genetics</i> , 2009 , 17, 1080-5	5.3	92
41	Genome-wide and fine-resolution association analysis of malaria in West Africa. <i>Nature Genetics</i> , 2009 , 41, 657-65	36.3	297
40	TLR9 polymorphisms in African populations: no association with severe malaria, but evidence of cis-variants acting on gene expression. <i>Malaria Journal</i> , 2009 , 8, 44	3.6	23
39	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	3.7	9
38	An Evolutionary Algorithm to Find Associations in Dense Genetic Maps. <i>IEEE Transactions on Evolutionary Computation</i> , 2008 , 12, 297-306	15.6	6
37	Genome-wide significance for dense SNP and resequencing data. <i>Genetic Epidemiology</i> , 2008 , 32, 179-85	2.6	164

36	Validating discovered Cis-acting regulatory genetic variants: application of an allele specific expression approach to HapMap populations. <i>PLoS ONE</i> , 2008 , 3, e4105	3.7	21
35	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007 , 447, 799-816	50.4	4121
34	On the usage of HWE for identifying genotyping errors. <i>Annals of Human Genetics</i> , 2007 , 71, 701-3; author reply 704	2.2	40
33	Estimating the number of coding mutations in genotypic and phenotypic driven N-ethyl-N-nitrosourea (ENU) screens: revisited. <i>Mammalian Genome</i> , 2007 , 18, 123-4	3.2	20
32	Sequence-level population simulations over large genomic regions. <i>Genetics</i> , 2007 , 177, 1725-31	4	84
31	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, 5669-70; author reply 5670-1	2.2	11
30	Personality and smoking status: a meta-analysis. <i>Nicotine and Tobacco Research</i> , 2007 , 9, 405-13	4.9	195
29	A genotype calling algorithm for the Illumina BeadArray platform. <i>Bioinformatics</i> , 2007 , 23, 2741-6	7.2	194
28	Bayesian logistic regression using a perfect phylogeny. <i>Biostatistics</i> , 2007 , 8, 32-52	3.7	14
27	Functional constraint and small insertions and deletions in the ENCODE regions of the human genome. <i>Genome Biology</i> , 2007 , 8, R180	18.3	30
26	Neuroticism mediates the association of the serotonin transporter gene with lifetime major depression. <i>Neuropsychobiology</i> , 2006 , 53, 1-8	4	81
25	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	2	9
24	Estimating the number of coding mutations in genotypic- and phenotypic-driven N-ethyl-N-nitrosourea (ENU) screens. <i>Mammalian Genome</i> , 2006 , 17, 230-8	3.2	56
23	Finding associations in dense genetic maps: a genetic algorithm approach. <i>Human Heredity</i> , 2005 , 60, 97-108	1.1	13
22	Association of the dopamine- β -hydroxylase gene with nicotine dependence: No evidence for mediation by personality. <i>Personality and Individual Differences</i> , 2005 , 39, 1113-1122	3.3	
21	The genetic basis for smoking behavior: a systematic review and meta-analysis. <i>Nicotine and Tobacco Research</i> , 2004 , 6, 583-97	4.9	240
20	Assessing publication bias in genetic association studies: evidence from a recent meta-analysis. <i>Psychiatry Research</i> , 2004 , 129, 39-44	9.9	152
19	Is body mass index a risk factor for motor vehicle driver injury? A cohort study with prospective and retrospective outcomes. <i>International Journal of Epidemiology</i> , 2003 , 32, 147-9	7.8	40

18	Missing... presumed at random: cost-analysis of incomplete data. <i>Health Economics (United Kingdom)</i> , 2003 , 12, 377-92	2.4	232
17	Expression profile of wild-type ETV6 in childhood acute leukaemia. <i>British Journal of Haematology</i> , 2003 , 122, 94-8	4.5	27
16	Developing a prognostic model in the presence of missing data: an ovarian cancer case study. <i>Journal of Clinical Epidemiology</i> , 2003 , 56, 28-37	5.7	161
15	Recurrence after abdominal surgery for Crohn's disease: relationship to disease site and surgical procedure. <i>Diseases of the Colon and Rectum</i> , 2002 , 45, 377-83	3.1	62
14	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, 585-7		22
13	Quantification of the completeness of follow-up. <i>Lancet, The</i> , 2002 , 359, 1309-10	4.0	303
12	The effect of missing values for covariates. <i>Epidemiology</i> , 2002 , 13, 113	3.1	1
11	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, 947-55	2.2	172
10	No effect of low-dose aspirin for the prevention of heterotopic bone formation after total hip replacement: a randomized trial of 2,649 patients. <i>Acta Orthopaedica</i> , 2000 , 71, 129-34		35
9	A systematic survey of 13 randomized trials of non-steroidal anti-inflammatory drugs for the prevention of heterotopic bone formation after major hip surgery. <i>Acta Orthopaedica</i> , 2000 , 71, 122-8		86
8	Randomized, placebo-controlled trial of the angiotensin-converting enzyme inhibitor, ramipril, in patients with coronary or other occlusive arterial disease. PART-2 Collaborative Research Group. Prevention of Atherosclerosis with Ramipril. <i>Journal of the American College of Cardiology</i> , 2000 , 36, 438-43	15.1	190
7	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. <i>Wellcome Open Research</i> , 3, 67	4.8	13
6	Discordant bioinformatic predictions of antimicrobial resistance from whole-genome sequencing data of bacterial isolates: An inter-laboratory study		1
5	Ribosome profiling in <i>Mycobacterium tuberculosis</i> reveals robust leaderless translation		2
4	Controlling the SARS-CoV-2 outbreak, insights from large scale whole genome sequences generated across the world		14
3	An integrated in silico immuno-genetic analytical platform provides insights into COVID-19 serological and vaccine targets		2
2	Rapid and iterative genome editing in the zoonotic malaria parasite <i>Plasmodium knowlesi</i> : New tools for <i>P. vivax</i> research		1
1	Studying accelerated cardiovascular ageing in Russian adults through a novel deep-learning ECG biomarker. <i>Wellcome Open Research</i> , 6, 12	4.8	3

