Jody E Phelan

List of Publications by Year
in descending order

		257450	265206
63 papers	**2,304** citations	**24** h-index	**42** g-index
72 all docs	**72** docs citations	**72** times ranked	**3165** citing authors

#	Article	IF	Citations
1	Genome-wide analysis of multi- and extensively drug-resistant Mycobacterium tuberculosis. Nature Genetics, 2018, 50, 307-316.	21.4	271
2	Integrating informatics tools and portable sequencing technology for rapid detection of resistance to anti-tuberculous drugs. Genome Medicine, 2019, 11, 41.	8.2	248
3	Outcomes, infectiousness, and transmission dynamics of patients with extensively drug-resistant tuberculosis and home-discharged patients with programmatically incurable tuberculosis: a prospective cohort study. Lancet Respiratory Medicine,the, 2017, 5, 269-281.	10.7	106
4	Mycobacterium tuberculosis whole genome sequencing and protein structure modelling provides insights into anti-tuberculosis drug resistance. BMC Medicine, 2016, 14, 31.	5.5	102
5	Primary macrophages and J774 cells respond differently to infection with Mycobacterium tuberculosis. Scientific Reports, 2017, 7, 42225.	3.3	84
6	Robust barcoding and identification of Mycobacterium tuberculosis lineages for epidemiological and clinical studies. Genome Medicine, 2020, 12, 114.	8.2	79
7	Discordant bioinformatic predictions of antimicrobial resistance from whole-genome sequencing data of bacterial isolates: an inter-laboratory study. Microbial Genomics, 2020, 6, .	2.0	69
8	Understanding molecular consequences of putative drug resistant mutations in Mycobacterium tuberculosis. Scientific Reports, 2018, 8, 15356.	3.3	64
9	Recombination in pe/ppe genes contributes to genetic variation in Mycobacterium tuberculosis lineages. BMC Genomics, 2016, 17, 151.	2.8	62
10	Identifying mixed Mycobacterium tuberculosis infections from whole genome sequence data. BMC Genomics, 2018, 19, 613.	2.8	57
11	PrimedRPA: primer design for recombinase polymerase amplification assays. Bioinformatics, 2019, 35, 682-684.	4.1	52
12	Machine Learning Predicts Accurately Mycobacterium tuberculosis Drug Resistance From Whole Genome Sequencing Data. Frontiers in Genetics, 2019, 10, 922.	2.3	51
13	Genome-wide diversity and differentiation in New World populations of the human malaria parasite Plasmodium vivax. PLoS Neglected Tropical Diseases, 2017, 11, e0005824.	3.0	47
14	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.	2.5	45
15	The variability and reproducibility of whole genome sequencing technology for detecting resistance to anti-tuberculous drugs. Genome Medicine, 2016, 8, 132.	8.2	44
16	Evidence for Host-Bacterial Co-evolution via Genome Sequence Analysis of 480 Thai Mycobacterium tuberculosis Lineage 1 Isolates. Scientific Reports, 2018, 8, 11597.	3.3	44
17	Genome-wide mutagenesis and multi-drug resistance in American trypanosomes induced by the front-line drug benznidazole. Scientific Reports, 2017, 7, 14407.	3.3	41
18	Genome-wide analysis of Mycobacterium tuberculosis polymorphisms reveals lineage-specific associations with drug resistance. BMC Genomics, 2019, 20, 252.	2.8	41

#	ARTICLE	IF	CITATIONS
19	A novel multiplex qPCR assay for detection of Plasmodium falciparum with histidine-rich protein 2 and 3 (pfhrp2 and pfhrp3) deletions in polyclonal infections. EBioMedicine, 2020, 55, 102757.	6.1	41
20	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.	2.3	40
21	Genetic diversity of candidate loci linked to Mycobacterium tuberculosis resistance to bedaquiline, delamanid and pretomanid. Scientific Reports, 2021, 11, 19431.	3.3	37
22	A novel Ancestral Beijing sublineage of Mycobacterium tuberculosis suggests the transition site to Modern Beijing sublineages. Scientific Reports, 2019, 9, 13718.	3.3	35
23	Mycobacterium tuberculosis whole genome sequencing provides insights into the Manila strain and drug-resistance mutations in the Philippines. Scientific Reports, 2019, 9, 9305.	3.3	33
24	Distinctive genetic structure and selection patterns in Plasmodium vivax from South Asia and East Africa. Nature Communications, 2021, 12, 3160.	12.8	32
25	Methylation in Mycobacterium tuberculosis is lineage specific with associated mutations present globally. Scientific Reports, 2018, 8, 160.	3.3	31
26	Whole genome sequencing of Mycobacterium tuberculosis isolates and clinical outcomes of patients treated for multidrug-resistant tuberculosis in Tanzania. BMC Genomics, 2020, 21, 174.	2.8	28
27	GenTB: A user-friendly genome-based predictor for tuberculosis resistance powered by machine learning. Genome Medicine, 2021, 13, 138.	8.2	27
28	Identification and validation of a novel panel of Plasmodium knowlesi biomarkers of serological exposure. PLoS Neglected Tropical Diseases, 2018, 12, e0006457.	3.0	26
29	An integrated whole genome analysis of Mycobacterium tuberculosis reveals insights into relationship between its genome, transcriptome and methylome. Scientific Reports, 2019, 9, 5204.	3.3	26
30	Using genomics to understand the origin and dispersion of multidrug and extensively drug resistant tuberculosis in Portugal. Scientific Reports, 2020, 10, 2600.	3.3	26
31	Single nucleotide polymorphisms in efflux pumps genes in extensively drug resistant Mycobacterium tuberculosis isolates from Pakistan. Tuberculosis, 2017, 107, 20-30.	1.9	24
32	Whole genome sequencing of drug resistant Mycobacterium tuberculosis isolates from a high burden tuberculosis region of North West Pakistan. Scientific Reports, 2019, 9, 14996.	3.3	24
33	A molecular barcode to inform the geographical origin and transmission dynamics of Plasmodium vivax malaria. PLoS Genetics, 2020, 16, e1008576.	3.5	24
34	Pyrazinamide resistance-conferring mutations in pncA and the transmission of multidrug resistant TB in Georgia. BMC Infectious Diseases, 2017, 17, 491.	2.9	21
35	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.	0.6	19
36	Combining structure and genomics to understand antimicrobial resistance. Computational and Structural Biotechnology Journal, 2020, 18, 3377-3394.	4.1	17

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37	An inter-laboratory study to investigate the impact of the bioinformatics component on microbiome analysis using mock communities. Scientific Reports, 2021, 11, 10590.	3.3	17
38	An integrated in silico immuno-genetic analytical platform provides insights into COVID-19 serological and vaccine targets. Genome Medicine, 2021, 13, 4.	8.2	16
39	A snapshot of translation in Mycobacterium tuberculosis during exponential growth and nutrient starvation revealed by ribosome profiling. Cell Reports, 2021, 34, 108695.	6.4	16
40	Whole-genome sequencing resolves a polyclonal outbreak by extended-spectrum beta-lactam and carbapenem-resistant Klebsiella pneumoniae in a Portuguese tertiary-care hospital. Microbial Genomics, 2019, 7, .	2.0	16
41	Genetic risk of obesity as a modifier of associations between neighbourhood environment and body mass index: an observational study of 335 046 UK Biobank participants. BMJ Nutrition, Prevention and Health, 2020, 3, 247-255.	3.7	15
42	Using deep learning to identify recent positive selection in malaria parasite sequence data. Malaria Journal, 2021, 20, 270.	2.3	15
43	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. Emerging Microbes and Infections, 2020, 9, 1342-1353.	6.5	14
44	Genomic Epidemiology of Carbapenemase Producing Klebsiella pneumoniae Strains at a Northern Portuguese Hospital Enables the Detection of a Misidentified Klebsiella variicola KPC-3 Producing Strain. Microorganisms, 2020, 8, 1986.	3.6	13
45	Clusters of Drug-Resistant <i>Mycobacterium tuberculosis</i> Detected by Whole-Genome Sequence Analysis of Nationwide Sample, Thailand, 2014â€"2017. Emerging Infectious Diseases, 2021, 27, 813-822.	4.3	13
46	Robust detection of point mutations involved in multidrug-resistant Mycobacterium tuberculosis in the presence of co-occurrent resistance markers. PLoS Computational Biology, 2020, 16, e1008518.	3.2	11
47	Methylation analysis of Klebsiella pneumoniae from Portuguese hospitals. Scientific Reports, 2021, 11, 6491.	3.3	10
48	A potential antigenic mimicry between viral and human proteins linking Myalgic Encephalomyelitis/Chronic Fatigue Syndrome (ME/CFS) with autoimmunity: The case of HPV immunization. Autoimmunity Reviews, 2020, 19, 102487.	5.8	9
49	Turkish and Japanese Mycobacterium tuberculosis sublineages share a remote common ancestor. Infection, Genetics and Evolution, 2016, 45, 461-473.	2.3	8
50	A modified decision tree approach to improve the prediction and mutation discovery for drug resistance in Mycobacterium tuberculosis. BMC Genomics, 2022, 23, 46.	2.8	8
51	Characterization of rifampicin-resistant Mycobacterium tuberculosis in Khyber Pakhtunkhwa, Pakistan. Scientific Reports, 2021, 11, 14194.	3.3	7
52	Characterisation of drug-resistant Mycobacterium tuberculosis mutations and transmission in Pakistan. Scientific Reports, 2022, 12, 7703.	3.3	7
53	Flavivirus integrations in Aedes aegypti are limited and highly conserved across samples from different geographic regions unlike integrations in Aedes albopictus. Parasites and Vectors, 2021, 14, 332.	2.5	6
54	Whole genome sequencing reveals large deletions and other loss of function mutations in Mycobacterium tuberculosis drug resistance genes. Microbial Genomics, 2021, 7, .	2.0	6

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55	Genomic evidence supporting the clonal expansion of extensively drug-resistant tuberculosis bacteria belonging to a rare proto - Beijing genotype. Emerging Microbes and Infections, 2020, 9, 2632-2641.	6.5	5
56	A phylogenomic approach for the analysis of colistin resistance-associated genes in Klebsiella pneumoniae, its mutational diversity and implications for phenotypic resistance. International Journal of Antimicrobial Agents, 2022, 59, 106581.	2.5	5
57	PowerBacGWAS: a computational pipeline to perform power calculations for bacterial genome-wide association studies. Communications Biology, 2022, 5, 266.	4.4	4
58	Molecular characterisation of second-line drug resistance among drug resistant tuberculosis patients tested in Uganda: a two and a half-year's review. BMC Infectious Diseases, 2022, 22, 363.	2.9	4
59	Whole-genome sequencing as a tool for studying the microevolution of drug-resistant serial Mycobacterium tuberculosis isolates. Tuberculosis, 2021, 131, 102137.	1.9	3
60	Genomic diversity and antimicrobial resistance among non-typhoidal Salmonella associated with human disease in The Gambia. Microbial Genomics, 2022, 8, .	2.0	3
61	COVID-profiler: a webserver for the analysis of SARS-CoV-2 sequencing data. BMC Bioinformatics, 2022, 23, 137.	2.6	3
62	Structural and Genomic Insights Into Pyrazinamide Resistance in Mycobacterium tuberculosis Underlie Differences Between Ancient and Modern Lineages. Frontiers in Molecular Biosciences, 2021, 8, 619403.	3.5	2
63	Molecular characterization of drug-resistant Mycobacterium tuberculosis among Filipino patients derived from the national tuberculosis prevalence survey Philippines 2016. Tuberculosis, 2022, , 102211.	1.9	0