

Jody E Phelan

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1592264/publications.pdf>

Version: 2024-02-01

63
papers

2,304
citations

257450

24
h-index

265206

42
g-index

72
all docs

72
docs citations

72
times ranked

3165
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	2.8	8
2	PowerBacGWAS: a computational pipeline to perform power calculations for bacterial genome-wide association studies. <i>Communications Biology</i> , 2022, 5, 266.	4.4	4
3	Genomic diversity and antimicrobial resistance among non-typhoidal <i>Salmonella</i> associated with human disease in The Gambia. <i>Microbial Genomics</i> , 2022, 8, .	2.0	3
4	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.	2.5	5
5	COVID-profiler: a webserver for the analysis of SARS-CoV-2 sequencing data. <i>BMC Bioinformatics</i> , 2022, 23, 137.	2.6	3
6	Molecular characterisation of second-line drug resistance among drug resistant tuberculosis patients tested in Uganda: a two and a half-yearâ€™s review. <i>BMC Infectious Diseases</i> , 2022, 22, 363.	2.9	4
7	Characterisation of drug-resistant <i>Mycobacterium tuberculosis</i> mutations and transmission in Pakistan. <i>Scientific Reports</i> , 2022, 12, 7703.	3.3	7
8	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.	1.9	0
9	An integrated in silico immuno-genetic analytical platform provides insights into COVID-19 serological and vaccine targets. <i>Genome Medicine</i> , 2021, 13, 4.	8.2	16
10	A snapshot of translation in <i>Mycobacterium tuberculosis</i> during exponential growth and nutrient starvation revealed by ribosome profiling. <i>Cell Reports</i> , 2021, 34, 108695.	6.4	16
11	Clusters of Drug-Resistant <i>Mycobacterium tuberculosis</i> Detected by Whole-Genome Sequence Analysis of Nationwide Sample, Thailand, 2014â€“2017. <i>Emerging Infectious Diseases</i> , 2021, 27, 813-822.	4.3	13
12	Methylation analysis of <i>Klebsiella pneumoniae</i> from Portuguese hospitals. <i>Scientific Reports</i> , 2021, 11, 6491.	3.3	10
13	Distinctive genetic structure and selection patterns in <i>Plasmodium vivax</i> from South Asia and East Africa. <i>Nature Communications</i> , 2021, 12, 3160.	12.8	32
14	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.	3.3	17
15	Using deep learning to identify recent positive selection in malaria parasite sequence data. <i>Malaria Journal</i> , 2021, 20, 270.	2.3	15
16	Flavivirus integrations in <i>Aedes aegypti</i> are limited and highly conserved across samples from different geographic regions unlike integrations in <i>Aedes albopictus</i> . <i>Parasites and Vectors</i> , 2021, 14, 332.	2.5	6
17	Characterization of rifampicin-resistant <i>Mycobacterium tuberculosis</i> in Khyber Pakhtunkhwa, Pakistan. <i>Scientific Reports</i> , 2021, 11, 14194.	3.3	7
18	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.	3.5	2

#	ARTICLE	IF	CITATIONS
19	GenTB: A user-friendly genome-based predictor for tuberculosis resistance powered by machine learning. <i>Genome Medicine</i> , 2021, 13, 138.	8.2	27
20	Genetic diversity of candidate loci linked to <i>Mycobacterium tuberculosis</i> resistance to bedaquiline, delamanid and pretomanid. <i>Scientific Reports</i> , 2021, 11, 19431.	3.3	37
21	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.	1.9	3
22	Whole genome sequencing reveals large deletions and other loss of function mutations in <i>Mycobacterium tuberculosis</i> drug resistance genes. <i>Microbial Genomics</i> , 2021, 7, .	2.0	6
23	Genomic evidence supporting the clonal expansion of extensively drug-resistant tuberculosis bacteria belonging to a rare proto Beijing genotype. <i>Emerging Microbes and Infections</i> , 2020, 9, 2632-2641.	6.5	5
24	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. <i>BMJ Nutrition, Prevention and Health</i> , 2020, 3, 247-255.	3.7	15
25	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.	3.6	13
26	Robust barcoding and identification of <i>Mycobacterium tuberculosis</i> lineages for epidemiological and clinical studies. <i>Genome Medicine</i> , 2020, 12, 114.	8.2	79
27	Combining structure and genomics to understand antimicrobial resistance. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3377-3394.	4.1	17
28	A novel multiplex qPCR assay for detection of <i>Plasmodium falciparum</i> with histidine-rich protein 2 and 3 (pfrhp2 and pfrhp3) deletions in polyclonal infections. <i>EBioMedicine</i> , 2020, 55, 102757.	6.1	41
29	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.	6.5	14
30	Whole genome sequencing of <i>Mycobacterium tuberculosis</i> isolates and clinical outcomes of patients treated for multidrug-resistant tuberculosis in Tanzania. <i>BMC Genomics</i> , 2020, 21, 174.	2.8	28
31	Using genomics to understand the origin and dispersion of multidrug and extensively drug resistant tuberculosis in Portugal. <i>Scientific Reports</i> , 2020, 10, 2600.	3.3	26
32	A potential antigenic mimicry between viral and human proteins linking Myalgic Encephalomyelitis/Chronic Fatigue Syndrome (ME/CFS) with autoimmunity: The case of HPV immunization. <i>Autoimmunity Reviews</i> , 2020, 19, 102487.	5.8	9
33	A molecular barcode to inform the geographical origin and transmission dynamics of <i>Plasmodium vivax</i> malaria. <i>PLoS Genetics</i> , 2020, 16, e1008576.	3.5	24
34	Discordant bioinformatic predictions of antimicrobial resistance from whole-genome sequencing data of bacterial isolates: an inter-laboratory study. <i>Microbial Genomics</i> , 2020, 6, .	2.0	69
35	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.	3.2	11
36	PrimedRPA: primer design for recombinase polymerase amplification assays. <i>Bioinformatics</i> , 2019, 35, 682-684.	4.1	52

#	ARTICLE	IF	CITATIONS
37	Mycobacterium tuberculosis whole genome sequencing provides insights into the Manila strain and drug-resistance mutations in the Philippines. <i>Scientific Reports</i> , 2019, 9, 9305.	3.3	33
38	Integrating informatics tools and portable sequencing technology for rapid detection of resistance to anti-tuberculous drugs. <i>Genome Medicine</i> , 2019, 11, 41.	8.2	248
39	Whole genome sequencing of drug resistant Mycobacterium tuberculosis isolates from a high burden tuberculosis region of North West Pakistan. <i>Scientific Reports</i> , 2019, 9, 14996.	3.3	24
40	A novel Ancestral Beijing sublineage of Mycobacterium tuberculosis suggests the transition site to Modern Beijing sublineages. <i>Scientific Reports</i> , 2019, 9, 13718.	3.3	35
41	Machine Learning Predicts Accurately Mycobacterium tuberculosis Drug Resistance From Whole Genome Sequencing Data. <i>Frontiers in Genetics</i> , 2019, 10, 922.	2.3	51
42	An integrated whole genome analysis of Mycobacterium tuberculosis reveals insights into relationship between its genome, transcriptome and methylome. <i>Scientific Reports</i> , 2019, 9, 5204.	3.3	26
43	Genome-wide analysis of Mycobacterium tuberculosis polymorphisms reveals lineage-specific associations with drug resistance. <i>BMC Genomics</i> , 2019, 20, 252.	2.8	41
44	Whole-genome sequencing resolves a polyclonal outbreak by extended-spectrum beta-lactam and carbapenem-resistant Klebsiella pneumoniae in a Portuguese tertiary-care hospital. <i>Microbial Genomics</i> , 2019, 7, .	2.0	16
45	Genome-wide analysis of multi- and extensively drug-resistant Mycobacterium tuberculosis. <i>Nature Genetics</i> , 2018, 50, 307-316.	21.4	271
46	Methylation in Mycobacterium tuberculosis is lineage specific with associated mutations present globally. <i>Scientific Reports</i> , 2018, 8, 160.	3.3	31
47	Understanding molecular consequences of putative drug resistant mutations in Mycobacterium tuberculosis. <i>Scientific Reports</i> , 2018, 8, 15356.	3.3	64
48	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.	2.3	40
49	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.	3.3	44
50	Identifying mixed Mycobacterium tuberculosis infections from whole genome sequence data. <i>BMC Genomics</i> , 2018, 19, 613.	2.8	57
51	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.	2.5	45
52	Identification and validation of a novel panel of Plasmodium knowlesi biomarkers of serological exposure. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006457.	3.0	26
53	Primary macrophages and J774 cells respond differently to infection with Mycobacterium tuberculosis. <i>Scientific Reports</i> , 2017, 7, 42225.	3.3	84
54	Genome-wide mutagenesis and multi-drug resistance in American trypanosomes induced by the front-line drug benznidazole. <i>Scientific Reports</i> , 2017, 7, 14407.	3.3	41

#	ARTICLE	IF	CITATIONS
55	Single nucleotide polymorphisms in efflux pumps genes in extensively drug resistant Mycobacterium tuberculosis isolates from Pakistan. <i>Tuberculosis</i> , 2017, 107, 20-30.	1.9	24
56	Genome-wide diversity and differentiation in New World populations of the human malaria parasite <i>Plasmodium vivax</i> . <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005824.	3.0	47
57	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.	2.9	21
58	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.	10.7	106
59	The variability and reproducibility of whole genome sequencing technology for detecting resistance to anti-tuberculous drugs. <i>Genome Medicine</i> , 2016, 8, 132.	8.2	44
60	<i>Mycobacterium tuberculosis</i> whole genome sequencing and protein structure modelling provides insights into anti-tuberculosis drug resistance. <i>BMC Medicine</i> , 2016, 14, 31.	5.5	102
61	Recombination in <i>pe/ppe</i> genes contributes to genetic variation in <i>Mycobacterium tuberculosis</i> lineages. <i>BMC Genomics</i> , 2016, 17, 151.	2.8	62
62	Turkish and Japanese <i>Mycobacterium tuberculosis</i> sublineages share a remote common ancestor. <i>Infection, Genetics and Evolution</i> , 2016, 45, 461-473.	2.3	8
63	The draft genome of <i>Mycobacterium aurum</i> , a potential model organism for investigating drugs against <i>Mycobacterium tuberculosis</i> and <i>Mycobacterium leprae</i> . <i>International Journal of Mycobacteriology</i> , 2015, 4, 207-216.	0.6	19