

Anzaan Dippenaar

List of Publications by Year in descending order

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40
papers

1,125
citations

528359

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445597

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43
all docs

43
docs citations

43
times ranked

1892
citing authors

#	ARTICLE	IF	CITATIONS
1	Exploring the potential of Oxford Nanopore Technologies sequencing for Mycobacterium tuberculosis sequencing: An assessment of R10 flowcells and V14 chemistry. PLoS ONE, 2024, 19, e0303938.	2.5	0
2	Emergence of Canonical and Noncanonical Genomic Variants following <i>In Vitro</i> Exposure of Clinical Mycobacterium tuberculosis Strains to Bedaquiline or Clofazimine. Antimicrobial Agents and Chemotherapy, 2023, 67, .	3.4	2
3	Nanopore Sequencing for Mycobacterium tuberculosis: a Critical Review of the Literature, New Developments, and Future Opportunities. Journal of Clinical Microbiology, 2022, 60, JCM0064621.	4.4	28
4	Optimizing liquefaction and decontamination of sputum for DNA extraction from Mycobacterium tuberculosis. Tuberculosis, 2022, 132, 102159.	2.0	7
5	Whole-Genome Sequencing Has the Potential To Improve Treatment for Rifampicin-Resistant Tuberculosis in High-Burden Settings: a Retrospective Cohort Study. Journal of Clinical Microbiology, 2022, 60, jcm0236221.	4.4	17
6	Ancient and recent differences in the intrinsic susceptibility of <i>Mycobacterium tuberculosis</i> complex to pretomanid. Journal of Antimicrobial Chemotherapy, 2022, 77, 1685-1693.	3.2	40
7	Transmission, distribution and drug resistance-conferring mutations of extensively drug-resistant tuberculosis in the Western Cape Province, South Africa. Microbial Genomics, 2022, 8, .	2.1	4
8	Variants in Bedaquiline-Candidate-Resistance Genes: Prevalence in Bedaquiline-Naive Patients, Effect on MIC, and Association with Mycobacterium tuberculosis Lineage. Antimicrobial Agents and Chemotherapy, 2022, 66, .	3.4	7
9	Capacity building for whole genome sequencing of <i>Mycobacterium tuberculosis</i> and bioinformatics in high TB burden countries. Briefings in Bioinformatics, 2021, 22, .	6.6	14
10	Characterizing epidemiological and genotypic features of <i>Mycobacterium bovis</i> infection in wild dogs (<i>Lycaon pictus</i>). Transboundary and Emerging Diseases, 2021, 68, 3433-3442.	3.0	7
11	Review of Diagnostic Tests for Detection of Mycobacterium bovis Infection in South African Wildlife. Frontiers in Veterinary Science, 2021, 8, 588697.	2.3	33
12	High frequency of bedaquiline resistance in programmatically treated drug-resistant TB patients with sustained culture-positivity in Cape Town, South Africa. International Journal of Mycobacteriology, 2021, 9, 9.	0.6	1
13	Rifampicin-Monoresistant Tuberculosis Is Not the Same as Multidrug-Resistant Tuberculosis: a Descriptive Study from Khayelitsha, South Africa. Antimicrobial Agents and Chemotherapy, 2021, 65, e0036421.	3.4	9
14	Potential contribution of HIV during first-line tuberculosis treatment to subsequent rifampicin-monoresistant tuberculosis and acquired tuberculosis drug resistance in South Africa: a retrospective molecular epidemiology study. Lancet Microbe, The, 2021, 2, e584-e593.	6.7	11
15	Drug resistant tuberculosis cases from the Copperbelt province and Northern regions of Zambia: Genetic diversity, demographic and clinical characteristics. Tuberculosis, 2021, 130, 102122.	2.0	1
16	Diagnostic accuracy of the FluoroType MTB and MTBDR VER 2.0 assays for the centralized high-throughput detection of Mycobacterium tuberculosis complex DNA and isoniazid and rifampicin resistance. Clinical Microbiology and Infection, 2021, 27, 1351.e1-1351.e4.	6.5	9
17	Emergence of resistance to bedaquiline. International Journal of Mycobacteriology, 2021, 9, 12.	0.6	0
18	Genetic Diversity in <i>Mycobacterium tuberculosis</i> Clinical Isolates and Resulting Outcomes of Tuberculosis Infection and Disease. Annual Review of Genetics, 2020, 54, 511-537.	7.8	27

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19	Rifampicin Resistant Tuberculosis in Lesotho: Diagnosis, Treatment Initiation and Outcomes. Scientific Reports, 2020, 10, 1917.	3.4	11
20	Phylogenomic assessment of drug-resistant Mycobacterium tuberculosis strains from Beira, Mozambique. Tuberculosis, 2020, 121, 101905.	2.0	3
21	A landscape of genomic alterations at the root of a near-untreatable tuberculosis epidemic. BMC Medicine, 2020, 18, 24.	5.7	22
22	Drug-Resistant Tuberculosis. , 2020, , 301-326.		0
23	Whole genome sequencing provides additional insights into recurrent tuberculosis classified as endogenous reactivation by IS6110 DNA fingerprinting. Infection, Genetics and Evolution, 2019, 75, 103948.	2.3	16
24	Comprehensive Characterization of the Attenuated Double Auxotroph Mycobacterium tuberculosis H37Rv as an Alternative to H37Rv. Frontiers in Microbiology, 2019, 10, 1922.	3.6	37
25	Fatal Tuberculosis in a Free-Ranging African Elephant and One Health Implications of Human Pathogens in Wildlife. Frontiers in Veterinary Science, 2019, 6, 18.	2.3	32
26	Whole genome sequencing of Mycobacterium tuberculosis: current standards and open issues. Nature Reviews Microbiology, 2019, 17, 533-545.	29.2	272
27	Xpert MTB/RIF performance to diagnose tuberculosis and rifampicin resistance in a reference centre in southern Brazil. ERJ Open Research, 2019, 5, 00043-2019.	2.7	12
28	Accuracy of whole genome sequencing versus phenotypic (MGIT) and commercial molecular tests for detection of drug-resistant Mycobacterium tuberculosis isolated from patients in Brazil and Mozambique. Tuberculosis, 2018, 110, 59-67.	2.0	26
29	Mutations in ppe38 block PE_PGRS secretion and increase virulence of Mycobacterium tuberculosis. Nature Microbiology, 2018, 3, 181-188.	13.1	117
30	The arms race between man and Mycobacterium tuberculosis: Time to regroup. Infection, Genetics and Evolution, 2018, 66, 361-375.	2.3	17
31	A New Phylogenetic Framework for the Animal-Adapted Mycobacterium tuberculosis Complex. Frontiers in Microbiology, 2018, 9, 2820.	3.6	154
32	Unexpected Genomic and Phenotypic Diversity of Mycobacterium africanum Lineage 5 Affects Drug Resistance, Protein Secretion, and Immunogenicity. Genome Biology and Evolution, 2018, 10, 1858-1874.	2.6	51
33	Progenitor strain introduction of Mycobacterium bovis at the wildlife-livestock interface can lead to clonal expansion of the disease in a single ecosystem. Infection, Genetics and Evolution, 2017, 51, 235-238.	2.3	40
34	Proteogenomic Investigation of Strain Variation in Clinical Mycobacterium tuberculosis Isolates. Journal of Proteome Research, 2017, 16, 3841-3851.	3.8	27
35	Whole genome sequence analysis of Mycobacterium suricattae. Tuberculosis, 2015, 95, 682-688.	2.0	54
36	Fighting an old disease with next-generation sequencing. ELife, 2015, 4, .	5.9	2

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37	New insights on tuberculosis transmission dynamics and drug susceptibility profiles among the prison population in Southern Brazil based on whole-genome sequencing. <i>Revista Da Sociedade Brasileira De Medicina Tropical</i> , 0, 56, .	1.2	2
38	Microfluidic Capture of <i>Mycobacterium tuberculosis</i> from Clinical Samples for Culture-Free Whole-Genome Sequencing. <i>Microbiology Spectrum</i> , 0, , .	3.0	1
39	Bridging the gap between molecular and genomic epidemiology in tuberculosis: inferring MIRU-VNTR patterns from genomic data. <i>Journal of Clinical Microbiology</i> , 0, , .	4.4	0
40	Collaborative learning in the digital age: empowering tuberculosis researchers through virtual training. <i>Journal of Microbiology and Biology Education</i> , 0, , .	1.1	0