

Anzaan Dippenaar

List of Publications by Year in descending order

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40
papers

1,125
citations

528359

15
h-index

445597

30
g-index

43
all docs

43
docs citations

43
times ranked

1892
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole genome sequencing of <i>Mycobacterium tuberculosis</i> : current standards and open issues. <i>Nature Reviews Microbiology</i> , 2019, 17, 533-545.	29.2	272
2	A New Phylogenetic Framework for the Animal-Adapted <i>Mycobacterium tuberculosis</i> Complex. <i>Frontiers in Microbiology</i> , 2018, 9, 2820.	3.6	154
3	Mutations in <i>ppe38</i> block PE_PGRS secretion and increase virulence of <i>Mycobacterium tuberculosis</i> . <i>Nature Microbiology</i> , 2018, 3, 181-188.	13.1	117
4	Whole genome sequence analysis of <i>Mycobacterium suricattae</i> . <i>Tuberculosis</i> , 2015, 95, 682-688.	2.0	54
5	Unexpected Genomic and Phenotypic Diversity of <i>Mycobacterium africanum</i> Lineage 5 Affects Drug Resistance, Protein Secretion, and Immunogenicity. <i>Genome Biology and Evolution</i> , 2018, 10, 1858-1874.	2.6	51
6	Progenitor strain introduction of <i>Mycobacterium bovis</i> at the wildlife-livestock interface can lead to clonal expansion of the disease in a single ecosystem. <i>Infection, Genetics and Evolution</i> , 2017, 51, 235-238.	2.3	40
7	Ancient and recent differences in the intrinsic susceptibility of <i>Mycobacterium tuberculosis</i> complex to pretomanid. <i>Journal of Antimicrobial Chemotherapy</i> , 2022, 77, 1685-1693.	3.2	40
8	Comprehensive Characterization of the Attenuated Double Auxotroph <i>Mycobacterium tuberculosis</i> <i>leuD1</i> panCD as an Alternative to H37Rv. <i>Frontiers in Microbiology</i> , 2019, 10, 1922.	3.6	37
9	Review of Diagnostic Tests for Detection of <i>Mycobacterium bovis</i> Infection in South African Wildlife. <i>Frontiers in Veterinary Science</i> , 2021, 8, 588697.	2.3	33
10	Fatal Tuberculosis in a Free-Ranging African Elephant and One Health Implications of Human Pathogens in Wildlife. <i>Frontiers in Veterinary Science</i> , 2019, 6, 18.	2.3	32
11	Nanopore Sequencing for <i>Mycobacterium tuberculosis</i> : a Critical Review of the Literature, New Developments, and Future Opportunities. <i>Journal of Clinical Microbiology</i> , 2022, 60, JCM0064621.	4.4	28
12	Proteogenomic Investigation of Strain Variation in Clinical <i>Mycobacterium tuberculosis</i> Isolates. <i>Journal of Proteome Research</i> , 2017, 16, 3841-3851.	3.8	27
13	Genetic Diversity in <i>Mycobacterium tuberculosis</i> Clinical Isolates and Resulting Outcomes of Tuberculosis Infection and Disease. <i>Annual Review of Genetics</i> , 2020, 54, 511-537.	7.8	27
14	Accuracy of whole genome sequencing versus phenotypic (MGIT) and commercial molecular tests for detection of drug-resistant <i>Mycobacterium tuberculosis</i> isolated from patients in Brazil and Mozambique. <i>Tuberculosis</i> , 2018, 110, 59-67.	2.0	26
15	A landscape of genomic alterations at the root of a near-untreatable tuberculosis epidemic. <i>BMC Medicine</i> , 2020, 18, 24.	5.7	22
16	The arms race between man and <i>Mycobacterium tuberculosis</i> : Time to regroup. <i>Infection, Genetics and Evolution</i> , 2018, 66, 361-375.	2.3	17
17	Whole-Genome Sequencing Has the Potential To Improve Treatment for Rifampicin-Resistant Tuberculosis in High-Burden Settings: a Retrospective Cohort Study. <i>Journal of Clinical Microbiology</i> , 2022, 60, jcm0236221.	4.4	17
18	Whole genome sequencing provides additional insights into recurrent tuberculosis classified as endogenous reactivation by IS6110 DNA fingerprinting. <i>Infection, Genetics and Evolution</i> , 2019, 75, 103948.	2.3	16

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19	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
20	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
21	Rifampicin Resistant Tuberculosis in Lesotho: Diagnosis, Treatment Initiation and Outcomes. Scientific Reports, 2020, 10, 1917.	3.4	11
22	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
23	Rifampicin-Mono-resistant 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
24	Diagnostic accuracy of the FluoroType MTB and MTBDR VER 2.0 assays for the centralized high-throughput detection of <i>Mycobacterium tuberculosis</i> complex DNA and isoniazid and rifampicin resistance. Clinical Microbiology and Infection, 2021, 27, 1351.e1-1351.e4.	6.5	9
25	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
26	Optimizing liquefaction and decontamination of sputum for DNA extraction from <i>Mycobacterium tuberculosis</i> . Tuberculosis, 2022, 132, 102159.	2.0	7
27	Variants in Bedaquiline-Candidate-Resistance Genes: Prevalence in Bedaquiline-Naive Patients, Effect on MIC, and Association with <i>Mycobacterium tuberculosis</i> Lineage. Antimicrobial Agents and Chemotherapy, 2022, 66, .	3.4	7
28	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
29	Phylogenomic assessment of drug-resistant <i>Mycobacterium tuberculosis</i> strains from Beira, Mozambique. Tuberculosis, 2020, 121, 101905.	2.0	3
30	Fighting an old disease with next-generation sequencing. ELife, 2015, 4, .	5.9	2
31	New insights on tuberculosis transmission dynamics and drug susceptibility profiles among the prison population in Southern Brazil based on whole-genome sequencing. Revista Da Sociedade Brasileira De Medicina Tropical, 0, 56, .	1.2	2
32	Emergence of Canonical and Noncanonical Genomic Variants following <i>In Vitro</i> Exposure of Clinical <i>Mycobacterium tuberculosis</i> Strains to Bedaquiline or Clofazimine. Antimicrobial Agents and Chemotherapy, 2023, 67, .	3.4	2
33	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
34	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
35	Microfluidic Capture of <i>Mycobacterium tuberculosis</i> from Clinical Samples for Culture-Free Whole-Genome Sequencing. Microbiology Spectrum, 0, , .	3.0	1
36	Emergence of resistance to bedaquiline. International Journal of Mycobacteriology, 2021, 9, 12.	0.6	0

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37	Drug-Resistant Tuberculosis. , 2020, , 301-326.		0
38	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
39	Bridging the gap between molecular and genomic epidemiology in tuberculosis: inferring MIRU-VNTR patterns from genomic data. Journal of Clinical Microbiology, 0, , .	4.4	0
40	Collaborative learning in the digital age: empowering tuberculosis researchers through virtual training. Journal of Microbiology and Biology Education, 0, , .	1.1	0