Robin M Warren

List of Publications by Year
in descending order

173 papers	10,352 citations	41323 49 h-index	38368 95 g-index
178 all docs	178 docs citations	178 times ranked	8447 citing authors

#	Article	IF	Citations
1	Mycobacterium tuberculosis complex genetic diversity: mining the fourth international spoligotyping database (SpolDB4) for classification, population genetics and epidemiology. BMC Microbiology, 2006, 6, 23.	1.3	900
2	Exogenous Reinfection as a Cause of Recurrent Tuberculosis after Curative Treatment. New England Journal of Medicine, 1999, 341, 1174-1179.	13.9	561
3	Evolutionary history and global spread of the Mycobacterium tuberculosis Beijing lineage. Nature Genetics, 2015, 47, 242-249.	9.4	466
4	The epidemiology, pathogenesis, transmission, diagnosis, and management of multidrug-resistant, extensively drug-resistant, and incurable tuberculosis. Lancet Respiratory Medicine,the, 2017, 5, 291-360.	5.2	459
5	Rate of Reinfection Tuberculosis after Successful Treatment Is Higher than Rate of New Tuberculosis. American Journal of Respiratory and Critical Care Medicine, 2005, 171, 1430-1435.	2.5	371
6	A standardised method for interpreting the association between mutations and phenotypic drug resistance inMycobacterium tuberculosis. European Respiratory Journal, 2017, 50, 1701354.	3.1	273
7	Patients with Active Tuberculosis often Have Different Strains in the Same Sputum Specimen. American Journal of Respiratory and Critical Care Medicine, 2004, 169, 610-614.	2.5	267
8	Proportion of tuberculosis transmission that takes place in households in a high-incidence area. Lancet, The, 2004, 363, 212-214.	6.3	261
9	Global control of tuberculosis: from extensively drug-resistant to untreatable tuberculosis. Lancet Respiratory Medicine,the, 2014, 2, 321-338.	5.2	237
10	Whole genome sequencing of Mycobacterium tuberculosis: current standards and open issues. Nature Reviews Microbiology, 2019, 17, 533-545.	13.6	237
11	Early treatment outcomes and HIV status of patients with extensively drug-resistant tuberculosis in South Africa: a retrospective cohort study. Lancet, The, 2010, 375, 1798-1807.	6.3	225
12	Long-term outcomes of patients with extensively drug-resistant tuberculosis in South Africa: a cohort study. Lancet, The, 2014, 383, 1230-1239.	6.3	211
13	Differentiation of Mycobacterium tuberculosis complex by PCR amplification of genomic regions of difference. International Journal of Tuberculosis and Lung Disease, 2006, 10, 818-22.	0.6	186
14	Reinfection and Mixed Infection Cause ChangingMycobacterium tuberculosisDrug-Resistance Patterns. American Journal of Respiratory and Critical Care Medicine, 2005, 172, 636-642.	2.5	173
15	Mixed-Strain Mycobacterium tuberculosis Infections and the Implications for Tuberculosis Treatment and Control. Clinical Microbiology Reviews, 2012, 25, 708-719.	5.7	172
16	COVID-19 cough classification using machine learning and global smartphone recordings. Computers in Biology and Medicine, 2021, 135, 104572.	3.9	171
17	Analysis for a Limited Number of Gene Codons Can Predict Drug Resistance of Mycobacterium tuberculosis in a High-Incidence Community. Journal of Clinical Microbiology, 2001, 39, 636-641.	1.8	154
18	A New Phylogenetic Framework for the Animal-Adapted Mycobacterium tuberculosis Complex. Frontiers in Microbiology, 2018, 9, 2820.	1.5	145

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19	Genetic Determinants of Drug Resistance in Mycobacterium tuberculosis and Their Diagnostic Value. American Journal of Respiratory and Critical Care Medicine, 2016, 194, 621-630.	2.5	131
20	Drug-Penetration Gradients Associated with Acquired Drug Resistance in Patients with Tuberculosis. American Journal of Respiratory and Critical Care Medicine, 2018, 198, 1208-1219.	2.5	130
21	Efflux pump inhibitors: targeting mycobacterial efflux systems to enhance TB therapy. Journal of Antimicrobial Chemotherapy, 2016, 71, 17-26.	1.3	123
22	The Temporal Dynamics of Relapse and Reinfection Tuberculosis After Successful Treatment: A Retrospective Cohort Study. Clinical Infectious Diseases, 2014, 58, 1676-1683.	2.9	119
23	Emergence of Increased Resistance and Extensively Drug-Resistant Tuberculosis Despite Treatment Adherence, South Africa. Emerging Infectious Diseases, 2010, 16, 264-271.	2.0	113
24	Mutations in ppe38 block PE_PGRS secretion and increase virulence of Mycobacterium tuberculosis. Nature Microbiology, 2018, 3, 181-188.	5.9	112
25	gyrA mutations and phenotypic susceptibility levels to ofloxacin and moxifloxacin in clinical isolates of Mycobacterium tuberculosis. Journal of Antimicrobial Chemotherapy, 2012, 67, 1088-1093.	1.3	107
26	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.	5.2	106
27	A Global Perspective on Pyrazinamide Resistance: Systematic Review and Meta-Analysis. PLoS ONE, 2015, 10, e0133869.	1.1	105
28	Detection and Quantification of Differentially Culturable Tubercle Bacteria in Sputum from Patients with Tuberculosis. American Journal of Respiratory and Critical Care Medicine, 2016, 194, 1532-1540.	2.5	105
29	Transmission of a Multidrugâ€ResistantMycobacterium tuberculosisStrain Resembling â€œStrain Wâ€• among Noninstitutionalized, Human Immunodeficiency Virusâ€“Seronegative Patients. Journal of Infectious Diseases, 1999, 180, 1608-1615.	1.9	94
30	The Lancet Respiratory Medicine Commission: 2019 update: epidemiology, pathogenesis, transmission, diagnosis, and management of multidrug-resistant and incurable tuberculosis. Lancet Respiratory Medicine,the, 2019, 7, 820-826.	5.2	92
31	Classification of drug-resistant tuberculosis in an epidemic area. Lancet, The, 2000, 356, 22-25.	6.3	88
32	Comparative Analysis of Mycobacterium tuberculosis pe and ppe Genes Reveals High Sequence Variation and an Apparent Absence of Selective Constraints. PLoS ONE, 2012, 7, e30593.	1.1	83
33	Novel Cause of Tuberculosis in Meerkats, South Africa. Emerging Infectious Diseases, 2013, 19, 2004-2007.	2.0	81
34	False-Positive Xpert MTB/RIF Results in Retested Patients with Previous Tuberculosis: Frequency, Profile, and Prospective Clinical Outcomes. Journal of Clinical Microbiology, 2018, 56, .	1.8	78
35	Integrating standardized whole genome sequence analysis with a global Mycobacterium tuberculosis antibiotic resistance knowledgebase. Scientific Reports, 2018, 8, 15382.	1.6	75
36	Multiple Mycobacterium tuberculosis Strains in Early Cultures from Patients in a High-Incidence Community Setting. Journal of Clinical Microbiology, 2002, 40, 2750-2754.	1.8	73

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37	Drug-Associated Adverse Events and Their Relationship with Outcomes in Patients Receiving Treatment for Extensively Drug-Resistant Tuberculosis in South Africa. PLoS ONE, 2013, 8, e63057.	1.1	71
38	The non-clonality of drug resistance in Beijing-genotype isolates of Mycobacterium tuberculosis from the Western Cape of South Africa. BMC Genomics, 2010, 11, 670.	1.2	69
39	Association of toll-like receptors with susceptibility to tuberculosis suggests sex-specific effects of TLR8 polymorphisms. Infection, Genetics and Evolution, 2015, 34, 221-229.	1.0	69
40	Safe Mycobacterium tuberculosis DNA Extraction Method That Does Not Compromise Integrity. Journal of Clinical Microbiology, 2006, 44, 254-256.	1.8	66
41	Phosphoproteomics analysis of a clinical Mycobacterium tuberculosis Beijing isolate: expanding the mycobacterial phosphoproteome catalog. Frontiers in Microbiology, 2015, 6, 6.	1.5	65
42	Emergence and treatment of multidrug resistant (MDR) and extensively drug-resistant (XDR) tuberculosis in South Africa. Infection, Genetics and Evolution, 2012, 12, 686-694.	1.0	62
43	The microbiome and tuberculosis: state of the art, potential applications, and defining the clinical research agenda. Lancet Respiratory Medicine,the, 2019, 7, 892-906.	5.2	62
44	Evolution of rifampicin treatment for tuberculosis. Infection, Genetics and Evolution, 2019, 74, 103937.	1.0	61
45	The Rationale for Using Rifabutin in the Treatment of MDR and XDR Tuberculosis Outbreaks. PLoS ONE, 2013, 8, e59414.	1.1	61
46	Mutations in therrsA1401G Gene and Phenotypic Resistance to Amikacin and Capreomycin inMycobacterium tuberculosis. Microbial Drug Resistance, 2012, 18, 193-197.	0.9	60
47	Xpert MTB/RIF Ultra and Xpert MTB/RIF for diagnosis of tuberculosis in an HIV-endemic setting with a high burden of previous tuberculosis: a two-cohort diagnostic accuracy study. Lancet Respiratory Medicine,the, 2020, 8, 368-382.	5.2	58
48	Molecular Detection of Mixed Infections of Mycobacterium tuberculosis Strains in Sputum Samples from Patients in Karonga District, Malawi. Journal of Clinical Microbiology, 2010, 48, 4512-4518.	1.8	57
49	Population Structure of Mixed Mycobacterium tuberculosis Infection Is Strain Genotype and Culture Medium Dependent. PLoS ONE, 2013, 8, e70178.	1.1	57
50	COVID-19 detection in cough, breath and speech using deep transfer learning and bottleneck features. Computers in Biology and Medicine, 2022, 141, 105153.	3.9	56
51	Geospatial distribution of Mycobacterium tuberculosis genotypes in Africa. PLoS ONE, 2018, 13, e0200632.	1.1	54
52	Iron acquisition strategies in mycobacteria. Tuberculosis, 2015, 95, 123-130.	0.8	53
53	Whole genome sequence analysis of Mycobacterium suricattae. Tuberculosis, 2015, 95, 682-688.	0.8	52
54	Population Structure of Multi- and Extensively Drug-Resistant Mycobacterium tuberculosis Strains in South Africa. Journal of Clinical Microbiology, 2012, 50, 995-1002.	1.8	50

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55	MDR M. tuberculosis outbreak clone in Eswatini missed by Xpert has elevated bedaquiline resistance dated to the pre-treatment era. Genome Medicine, 2020, 12, 104.	3.6	50
56	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.	1.1	47
57	Transmission of drug-resistant tuberculosis in HIV-endemic settings. Lancet Infectious Diseases, The, 2019, 19, e77-e88.	4.6	47
58	Molecular Characteristics and Global Spread of Mycobacterium tuberculosis with a Western Cape F11 Genotype. Journal of Clinical Microbiology, 2004, 42, 769-772.	1.8	46
59	Agreement between assays of cell-mediated immunity utilizing Mycobacterium bovis-specific antigens for the diagnosis of tuberculosis in African buffaloes (Syncerus caffer). Veterinary Immunology and Immunopathology, 2014, 160, 133-138.	0.5	46
60	Alcohol, Hospital Discharge, and Socioeconomic Risk Factors for Default from Multidrug Resistant Tuberculosis Treatment in Rural South Africa: A Retrospective Cohort Study. PLoS ONE, 2013, 8, e83480.	1.1	45
61	Programmatically Selected Multidrug-Resistant Strains Drive the Emergence of Extensively Drug-Resistant Tuberculosis in South Africa. PLoS ONE, 2013, 8, e70919.	1.1	44
62	Clonal Expansion of a Globally Disseminated Lineage of Mycobacterium tuberculosis with Low IS 6110 Copy Numbers. Journal of Clinical Microbiology, 2004, 42, 5774-5782.	1.8	42
63	Mapping of Mycobacterium tuberculosis Complex Genetic Diversity Profiles in Tanzania and Other African Countries. PLoS ONE, 2016, 11, e0154571.	1.1	41
64	Prediction of Drug Resistance in M. tuberculosis: Molecular Mechanisms, Tools, and Applications. IUBMB Life, 2002, 53, 231-237.	1.5	40
65	Potential of Rapid Diagnosis for Controlling Drug-Susceptible and Drug-Resistant Tuberculosis in Communities Where Mycobacterium tuberculosis Infections Are Highly Prevalent. Journal of Clinical Microbiology, 2009, 47, 1484-1490.	1.8	39
66	Mycobacterium tuberculosis Subculture Results in Loss of Potentially Clinically Relevant Heteroresistance. Antimicrobial Agents and Chemotherapy, 2017, 61, .	1.4	38
67	Bacterial and host determinants of cough aerosol culture positivity in patients with drug-resistant versus drug-susceptible tuberculosis. Nature Medicine, 2020, 26, 1435-1443.	15.2	38
68	An All-Oral 6-Month Regimen for Multidrug-Resistant Tuberculosis: A Multicenter, Randomized Controlled Clinical Trial (the NExT Study). American Journal of Respiratory and Critical Care Medicine, 2022, 205, 1214-1227.	2.5	38
69	The clinical relevance of Mycobacterial pharmacogenetics. Tuberculosis, 2009, 89, 199-202.	0.8	37
70	Mycobacterium tuberculosis pncA Polymorphisms That Do Not Confer Pyrazinamide Resistance at a Breakpoint Concentration of 100 Micrograms per Milliliter in MGIT. Journal of Clinical Microbiology, 2015, 53, 3633-3635.	1.8	35
71	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.	1.0	35
72	Modification of the QuantiFERON-TB Gold (In-Tube) assay for the diagnosis of Mycobacterium bovis infection in African buffaloes (Syncerus caffer). Veterinary Immunology and Immunopathology, 2011, 142, 113-118.	0.5	34

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73	Automatic cough classification for tuberculosis screening in a real-world environment. Physiological Measurement, 2021, 42, 105014.	1.2	34
74	Ancient and recent differences in the intrinsic susceptibility of Mycobacterium tuberculosis complex to pretomanid. Journal of Antimicrobial Chemotherapy, 2022, 77, 1685-1693.	1.3	34
75	Diagnostic Accuracy and Utility of FluoroType MTBDR, a New Molecular Assay for Multidrug-Resistant Tuberculosis. Journal of Clinical Microbiology, 2018, 56, .	1.8	33
76	Mixed Mycobacterium tuberculosisâ€“Strain Infections Are Associated With Poor Treatment Outcomes Among Patients With Newly Diagnosed Tuberculosis, Independent of Pretreatment Heteroresistance. Journal of Infectious Diseases, 2018, 218, 1974-1982.	1.9	32
77	Review of Diagnostic Tests for Detection of Mycobacterium bovis Infection in South African Wildlife. Frontiers in Veterinary Science, 2021, 8, 588697.	0.9	31
78	Impact of alcohol consumption on tuberculosis treatment outcomes: a prospective longitudinal cohort study protocol. BMC Infectious Diseases, 2018, 18, 488.	1.3	30
79	Regulatory T Cells Subvert Mycobacterial Containment in Patients Failing Extensively Drug-Resistant Tuberculosis Treatment. American Journal of Respiratory and Critical Care Medicine, 2018, 198, 104-116.	2.5	28
80	Fatal Tuberculosis in a Free-Ranging African Elephant and One Health Implications of Human Pathogens in Wildlife. Frontiers in Veterinary Science, 2019, 6, 18.	0.9	28
81	Proteogenomic Investigation of Strain Variation in Clinical Mycobacterium tuberculosis Isolates. Journal of Proteome Research, 2017, 16, 3841-3851.	1.8	27
82	Spatial Network Mapping of Pulmonary Multidrug-Resistant Tuberculosis Cavities Using RNA Sequencing. American Journal of Respiratory and Critical Care Medicine, 2019, 200, 370-380.	2.5	27
83	Mycobacterial nucleoid associated proteins: An added dimension in gene regulation. Tuberculosis, 2018, 108, 169-177.	0.8	26
84	Rv1460, a SufR homologue, is a repressor of the suf operon in Mycobacterium tuberculosis. PLoS ONE, 2018, 13, e0200145.	1.1	26
85	Genetic diversity of Mycobacterium tuberculosis isolated from tuberculosis patients in the Serengeti ecosystem in Tanzania. Tuberculosis, 2015, 95, 170-178.	0.8	24
86	Distinct serum biosignatures are associated with different tuberculosis treatment outcomes. Tuberculosis, 2019, 118, 101859.	0.8	24
87	The Xpert MTB/RIF Ultra assay detects Mycobacterium tuberculosis complex DNA in white rhinoceros (Ceratotherium simum) and African elephants (Loxodonta africana). Scientific Reports, 2020, 10, 14482.	1.6	22
88	Genetic Diversity in Mycobacterium tuberculosis Clinical Isolates and Resulting Outcomes of Tuberculosis Infection and Disease. Annual Review of Genetics, 2020, 54, 511-537.	3.2	22
89	Anaerobe-enriched gut microbiota predicts pro-inflammatory responses in pulmonary tuberculosis. EBioMedicine, 2021, 67, 103374.	2.7	22
90	Detection of Mycobacterium tuberculosis infection in chacma baboons (Papio ursinus) using the QuantiFERONâ€TB Gold (Inâ€Tube) assay. Journal of Medical Primatology, 2009, 38, 411-417.	0.3	20

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91	Face masks in the post-COVID-19 era: a silver lining for the damaged tuberculosis public health response?. Lancet Respiratory Medicine,the, 2021, 9, 340-342.	5.2	20
92	Antimicrobial resistance in tuberculosis: an international perspective. Expert Review of Anti-Infective Therapy, 2006, 4, 759-766.	2.0	19
93	High Frequency of Resistance, Lack of Clinical Benefit, and Poor Outcomes in Capreomycin Treated South African Patients with Extensively Drug-Resistant Tuberculosis. PLoS ONE, 2015, 10, e0123655.	1.1	19
94	Linezolid Pharmacokinetics in South African Patients with Drug-Resistant Tuberculosis and a High Prevalence of HIV Coinfection. Antimicrobial Agents and Chemotherapy, 2019, 63, .	1.4	19
95	The Risk of Tuberculosis Reinfection Soon after Cure of a First Disease Episode Is Extremely High in a Hyperendemic Community. PLoS ONE, 2015, 10, e0144487.	1.1	19
96	Rapid Sequencing of the Mycobacterium tuberculosis pncA Gene for Detection of Pyrazinamide Susceptibility. Journal of Clinical Microbiology, 2014, 52, 4056-4057.	1.8	17
97	Prevalence of pyrazinamide resistance across the spectrum of drug resistant phenotypes of Mycobacterium tuberculosis. Tuberculosis, 2016, 99, 128-130.	0.8	17
98	Implications of Failure to Routinely Diagnose Resistance to Second-Line Drugs in Patients With Rifampicin-Resistant Tuberculosis on Xpert MTB/RIF: A Multisite Observational Study. Clinical Infectious Diseases, 2017, 64, 1502-1508.	2.9	17
99	The potential use of rifabutin for treatment of patients diagnosed with rifampicin-resistant tuberculosis. Journal of Antimicrobial Chemotherapy, 2018, 73, 2667-2674.	1.3	17
100	An interferon-gamma release assay for the diagnosis of the Mycobacterium bovis infection in white rhinoceros (Ceratotherium simum). Veterinary Immunology and Immunopathology, 2019, 217, 109931.	0.5	17
101	Parallel measurement of IFN-Î³ and IP-10 in QuantiFERONÂ®-TB Gold (QFT) plasma improves the detection of Mycobacterium bovis infection in African buffaloes (Syncerus caffer). Preventive Veterinary Medicine, 2019, 169, 104700.	0.7	16
102	Prevalence, Predictors, and Successful Treatment Outcomes of Xpert MTB/RIFâ€“identified Rifampicin-resistant Tuberculosis in Post-conflict Eastern Democratic Republic of the Congo, 2012â€“2017: A Retrospective Province-Wide Cohort Study. Clinical Infectious Diseases, 2019, 69, 1278-1287.	2.9	16
103	The evaluation of candidate biomarkers of cell-mediated immunity for the diagnosis of Mycobacterium bovis infection in African buffaloes (Syncerus caffer). Veterinary Immunology and Immunopathology, 2014, 162, 198-202.	0.5	15
104	Spatial distribution of Mycobacterium Tuberculosis in metropolitan Harare, Zimbabwe. PLoS ONE, 2020, 15, e0231637.	1.1	15
105	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.	1.8	14
106	Of Testing and Treatment: Implications of Implementing New Regimens for Multidrug-Resistant Tuberculosis. Clinical Infectious Diseases, 2017, 65, 1206-1211.	2.9	13
107	Parallel testing increases detection of Mycobacterium bovis-infected African buffaloes (Syncerus) Tj ETQq1 1 0.784314 rgBT /Overloc	0.5	13
108	IP-10: A potential biomarker for detection of Mycobacterium bovis infection in warthogs (Phacochoerus africanus). Veterinary Immunology and Immunopathology, 2018, 201, 43-48.	0.5	13

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109	Whole genome sequencing provides additional insights into recurrent tuberculosis classified as endogenous reactivation by IS6110 DNA fingerprinting. Infection, Genetics and Evolution, 2019, 75, 103948.	1.0	13
110	Novel molecular transport medium used in combination with Xpert MTB/RIF ultra provides rapid detection of Mycobacterium bovis in African buffaloes. Scientific Reports, 2021, 11, 7061.	1.6	13
111	Molecular Detection of Early Appearance of Drug Resistance during Mycobacterium tuberculosis Infection. Clinical Chemistry and Laboratory Medicine, 2002, 40, 876-81.	1.4	12
112	Assessing the progress of Mycobacterium tuberculosis H37Rv structural genomics. Tuberculosis, 2015, 95, 131-136.	0.8	12
113	Cell-Mediated Immunological Biomarkers and Their Diagnostic Application in Livestock and Wildlife Infected With Mycobacterium bovis. Frontiers in Immunology, 2021, 12, 639605.	2.2	12
114	Multiple, independent, identical IS6110 insertions in Mycobacterium tuberculosis PPE genes. Tuberculosis, 2009, 89, 439-442.	0.8	11
115	Molecular Epidemiological Interpretation of the Epidemic of Extensively Drug-Resistant Tuberculosis in South Africa. Journal of Clinical Microbiology, 2015, 53, 3650-3653.	1.8	11
116	Mycobacterial genomic DNA from used Xpert MTB/RIF cartridges can be utilised for accurate second-line genotypic drug susceptibility testing and spoligotyping. Scientific Reports, 2017, 7, 14854.	1.6	11
117	A commercial ELISA for detection of interferon gamma in white rhinoceros. Journal of Veterinary Diagnostic Investigation, 2019, 31, 531-536.	0.5	11
118	Minority Mycobacterium tuberculosis Genotypic Populations as an Indicator of Subsequent Phenotypic Resistance. American Journal of Respiratory Cell and Molecular Biology, 2019, 61, 789-791.	1.4	11
119	Xpert Mycobacterium tuberculosis/Rifampicinâ€"Detected Rifampicin Resistance is a Suboptimal Surrogate for Multidrug-resistant Tuberculosis in Eastern Democratic Republic of the Congo: Diagnostic and Clinical Implications. Clinical Infectious Diseases, 2020, 73, e362-e370.	2.9	11
120	Rifampicin Resistant Tuberculosis in Lesotho: Diagnosis, Treatment Initiation and Outcomes. Scientific Reports, 2020, 10, 1917.	1.6	11
121	Improved detection of Mycobacterium tuberculosis and M. bovis in African wildlife samples using cationic peptide decontamination and mycobacterial culture supplementation. Journal of Veterinary Diagnostic Investigation, 2022, 34, 61-67.	0.5	11
122	TB Epidemiology and Human Genetics. Novartis Foundation Symposium, 0, , 17-41.	1.2	11
123	Isoniazid Resistance and Dosage as Treatment for Patients with Tuberculosis. Current Drug Metabolism, 2018, 18, 1030-1039.	0.7	11
124	The stability of plasma IP-10 enhances its utility for the diagnosis of Mycobacterium bovis infection in African buffaloes (Syncerus caffer). Veterinary Immunology and Immunopathology, 2016, 173, 17-20.	0.5	10
125	Measuring antigen-specific responses in Mycobacterium bovis-infected warthogs (Phacochoerus) Tj ETQq1 1 0.784314 rgBT /Overloc	0.7	10
126	Human whole genome sequencing in South Africa. Scientific Reports, 2021, 11, 606.	1.6	10

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127	Alcohol and Tobacco Use in a Tuberculosis Treatment Cohort during South Africaâ€™s COVID-19 Sales Bans: A Case Series. International Journal of Environmental Research and Public Health, 2021, 18, 5449.	1.2	10
128	Comprehensive and accurate genetic variant identification from contaminated and low-coverage Mycobacterium tuberculosis whole genome sequencing data. Microbial Genomics, 2021, 7, .	1.0	10
129	Low Frequency of Acquired Isoniazid and Rifampicin Resistance in Rifampicin-Susceptible Pulmonary Tuberculosis in a Setting of High HIV-1 Infection and Tuberculosis Coprevalence. Journal of Infectious Diseases, 2017, 216, 632-640.	1.9	9
130	Detection of Second Line Drug Resistance among Drug Resistant Mycobacterium Tuberculosis Isolates in Botswana. Pathogens, 2019, 8, 208.	1.2	9
131	Genetic diversity of Mycobacterium tuberculosis strains circulating in Botswana. PLoS ONE, 2019, 14, e0216306.	1.1	9
132	The VetMAXâ„¢ M. tuberculosis complex PCR kit detects MTBC DNA in antemortem and postmortem samples from white rhinoceros (Ceratotherium simum), African elephants (Loxodonta africana) and African buffaloes (Syncerus caffer). BMC Veterinary Research, 2020, 16, 220.	0.7	9
133	Discordances between molecular assays for rifampicin resistance in Mycobacterium tuberculosis: frequency, mechanisms and clinical impact. Journal of Antimicrobial Chemotherapy, 2020, 75, 1123-1129.	1.3	9
134	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.	3.4	9
135	Using routinely collected laboratory data to identify high rifampicin-resistant tuberculosis burden communities in the Western Cape Province, South Africa: A retrospective spatiotemporal analysis. PLoS Medicine, 2018, 15, e1002638.	3.9	8
136	Impact of Mycobacterium bovis-induced pathology on interpretation of QuantiFERONÂ®-TB Gold assay results in African buffaloes (Syncerus caffer). Veterinary Immunology and Immunopathology, 2019, 217, 109923.	0.5	8
137	Evidence for the Effect of Vaccination on Host-Pathogen Interactions in a Murine Model of Pulmonary Tuberculosis by Mycobacterium tuberculosis. Frontiers in Immunology, 2020, 11, 930.	2.2	8
138	A multi-phenotype genome-wide association study of clades causing tuberculosis in a Ghanaian- and South African cohort. Genomics, 2021, 113, 1802-1815.	1.3	8
139	Cytokine gene expression assay as a diagnostic tool for detection of Mycobacterium bovis infection in warthogs (Phacochoerus africanus). Scientific Reports, 2019, 9, 16525.	1.6	7
140	Identifying nucleic acid-associated proteins in Mycobacterium smegmatis by mass spectrometry-based proteomics. BMC Molecular and Cell Biology, 2020, 21, 19.	1.0	7
141	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.	1.4	7
142	Insertion Element IS6110-Based Restriction Fragment Length Polymorphism Genotyping of Mycobacterium tuberculosis. Methods in Molecular Biology, 2009, 465, 353-370.	0.4	7
143	A treatment recommender clinical decision support system for personalized medicine: method development and proof-of-concept for drug resistant tuberculosis. BMC Medical Informatics and Decision Making, 2022, 22, 56.	1.5	7
144	Extract from used Xpert MTB/RIF Ultra cartridges is useful for accurate second-line drug-resistant tuberculosis diagnosis with minimal rpoB-amplicon cross-contamination risk. Scientific Reports, 2020, 10, 2633.	1.6	6

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145	Optimized interferon-gamma release assays for detection of Mycobacterium bovis infection in African buffaloes (Syncerus caffer). Veterinary Immunology and Immunopathology, 2021, 231, 110163.	0.5	6
146	Optimisation of the tuberculin skin test for detection of Mycobacterium bovis in African buffaloes (Syncerus caffer). Preventive Veterinary Medicine, 2021, 188, 105254.	0.7	6
147	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.	2.8	6
148	Comparative Performance of Genomic Methods for the Detection of Pyrazinamide Resistance and Heteroresistance in Mycobacterium tuberculosis. Journal of Clinical Microbiology, 2022, 60, JCM0190721.	1.8	6
149	Optimizing liquefaction and decontamination of sputum for DNA extraction from Mycobacterium tuberculosis. Tuberculosis, 2022, 132, 102159.	0.8	6
150	The quantitation of biotinylated compounds by a solid-phase assay using a125I-labelled biotin derivative. FEBS Letters, 1987, 215, 305-310.	1.3	5
151	MDR tuberculosis control: time to change the dogma?. Lancet Respiratory Medicine,the, 2015, 3, 907-909.	5.2	5
152	Switching to bedaquiline for treatment of rifampicin-resistant tuberculosis in South Africa: AÂretrospective cohort analysis. PLoS ONE, 2019, 14, e0223308.	1.1	5
153	Diagnosis of Mycobacterium bovis infection in freeâ€ranging common hippopotamus () Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.3	5
154	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, .	1.4	5
155	Adaptation and Diagnostic Potential of a Commercial Cat Interferon Gamma Release Assay for the Detection of Mycobacterium bovis Infection in African Lions (Panthera leo). Pathogens, 2022, 11, 765.	1.2	5
156	Exploring the potential of T7 bacteriophage protein Gp2 as a novel inhibitor of mycobacterial RNA polymerase. Tuberculosis, 2017, 106, 82-90.	0.8	4
157	Frequent Suboptimal Thermocycler Ramp Rate Usage Negatively Impacts GenoType MTBDRsl VER 2.0 Performance for Second-Line Drug-Resistant Tuberculosis Diagnosis. Journal of Molecular Diagnostics, 2022, 24, 494-502.	1.2	4
158	Identification of gene fusion events in Mycobacterium tuberculosis that encode chimeric proteins. NAR Genomics and Bioinformatics, 2020, 2, lqaa033.	1.5	3
159	Phylogenomic assessment of drug-resistant Mycobacterium tuberculosis strains from Beira, Mozambique. Tuberculosis, 2020, 121, 101905.	0.8	3
160	Use of the MILLIPLEXÂ® bovine cytokine/chemokine multiplex assay to identify Mycobacterium bovis-infection biomarkers in African buffaloes (Syncerus caffer). Veterinary Immunology and Immunopathology, 2021, 231, 110152.	0.5	3
161	Implementation of new tools for multidrug-resistant tuberculosis detection and control. International Journal of Mycobacteriology, 2016, 5, S67.	0.3	2
162	Cytokine biomarker discovery in the white rhinoceros (Ceratotherium simum). Veterinary Immunology and Immunopathology, 2021, 232, 110168.	0.5	2

#	Article	IF	Citations
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