Bouke Catherine de Jong

List of Publications by Year in descending order

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147 papers 7,498 citations

87723 38 h-index 79 g-index

160 all docs 160 docs citations

160 times ranked 6952 citing authors

#	Article	IF	CITATIONS
1	Variable host-pathogen compatibility in Mycobacterium tuberculosis. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 2869-2873.	3.3	897
2	A Four-Month Gatifloxacin-Containing Regimen for Treating Tuberculosis. New England Journal of Medicine, 2014, 371, 1588-1598.	13.9	352
3	Mycobacterium tuberculosis lineage 4 comprises globally distributed and geographically restricted sublineages. Nature Genetics, 2016, 48, 1535-1543.	9.4	326
4	Acquired Resistance of Mycobacterium tuberculosis to Bedaquiline. PLoS ONE, 2014, 9, e102135.	1.1	320
5	Progression to Active Tuberculosis, but Not Transmission, Varies by (i>Mycobacterium tuberculosis (/i>Lineage in The Gambia. Journal of Infectious Diseases, 2008, 198, 1037-1043.	1.9	269
6	Whole genome sequencing of Mycobacterium tuberculosis: current standards and open issues. Nature Reviews Microbiology, 2019, 17, 533-545.	13.6	237
7	Mycobacterium africanum—Review of an Important Cause of Human Tuberculosis in West Africa. PLoS Neglected Tropical Diseases, 2010, 4, e744.	1.3	221
8	Rifampin Drug Resistance Tests for Tuberculosis: Challenging the Gold Standard. Journal of Clinical Microbiology, 2013, 51, 2633-2640.	1.8	216
9	Factors associated with mortality in patients with drug-susceptible pulmonary tuberculosis. BMC Infectious Diseases, 2011, 11, 1.	1.3	204
10	Rifampin Resistance Missed in Automated Liquid Culture System for Mycobacterium tuberculosis Isolates with Specific <i>rpoB</i> Mutations. Journal of Clinical Microbiology, 2013, 51, 2641-2645.	1.8	186
11	Longitudinal Assessment of an ELISPOT Test for Mycobacterium tuberculosis Infection. PLoS Medicine, 2007, 4, e192.	3.9	150
12	M.Âtuberculosis T Cell Epitope Analysis Reveals Paucity of Antigenic Variation and Identifies Rare Variable TB Antigens. Cell Host and Microbe, 2015, 18, 538-548.	5.1	142
13	Treatment Outcomes of Patients with HIV and Tuberculosis. American Journal of Respiratory and Critical Care Medicine, 2007, 175, 1199-1206.	2.5	136
14	A sister lineage of the Mycobacterium tuberculosis complex discovered in the African Great Lakes region. Nature Communications, 2020, 11, 2917.	5.8	136
15	Unexpected high prevalence of resistance-associated <i>Rv0678 </i> variants in MDR-TB patients without documented prior use of clofazimine or bedaquiline. Journal of Antimicrobial Chemotherapy, 2017, 72, dkw502.	1.3	134
16	Infection with Helicobacter pylori Is Associated with Protection against Tuberculosis. PLoS ONE, 2010, 5, e8804.	1.1	133
17	Outbreak of multidrug-resistant tuberculosis in South Africa undetected by WHO-endorsed commercial tests: an observational study. Lancet Infectious Diseases, The, 2018, 18, 1350-1359.	4.6	118
18	Incidence of Tuberculosis and the Predictive Value of ELISPOT and Mantoux Tests in Gambian Case Contacts. PLoS ONE, 2008, 3, e1379.	1.1	116

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19	The relationship between transmission time and clustering methods in Mycobacterium tuberculosis epidemiology. EBioMedicine, 2018, 37, 410-416.	2.7	106
20	Clinical Management of Tuberculosis in the Context of HIV Infection. Annual Review of Medicine, 2004, 55, 283-301.	5.0	91
21	Disputed <l>rpo</l> B mutations can frequently cause important rifampicin resistance among new tuberculosis patients. International Journal of Tuberculosis and Lung Disease, 2015, 19, 185-190.	0.6	90
22	Production of TNF-α, IL-12(p40) and IL-17 Can Discriminate between Active TB Disease and Latent Infection in a West African Cohort. PLoS ONE, 2010, 5, e12365.	1.1	90
23	Isoniazid resistance levels of Mycobacterium tuberculosis can largely be predicted by high-confidence resistance-conferring mutations. Scientific Reports, 2018, 8, 3246.	1.6	87
24	Specific <i>gyrA</i> gene mutations predict poor treatment outcome in MDR-TB. Journal of Antimicrobial Chemotherapy, 2016, 71, 314-323.	1.3	86
25	Transcriptional Adaptation of Drug-tolerant <i>Mycobacterium tuberculosis</i> During Treatment of Human Tuberculosis. Journal of Infectious Diseases, 2015, 212, 990-998.	1.9	82
26	Mycobacterium africanumElicits an Attenuated T Cell Response to Early Secreted Antigenic Target, 6 kDa, in Patients with Tuberculosis and Their Household Contacts. Journal of Infectious Diseases, 2006, 193, 1279-1286.	1.9	77
27	Marijuana Use and Its Association With Adherence to Antiretroviral Therapy Among HIV-Infected Persons With Moderate to Severe Nausea. Journal of Acquired Immune Deficiency Syndromes (1999), 2005, 38, 43-46.	0.9	73
28	Phylogenomics of Mycobacterium africanum reveals a new lineage and a complex evolutionary history. Microbial Genomics, 2021, 7, .	1.0	71
29	The Genome of Mycobacterium Africanum West African 2 Reveals a Lineage-Specific Locus and Genome Erosion Common to the M. tuberculosis Complex. PLoS Neglected Tropical Diseases, 2012, 6, e1552.	1.3	69
30	Targeting multidrug-resistant tuberculosis (MDR-TB) by therapeutic vaccines. Medical Microbiology and Immunology, 2013, 202, 95-104.	2.6	63
31	HIV Prevention Fatigue Among High-Risk Populations in San Francisco. Journal of Acquired Immune Deficiency Syndromes (1999), 2004, 35, 432-434.	0.9	62
32	Differences between tuberculosis cases infected withMycobacterium africanum, West African type 2, relative to Euro-AmericanMycobacterium tuberculosis: an update. FEMS Immunology and Medical Microbiology, 2010, 58, 102-105.	2.7	61
33	Deep amplicon sequencing for culture-free prediction of susceptibility or resistance to 13 anti-tuberculous drugs. European Respiratory Journal, 2021, 57, 2002338.	3.1	58
34	Reference set of Mycobacterium tuberculosis clinical strains: A tool for research and product development. PLoS ONE, 2019, 14, e0214088.	1.1	56
35	Use of Spoligotyping and Large Sequence Polymorphisms To Study the Population Structure of the <i>Mycobacterium tuberculosis</i> Complex in a Cohort Study of Consecutive Smear-Positive Tuberculosis Cases in The Gambia. Journal of Clinical Microbiology, 2009, 47, 994-1001.	1.8	53
36	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

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37	GeneXpert MTB/RIF Assay for the Diagnosis of Tuberculous Lymphadenitis on Concentrated Fine Needle Aspirates in High Tuberculosis Burden Settings. PLoS ONE, 2015, 10, e0137471.	1.1	47
38	Does Resistance to Pyrazinamide Accurately Indicate the Presence of Mycobacterium bovis?. Journal of Clinical Microbiology, 2005, 43, 3530-3532.	1.8	44
39	Bedaquiline susceptibility testing of <i>Mycobacterium tuberculosis</i> in an automated liquid culture system. Journal of Antimicrobial Chemotherapy, 2015, 70, 2300-2305.	1.3	41
40	Impaired Fitness of Mycobacterium africanum Despite Secretion of ESAT-6. Journal of Infectious Diseases, 2012, 205, 984-990.	1.9	39
41	Identification of Probable Early-Onset Biomarkers for Tuberculosis Disease Progression. PLoS ONE, 2011, 6, e25230.	1.1	39
42	Variable ability of rapid tests to detect Mycobacterium tuberculosis rpoB mutations conferring phenotypically occult rifampicin resistance. Scientific Reports, 2019, 9, 11826.	1.6	38
43	Mycobacterium tuberculosis precursor rRNA as a measure of treatment-shortening activity of drugs and regimens. Nature Communications, 2021, 12, 2899.	5.8	38
44	Mycobacterium africanum: a new opportunistic pathogen in HIV infection?. Aids, 2005, 19, 1714-1715.	1.0	36
45	The TDR Tuberculosis Strain Bank: a resource for basic science, tool development and diagnostic services. International Journal of Tuberculosis and Lung Disease, 2012, 16, 24-31.	0.6	36
46	Deciphering the Growth Behaviour of Mycobacterium africanum. PLoS Neglected Tropical Diseases, 2013, 7, e2220.	1.3	36
47	How Well Do Routine Molecular Diagnostics Detect Rifampin Heteroresistance in Mycobacterium tuberculosis?. Journal of Clinical Microbiology, 2019, 57, .	1.8	36
48	Prevalence and drivers of false-positive rifampicin-resistant Xpert MTB/RIF results: a prospective observational study in Rwanda. Lancet Microbe, The, 2020, 1, e74-e83.	3.4	35
49	A Mycobacterial Perspective on Tuberculosis in West Africa: Significant Geographical Variation of M. africanum and Other M. tuberculosis Complex Lineages. PLoS Neglected Tropical Diseases, 2016, 10, e0004408.	1.3	35
50	Comparative genomics of Mycobacterium africanum Lineage 5 and Lineage 6 from Ghana suggests distinct ecological niches. Scientific Reports, 2018, 8, 11269.	1.6	34
51	Using ELISPOT to Expose False Positive Skin Test Conversion in Tuberculosis Contacts. PLoS ONE, 2007, 2, e183.	1.1	33
52	Correlation of different phenotypic drug susceptibility testing methods for four fluoroquinolones in <i>Mycobacterium tuberculosis</i>). Journal of Antimicrobial Chemotherapy, 2016, 71, 1233-1240.	1.3	32
53	Multiple introductions and recent spread of the emerging human pathogen <i>Mycobacterium ulcerans</i> across Africa. Genome Biology and Evolution, 2017, 9, evx003.	1.1	32
54	Comparative Genomics Shows That Mycobacterium ulcerans Migration and Expansion Preceded the Rise of Buruli Ulcer in Southeastern Australia. Applied and Environmental Microbiology, 2018, 84, .	1.4	32

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55	Some Synonymous and Nonsynonymous <i>gyrA</i> Mutations in Mycobacterium tuberculosis Lead to Systematic False-Positive Fluoroquinolone Resistance Results with the Hain GenoType MTBDR <i>sl</i> Assays. Antimicrobial Agents and Chemotherapy, 2017, 61, .	1.4	29
56	Multicenter External Quality Assessment Program for PCR Detection of Mycobacterium ulcerans in Clinical and Environmental Specimens. PLoS ONE, 2014, 9, e89407.	1.1	29
57	Whole genome sequencing to complement tuberculosis drug resistance surveys in Uganda. Infection, Genetics and Evolution, 2016, 40, 8-16.	1.0	28
58	The predominance of Ethiopian specific Mycobacterium tuberculosis families and minimal contribution of Mycobacterium bovis in tuberculous lymphadenitis patients in Southwest Ethiopia. Infection, Genetics and Evolution, 2017, 55, 251-259.	1.0	28
59	Sputum is a surrogate for bronchoalveolar lavage for monitoring Mycobacterium tuberculosis transcriptional profiles in TB patients. Tuberculosis, 2016, 100, 89-94.	0.8	27
60	Whole-genome sequencing illuminates the evolution and spread of multidrug-resistant tuberculosis in Southwest Nigeria. PLoS ONE, 2017, 12, e0184510.	1.1	27
61	Diagnostic Accuracy of Clinical and Microbiological Signs in Patients With Skin Lesions Resembling Buruli Ulcer in an Endemic Region. Clinical Infectious Diseases, 2018, 67, 827-834.	2.9	27
62	Management of multidrug-resistant tuberculosis with shorter treatment regimen in Niger: Nationwide programmatic achievements. Respiratory Medicine, 2020, 161, 105844.	1.3	26
63	The First Phylogeographic Population Structure and Analysis of Transmission Dynamics of M. africanum West African 1— Combining Molecular Data from Benin, Nigeria and Sierra Leone. PLoS ONE, 2013, 8, e77000.	1.1	26
64	The Biology and Epidemiology of Mycobacterium africanum. Advances in Experimental Medicine and Biology, 2017, 1019, 117-133.	0.8	24
65	Genotypic characterization directly applied to sputum improves the detection of Mycobacterium africanum West African 1, under-represented in positive cultures. PLoS Neglected Tropical Diseases, 2017, 11, e0005900.	1.3	24
66	Fluorescein diacetate vital staining allows earlier diagnosis of rifampicin-resistant tuberculosis. International Journal of Tuberculosis and Lung Disease, 2012, 16, 1174-1179.	0.6	23
67	Whole Genome Comparisons Suggest Random Distribution of Mycobacterium ulcerans Genotypes in a Buruli Ulcer Endemic Region of Ghana. PLoS Neglected Tropical Diseases, 2015, 9, e0003681.	1.3	23
68	Evolution of Mycobacterium tuberculosis complex lineages and their role in an emerging threat of multidrug resistant tuberculosis in Bamako, Mali. Scientific Reports, 2020, 10, 327.	1.6	23
69	Effects of cryopreservation on CD4+ CD25+ T cells of HIV-1 infected individuals. Journal of Clinical Laboratory Analysis, 2008, 22, 153-158.	0.9	22
70	Burden of Mycobacterium ulcerans Disease (Buruli Ulcer) and the Underreporting Ratio in the Territory of Songololo, Democratic Republic of Congo. PLoS Neglected Tropical Diseases, 2013, 7, e2563.	1.3	22
71	Predominant Mycobacterium tuberculosis Families and High Rates of Recent Transmission among New Cases Are Not Associated with Primary Multidrug Resistance in Lima, Peru. Journal of Clinical Microbiology, 2015, 53, 1854-1863.	1.8	22
72	Clustering of leprosy beyond the household level in a highly endemic setting on the Comoros, an observational study. BMC Infectious Diseases, 2019, 19, 501.	1.3	22

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73	Differences in <scp>T</scp> â€cell responses between <i><scp>M</scp>ycobacterium tuberculosis</i> and <i><scp>M</scp>ycobacterium africanum</i> â€infected patients. European Journal of Immunology, 2014, 44, 1387-1398.	1.6	21
74	Effect of efavirenz-based antiretroviral therapy and high-dose rifampicin on the pharmacokinetics of isoniazid and acetyl-isoniazid. Journal of Antimicrobial Chemotherapy, 2018, 74, 139-148.	1.3	21
75	Outbreak of Tuberculosis and Multidrug-Resistant Tuberculosis, Mbuji-Mayi Central Prison, Democratic Republic of the Congo. Emerging Infectious Diseases, 2018, 24, 2029-2035.	2.0	21
76	Impact of the Mycobaterium africanum West Africa 2 Lineage on TB Diagnostics in West Africa: Decreased Sensitivity of Rapid Identification Tests in The Gambia. PLoS Neglected Tropical Diseases, 2016, 10, e0004801.	1.3	20
77	Effect of a Control Project on Clinical Profiles and Outcomes in Buruli Ulcer: A Before/After Study in Bas-Congo, Democratic Republic of Congo. PLoS Neglected Tropical Diseases, 2011, 5, e1402.	1.3	19
78	Adaptation of Mycobacterium tuberculosis to Impaired Host Immunity in HIV-Infected Patients. Journal of Infectious Diseases, 2016, 214, 1205-1211.	1.9	19
79	World Health Organization 2018 treatment guidelines for rifampicin-resistant tuberculosis: uncertainty, potential risks and the way forward. International Journal of Antimicrobial Agents, 2020, 55, 105822.	1.1	19
80	Insertion Sequence Element Single Nucleotide Polymorphism Typing Provides Insights into the Population Structure and Evolution of Mycobacterium ulcerans across Africa. Applied and Environmental Microbiology, 2014, 80, 1197-1209.	1.4	18
81	Pseudo-Outbreak of Pre-Extensively Drug-Resistant (Pre-XDR) Tuberculosis in Kinshasa: Collateral Damage Caused by False Detection of Fluoroquinolone Resistance by GenoType MTBDR <i>sl</i> Journal of Clinical Microbiology, 2014, 52, 2876-2880.	1.8	18
82	Xpert Ultra Can Unambiguously Identify Specific Rifampin Resistance-Conferring Mutations. Journal of Clinical Microbiology, 2018, 56, .	1.8	18
83	Protocol, rationale and design of PEOPLE (Post ExpOsure Prophylaxis for LEprosy in the Comoros and) Tj ETQq1 1 post-exposure prophylaxis of leprosy contacts. BMC Infectious Diseases, 2019, 19, 1033.	. 0.784314 1.3	
84	Mycobacterium africanum (Lineage 6) shows slower sputum smear conversion on tuberculosis treatment than Mycobacterium tuberculosis (Lineage 4) in Bamako, Mali. PLoS ONE, 2018, 13, e0208603.	1.1	17
85	A tuberculosis nationwide prevalence survey in Gambia, 2012. Bulletin of the World Health Organization, 2016, 94, 433-441.	1.5	17
86	Comparative evaluation of BACTEC MGIT 960 with BACTEC 9000 MB and LJ for isolation of mycobacteria in The Gambia. Journal of Infection in Developing Countries, 2008, 2, 200-5.	0.5	17
87	Analysis of flow cytometry data using an automatic processing tool. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2008, 73A, 857-867.	1.1	16
88	The perceived impact of isoniazid resistance on outcome of first-line rifampicin-throughout regimens is largely due to missed rifampicin resistance. PLoS ONE, 2020, 15, e0233500.	1.1	16
89	High Genotypic Discordance of Concurrent Mycobacterium tuberculosis Isolates from Sputum and Blood of HIV-Infected Individuals. PLoS ONE, 2015, 10, e0132581.	1.1	15
90	Significant under expression of the DosR regulon in M.Âtuberculosis complex lineage 6 in sputum. Tuberculosis, 2017, 104, 58-64.	0.8	15

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91	Systematic screening for tuberculosis among hospital outpatients in Cameroon: The role of screening and testing algorithms to improve case detection. Journal of Clinical Tuberculosis and Other Mycobacterial Diseases, 2019, 15, 100095.	0.6	15
92	Comparative genomics shows differences in the electron transport and carbon metabolic pathways of Mycobacterium africanum relative to Mycobacterium tuberculosis and suggests an adaptation to low oxygen tension. Tuberculosis, 2020, 120, 101899.	0.8	15
93	A Genomic Approach to Resolving Relapse versus Reinfection among Four Cases of Buruli Ulcer. PLoS Neglected Tropical Diseases, 2015, 9, e0004158.	1.3	14
94	First insights into circulating Mycobacterium tuberculosis complex lineages and drug resistance in Guinea. Infection, Genetics and Evolution, 2015, 33, 314-319.	1.0	14
95	Mycobacterium ulcerans Population Genomics To Inform on the Spread of Buruli Ulcer across Central Africa. MSphere, 2019, 4, .	1.3	14
96	Do Xpert MTB/RIF Cycle Threshold Values Provide Information about Patient Delays for Tuberculosis Diagnosis?. PLoS ONE, 2016, 11, e0162833.	1.1	13
97	Targeted next-generation sequencing of sputum for diagnosis ofÂdrug-resistant TB: results of a national survey in DemocraticÂRepublic of theÂCongo. Scientific Reports, 2020, 10, 10786.	1.6	13
98	Quantifying transmission fitness costs of multi-drug resistant tuberculosis. Epidemics, 2021, 36, 100471.	1.5	13
99	Low sensitivity of the MPT64 identification test to detect lineage 5 of the Mycobacterium tuberculosis complex. Journal of Medical Microbiology, 2018, 67, 1718-1727.	0.7	13
100	Bacterial diversity in Buruli ulcer skin lesions: Challenges in the clinical microbiome analysis of a skin disease. PLoS ONE, 2017, 12, e0181994.	1.1	13
101	Immune Reconstitution Inflammatory Syndrome and the Influence of T Regulatory Cells: A Cohort Study in the Gambia. PLoS ONE, 2012, 7, e39213.	1.1	12
102	Genetic variability of Mycobacterium tuberculosiscomplex in patients with no known risk factors for MDR-TB in the North-eastern part of Lima, Peru. BMC Infectious Diseases, 2013, 13, 397.	1.3	12
103	ImmunogenicMycobacterium africanumStrains Associated with Ongoing Transmission in The Gambia. Emerging Infectious Diseases, 2013, 19, 1598-1604.	2.0	12
104	Initial resistance to companion drugs should not be considered an exclusion criterion for the shorter multidrug-resistant tuberculosis treatment regimen. International Journal of Infectious Diseases, 2020, 100, 357-365.	1.5	12
105	High rifampicin-resistant TB cure rates and prevention of severe ototoxicity after replacing the injectable by linezolid in early stage of hearing loss. European Respiratory Journal, 2021, 57, 2002250.	3.1	12
106	Whole genome sequencing reveals mycobacterial microevolution among concurrent isolates from sputum and blood in HIV infected TB patients. BMC Infectious Diseases, 2016, 16, 371.	1.3	11
107	Potential Application of Digitally Linked Tuberculosis Diagnostics for Real-Time Surveillance of Drug-Resistant Tuberculosis Transmission: Validation and Analysis of Test Results. JMIR Medical Informatics, 2018, 6, e12.	1.3	11
108	The thin-layer agar method for direct phenotypic detection of multi- and extensively drug-resistant tuberculosis. International Journal of Tuberculosis and Lung Disease, 2015, 19, 1547-1552.	0.6	9

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109	Second-line injectable drugs for rifampicin-resistant tuberculosis: better the devil we know?. Journal of Antimicrobial Chemotherapy, 2021, 76, 831-835.	1.3	9
110	<i>Mycobacterium tuberculosis</i> borderline <i>rpoB</i> mutations: emerging from the unknown. European Respiratory Journal, 2021, 58, 2100783.	3.1	9
111	Mycobacterium tuberculosis complex lineage 5 exhibits high levels of within-lineage genomic diversity and differing gene content compared to the type strain H37Rv. Microbial Genomics, 2021, 7, .	1.0	9
112	Investigating drug resistance of Mycobacterium leprae in the Comoros: an observational deep-sequencing study. Lancet Microbe, The, 2022, 3, e693-e700.	3.4	9
113	AdvISER-PYRO: Amplicon Identification using SparsE Representation of PYROsequencing signal. Bioinformatics, 2013, 29, 1963-1969.	1.8	8
114	High-Dose First-Line Treatment Regimen for Recurrent Rifampicin-Susceptible Tuberculosis. American Journal of Respiratory and Critical Care Medicine, 2020, 201, 1578-1579.	2.5	8
115	Shifts in Mycobacterial Populations and Emerging Drug-Resistance in West and Central Africa. PLoS ONE, 2014, 9, e110393.	1.1	8
116	Half of rifampicin-resistant Mycobacterium tuberculosis complex isolated from tuberculosis patients in Sub-Saharan Africa have concomitant resistance to pyrazinamide. PLoS ONE, 2017, 12, e0187211.	1.1	8
117	Buruli Ulcer in Traveler from Suriname, South America, to the Netherlands. Emerging Infectious Diseases, 2015, 21, 497-499.	2.0	7
118	Tuberculosis treatment: one-shot approach or cascade of regimens?. Lancet Respiratory Medicine, the, 2020, 8, e4-e5.	5.2	7
119	Genetic diversity of the Mycobacterium tuberculosis complex strains from newly diagnosed tuberculosis patients in Northwest Ethiopia reveals a predominance of East-African-Indian and Euro-American lineages. International Journal of Infectious Diseases, 2021, 103, 72-80.	1.5	7
120	Exploring clustering of leprosy in the Comoros and Madagascar: A geospatial analysis. International Journal of Infectious Diseases, 2021, 108, 96-101.	1.5	7
121	Extensively drug resistant tuberculosis in Mali: a case report. BMC Research Notes, 2017, 10, 561.	0.6	6
122	Characterization of Mycobacterium tuberculosis var. africanum isolated from a patient with pulmonary tuberculosis in Brazil. Infection, Genetics and Evolution, 2020, 85, 104550.	1.0	6
123	Injectables' key role in rifampicin-resistant tuberculosis shorter treatment regimen outcomes. PLoS ONE, 2020, 15, e0238016.	1.1	6
124	Multidrug-resistant patients receiving treatment in Niger who are infected with M. tuberculosis Cameroon family convert faster in smear and culture than those with M. tuberculosis Ghana family. Tuberculosis, 2020, 122, 101922.	0.8	6
125	Case Report: Dynamics of Acquired Fluoroquinolone Resistance under Standardized Short-Course Treatment of Multidrug-Resistant Tuberculosis. American Journal of Tropical Medicine and Hygiene, 2020, 103, 1443-1446.	0.6	6
126	Introduction of Mycobacterium ulcerans disease in the Bankim Health District of Cameroon follows damming of the Mapé River. PLoS Neglected Tropical Diseases, 2020, 14, e0008501.	1.3	5

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127	Supervised learning for the automated transcription of spacer classification from spoligotype films. BMC Bioinformatics, 2009, 10, 248.	1.2	4
128	Bridging the TB data gap: <i>in silico</i> extraction of rifampicin-resistant tuberculosis diagnostic test results from whole genome sequence data. Peerl, 2019, 7, e7564.	0.9	4
129	Skewing of the CD4+ T-Cell Pool Toward Monofunctional Antigen-Specific Responses in Patients With Immune Reconstitution Inflammatory Syndrome in The Gambia. Clinical Infectious Diseases, 2013, 57, 594-603.	2.9	3
130	Decontamination methods for samples preserved in cetylpyridinium chloride and cultured on thin-layer agar. International Journal of Tuberculosis and Lung Disease, 2014, 18, 972-977.	0.6	3
131	An operational study comparing microscopes and staining variations for tuberculosis LED FM. International Journal of Tuberculosis and Lung Disease, 2014, 18, 964-971.	0.6	3
132	Improving clinical and epidemiological predictors of Buruli ulcer. PLoS Neglected Tropical Diseases, 2018, 12, e0006713.	1.3	3
133	Performance of OMNIgene•SPUTUM (DNA Genotek) and cetylpyridinium chloride for sputum storage prior to mycobacterial culture. Journal of Medical Microbiology, 2018, 67, 798-805.	0.7	3
134	Minimally invasive sampling to identify leprosy patients with a high bacterial burden in the Union of the Comoros. PLoS Neglected Tropical Diseases, 2021, 15, e0009924.	1.3	3
135	High yield of retrospective active case finding for leprosy in Comoros. PLoS Neglected Tropical Diseases, 2022, 16, e0010158.	1.3	3
136	Catch Them While You Can!. American Journal of Respiratory and Critical Care Medicine, 2008, 178, 5-6.	2.5	2
137	Immunogenicity of antigens from the TbD1 region present in M. africanum and missing from "modern" M. tuberculosis: a cross- sectional study. BMC Infectious Diseases, 2010, 10, 11.	1.3	2
138	Low Cycle Threshold Value in Xpert MTB/RIF Assay May Herald False Detection of Tuberculosis and Rifampicin Resistance: A Study of Two Cases. Open Forum Infectious Diseases, 2021, 8, ofab034.	0.4	2
139	Bedaquiline can act as core drug in a standardized treatment regimen for fluoroquinolone-resistant rifampicin-resistant tuberculosis. European Respiratory Journal, 2021, , 2102124.	3.1	2
140	Multidrug-resistant tuberculosis control in Rwanda overcomes a successful clone that causes most disease over a quarter century. Journal of Clinical Tuberculosis and Other Mycobacterial Diseases, 2022, 27, 100299.	0.6	2
141	Use of RODAC plates to measure containment of Mycobacterium tuberculosis in a Class IIB biosafety cabinet during routine operations. International Journal of Mycobacteriology, 2016, 5, 148-154.	0.3	1
142	False Rifampicin Resistance in Xpert Ultra Applied to Lymph Node Aspirate: A Case Report. Open Forum Infectious Diseases, 2020, 7, ofaa204.	0.4	1
143	Definitive outcomes in patients with rifampicin-resistant tuberculosis treated in Niger from 2012 to 2019: A retrospective cohort study. International Health, 2023, 15, 258-264.	0.8	1
144	On Treatment Outcomes of Patients with HIV and Tuberculosis. American Journal of Respiratory and Critical Care Medicine, 2008, 177, 121-122.	2.5	0

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145	Multidrug-resistant tuberculosis outbreak in South Africa – Authors' reply. Lancet Infectious Diseases, The, 2019, 19, 135-136.	4.6	0
146	Management of falsepositive rifampicin resistant Xpert MTB/RIF – Authors' reply. Lancet Microbe, The, 2020, 1, e239.	3.4	0
147	Acquired rifampicin resistance during first TB treatment: magnitude, relative importance, risk factors and keys to control in low-income settings. JAC-Antimicrobial Resistance, 2022, 4, dlac037.	0.9	0