

Ruth McNerney

List of Publications by Year in descending order

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83
papers

6,427
citations

70961

41
h-index

71532

76
g-index

86
all docs

86
docs citations

86
times ranked

7102
citing authors

#	ARTICLE	IF	CITATIONS
1	A robust SNP barcode for typing Mycobacterium tuberculosis complex strains. Nature Communications, 2014, 5, 4812.	5.8	531
2	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
3	Advances in tuberculosis diagnostics: the Xpert MTB/RIF assay and future prospects for a point-of-care test. Lancet Infectious Diseases, The, 2013, 13, 349-361.	4.6	385
4	Rapid determination of anti-tuberculosis drug resistance from whole-genome sequences. Genome Medicine, 2015, 7, 51.	3.6	323
5	A standardised method for interpreting the association between mutations and phenotypic drug resistance in Mycobacterium tuberculosis. European Respiratory Journal, 2017, 50, 1701354.	3.1	273
6	Genome-wide analysis of multi- and extensively drug-resistant Mycobacterium tuberculosis. Nature Genetics, 2018, 50, 307-316.	9.4	271
7	Integrating informatics tools and portable sequencing technology for rapid detection of resistance to anti-tuberculous drugs. Genome Medicine, 2019, 11, 41.	3.6	248
8	Tuberculosis: advances and challenges in development of new diagnostics and biomarkers. Lancet Infectious Diseases, The, 2018, 18, e199-e210.	4.6	244
9	Drug-resistant tuberculosis: time for visionary political leadership. Lancet Infectious Diseases, The, 2013, 13, 529-539.	4.6	243
10	Towards a point-of-care test for active tuberculosis: obstacles and opportunities. Nature Reviews Microbiology, 2011, 9, 204-213.	13.6	178
11	Tuberculosis Diagnostics and Biomarkers: Needs, Challenges, Recent Advances, and Opportunities. Journal of Infectious Diseases, 2012, 205, S147-S158.	1.9	154
12	Recurrence due to Relapse or Reinfection With Mycobacterium tuberculosis: A Whole-Genome Sequencing Approach in a Large, Population-Based Cohort With a High HIV Infection Prevalence and Active Follow-up. Journal of Infectious Diseases, 2015, 211, 1154-1163.	1.9	149
13	Drug-Resistant Tuberculosis—Current Dilemmas, Unanswered Questions, Challenges, and Priority Needs. Journal of Infectious Diseases, 2012, 205, S228-S240.	1.9	140
14	Evaluation of a new rapid bacteriophage-based method for the drug susceptibility testing of Mycobacterium tuberculosis. Nature Medicine, 1997, 3, 465-468.	15.2	137
15	Rapid Detection of Mycobacterium tuberculosis by Recombinase Polymerase Amplification. PLoS ONE, 2014, 9, e103091.	1.1	125
16	Multidrug-resistant tuberculosis. BMC Infectious Diseases, 2008, 8, 10.	1.3	109
17	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
18	The analysis of para-cresol production and tolerance in Clostridium difficile O27 and O12 strains. BMC Microbiology, 2011, 11, 86.	1.3	105

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19	Mycobacterium tuberculosis whole genome sequencing and protein structure modelling provides insights into anti-tuberculosis drug resistance. BMC Medicine, 2016, 14, 31.	2.3	102
20	Whole Genome Sequencing Shows a Low Proportion of Tuberculosis Disease Is Attributable to Known Close Contacts in Rural Malawi. PLoS ONE, 2015, 10, e0132840.	1.1	84
21	SpolPred: rapid and accurate prediction of <i>Mycobacterium tuberculosis</i> spoligotypes from short genomic sequences. Bioinformatics, 2012, 28, 2991-2993.	1.8	80
22	PolyTB: A genomic variation map for Mycobacterium tuberculosis. Tuberculosis, 2014, 94, 346-354.	0.8	79
23	Diagnostics for Developing Countries. Diagnostics, 2015, 5, 200-209.	1.3	77
24	Elucidating Emergence and Transmission of Multidrug-Resistant Tuberculosis in Treatment Experienced Patients by Whole Genome Sequencing. PLoS ONE, 2013, 8, e83012.	1.1	75
25	Integrating standardized whole genome sequence analysis with a global Mycobacterium tuberculosis antibiotic resistance knowledgebase. Scientific Reports, 2018, 8, 15382.	1.6	75
26	Perspectives on Advances in Tuberculosis Diagnostics, Drugs, and Vaccines. Clinical Infectious Diseases, 2015, 61, S102-S118.	2.9	74
27	Effect of new tuberculosis diagnostic technologies on community-based intensified case finding: a multicentre randomised controlled trial. Lancet Infectious Diseases, The, 2017, 17, 441-450.	4.6	71
28	Tuberculosis in Sudan: a study of Mycobacterium tuberculosis strain genotype and susceptibility to anti-tuberculosis drugs. BMC Infectious Diseases, 2011, 11, 219.	1.3	64
29	Rate and Amplification of Drug Resistance among Previously Treated Patients with Tuberculosis in Kampala, Uganda. Clinical Infectious Diseases, 2008, 47, 1126-1134.	2.9	63
30	Recombination in <i>pe/ppe</i> genes contributes to genetic variation in Mycobacterium tuberculosis lineages. BMC Genomics, 2016, 17, 151.	1.2	62
31	Whole Genome Sequencing Based Characterization of Extensively Drug-Resistant Mycobacterium tuberculosis Isolates from Pakistan. PLoS ONE, 2015, 10, e0117771.	1.1	59
32	Association of Schistosomiasis with False-Positive HIV Test Results in an African Adolescent Population. Journal of Clinical Microbiology, 2010, 48, 1570-1577.	1.8	58
33	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
34	Identifying mixed Mycobacterium tuberculosis infections from whole genome sequence data. BMC Genomics, 2018, 19, 613.	1.2	57
35	Development of a Bacteriophage Phage Replication Assay for Diagnosis of Pulmonary Tuberculosis. Journal of Clinical Microbiology, 2004, 42, 2115-2120.	1.8	53
36	Unraveling Mycobacterium tuberculosis genomic diversity and evolution in Lisbon, Portugal, a highly drug resistant setting. BMC Genomics, 2014, 15, 991.	1.2	52

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37	Emerging technologies in point-of-care molecular diagnostics for resource-limited settings. <i>Expert Review of Molecular Diagnostics</i> , 2014, 14, 525-534.	1.5	52
38	Machine Learning Predicts Accurately Mycobacterium tuberculosis Drug Resistance From Whole Genome Sequencing Data. <i>Frontiers in Genetics</i> , 2019, 10, 922.	1.1	51
39	Regulation of medical diagnostics and medical devices in the East African community partner states. <i>BMC Health Services Research</i> , 2014, 14, 524.	0.9	50
40	Effectiveness of the Standard WHO Recommended Retreatment Regimen (Category II) for Tuberculosis in Kampala, Uganda: A Prospective Cohort Study. <i>PLoS Medicine</i> , 2011, 8, e1000427.	3.9	49
41	Removing the bottleneck in whole genome sequencing of Mycobacterium tuberculosis for rapid drug resistance analysis: a call to action. <i>International Journal of Infectious Diseases</i> , 2017, 56, 130-135.	1.5	49
42	New tuberculosis diagnostics and rollout. <i>International Journal of Infectious Diseases</i> , 2015, 32, 81-86.	1.5	46
43	The variability and reproducibility of whole genome sequencing technology for detecting resistance to anti-tuberculous drugs. <i>Genome Medicine</i> , 2016, 8, 132.	3.6	44
44	Low-cost rapid detection of rifampicin resistant tuberculosis using bacteriophage in Kampala, Uganda. <i>Annals of Clinical Microbiology and Antimicrobials</i> , 2007, 6, 1.	1.7	39
45	Field test of a novel detection device for Mycobacterium tuberculosis antigen in cough. <i>BMC Infectious Diseases</i> , 2010, 10, 161.	1.3	37
46	Production of volatile organic compounds by mycobacteria. <i>FEMS Microbiology Letters</i> , 2012, 328, 150-156.	0.7	36
47	Improving access to new diagnostics through harmonised regulation: priorities for action. <i>African Journal of Laboratory Medicine</i> , 2014, 3, 123.	0.2	36
48	Methylation in Mycobacterium tuberculosis is lineage specific with associated mutations present globally. <i>Scientific Reports</i> , 2018, 8, 160.	1.6	31
49	In-House Phage Amplification Assay Is a Sound Alternative for Detecting Rifampin-Resistant Mycobacterium tuberculosis in Low-Resource Settings. <i>Antimicrobial Agents and Chemotherapy</i> , 2005, 49, 425-427.	1.4	30
50	Propagation of Respiratory Aerosols by the Vuvuzela. <i>PLoS ONE</i> , 2011, 6, e20086.	1.1	30
51	Changes in Mycobacterium tuberculosis Genotype Families Over 20 Years in a Population-Based Study in Northern Malawi. <i>PLoS ONE</i> , 2010, 5, e12259.	1.1	28
52	Regulatory In Vitro Diagnostics Landscape in Africa: Update on Regional Activities. <i>Clinical Infectious Diseases</i> , 2015, 61, S135-S140.	2.9	28
53	Spatial Network Mapping of Pulmonary Multidrug-Resistant Tuberculosis Cavities Using RNA Sequencing. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2019, 200, 370-380.	2.5	27
54	A multiple genome analysis of Mycobacterium tuberculosis reveals specific novel genes and mutations associated with pyrazinamide resistance. <i>BMC Genomics</i> , 2017, 18, 769.	1.2	26

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55	Detection of Mycobacterium tuberculosis in Sputum by Gas Chromatography-Mass Spectrometry of Methyl Mycocerosates Released by Thermochemolysis. PLoS ONE, 2012, 7, e32836.	1.1	24
56	Treatment Outcomes of New Tuberculosis Patients Hospitalized in Kampala, Uganda: A Prospective Cohort Study. PLoS ONE, 2014, 9, e90614.	1.1	24
57	Single nucleotide polymorphisms in efflux pumps genes in extensively drug resistant Mycobacterium tuberculosis isolates from Pakistan. Tuberculosis, 2017, 107, 20-30.	0.8	24
58	PhyTB: Phylogenetic tree visualisation and sample positioning for M. tuberculosis. BMC Bioinformatics, 2015, 16, 155.	1.2	23
59	Use of whole genome sequencing in surveillance of drug resistant tuberculosis. Expert Review of Anti-Infective Therapy, 2018, 16, 433-442.	2.0	22
60	Impact of the Xpert MTB/RIF diagnostic test for tuberculosis in countries with a high burden of disease. Current Opinion in Pulmonary Medicine, 2015, 21, 304-308.	1.2	20
61	The draft genome of Mycobacterium aurum, a potential model organism for investigating drugs against Mycobacterium tuberculosis and Mycobacterium leprae. International Journal of Mycobacteriology, 2015, 4, 207-216.	0.3	19
62	Achieving STOP TB Partnership goals: perspectives on development of new diagnostics, drugs and vaccines for tuberculosis. Tropical Medicine and International Health, 2011, 16, 819-827.	1.0	18
63	Clonal expansion across the seas as seen through CPLP-TB database: A joint effort in cataloguing Mycobacterium tuberculosis genetic diversity in Portuguese-speaking countries. Infection, Genetics and Evolution, 2019, 72, 44-58.	1.0	18
64	Colorimetric Phage-Based Assay for Detection of Rifampin-Resistant Mycobacterium tuberculosis. Journal of Clinical Microbiology, 2007, 45, 1330-1332.	1.8	17
65	Development and optimization of a gas chromatography/mass spectrometry method for the analysis of thermochemolytic degradation products of phthiocerol dimycocerosate waxes found in Mycobacterium tuberculosis. Rapid Communications in Mass Spectrometry, 2013, 27, 2374-2382.	0.7	14
66	Emergence of multidrug-resistant Mycobacterium tuberculosis of the Beijing lineage in Portugal and Guinea-Bissau: a snapshot of moving clones by whole-genome sequencing. Emerging Microbes and Infections, 2020, 9, 1342-1353.	3.0	14
67	Evaluation of phage assay for rapid phenotypic detection of rifampicin resistance in Mycobacterium tuberculosis. Annals of Clinical Microbiology and Antimicrobials, 2006, 5, 11.	1.7	12
68	Comparison of rapid tests for detection of rifampicin-resistant Mycobacterium tuberculosis in Kampala, Uganda. BMC Infectious Diseases, 2009, 9, 139.	1.3	12
69	Lifestyle, attitudes and needs of uncured XDR-TB patients living in the communities of South Africa: a qualitative study. Tropical Medicine and International Health, 2015, 20, 1155-1161.	1.0	10
70	Turkish and Japanese Mycobacterium tuberculosis sublineages share a remote common ancestor. Infection, Genetics and Evolution, 2016, 45, 461-473.	1.0	8
71	Alternate efflux pump mechanism may contribute to drug resistance in extensively drug-resistant isolates of Mycobacterium tuberculosis. International Journal of Mycobacteriology, 2016, 5, S97-S98.	0.3	6
72	A proportion of mutations fixed in the genomes of in vitro selected isogenic drug-resistant Mycobacterium tuberculosis mutants can be detected as minority variants in the parent culture. FEMS Microbiology Letters, 2015, 362, 1-7.	0.7	5

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73	Development of sample clean up methods for the analysis of Mycobacterium tuberculosis methyl mycocerosate biomarkers in sputum extracts by gas chromatography-mass spectrometry. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2015, 986-987, 135-142.	1.2	5
74	Micro-Well Phage Replication Assay for Screening Mycobacteria for Resistance to Rifampin and Streptomycin. , 2001, 48, 21-30.		3
75	Characterization of genomic variations in SNPs of PE_PGRS genes reveals deletions and insertions in extensively drug resistant (XDR) M. tuberculosis strains from Pakistan. <i>International Journal of Mycobacteriology</i> , 2015, 4, 73-79.	0.3	3
76	Phage Replication Technology for Diagnosis and Drug Susceptibility Testing. , 2001, 54, 145-154.		2
77	Screening of immigrants in the UK for latent tuberculosis. <i>Expert Review of Respiratory Medicine</i> , 2011, 5, 483-486.	1.0	2
78	Simplicio: Testes rápidos para o rastreio preliminar da tuberculose. <i>Revista Portuguesa De Pneumologia</i> , 2010, 16, S49-S55.	0.7	1
79	Sociodemographic basis of tuberculosis knowledge in Bolivia [Correspondence]. <i>International Journal of Tuberculosis and Lung Disease</i> , 2013, 17, 1245-1246.	0.6	1
80	Whole genome sequencing-based characterization of extensively drug resistant (XDR) strains of Mycobacterium tuberculosis from Pakistan. <i>International Journal of Mycobacteriology</i> , 2015, 4, 11-12.	0.3	1
81	The emergence and spread of incurable tuberculosis in South Africa. <i>International Journal of Mycobacteriology</i> , 2016, 5, S68.	0.3	1
82	ScreenTape as a tool for the rapid differentiation of Mycobacterium tuberculosis isolates. <i>Journal of Medical Microbiology</i> , 2009, 58, 1266-1268.	0.7	1
83	Clinical Tuberculosis, 2nd edn. Ed. P. D. O. Davies. Chapman & Hall, 1998. Pp. 711+112 (approx.) illus. £99.. <i>Epidemiology and Infection</i> , 2000, 124, 341-342.	1.0	0