

Ruth McNerney

List of Publications by Year in descending order

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83
papers

6,427
citations

71102

41
h-index

71685

76
g-index

86
all docs

86
docs citations

86
times ranked

7102
citing authors

#	ARTICLE	IF	CITATIONS
1	Emergence of multidrug-resistant <i>Mycobacterium tuberculosis</i> of the Beijing lineage in Portugal and Guinea-Bissau: a snapshot of moving clones by whole-genome sequencing. <i>Emerging Microbes and Infections</i> , 2020, 9, 1342-1353.	6.5	14
2	Integrating informatics tools and portable sequencing technology for rapid detection of resistance to anti-tuberculous drugs. <i>Genome Medicine</i> , 2019, 11, 41.	8.2	248
3	Machine Learning Predicts Accurately <i>Mycobacterium tuberculosis</i> Drug Resistance From Whole Genome Sequencing Data. <i>Frontiers in Genetics</i> , 2019, 10, 922.	2.3	51
4	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.	5.6	27
5	Clonal expansion across the seas as seen through CPLP-TB database: A joint effort in cataloguing <i>Mycobacterium tuberculosis</i> genetic diversity in Portuguese-speaking countries. <i>Infection, Genetics and Evolution</i> , 2019, 72, 44-58.	2.3	18
6	Genome-wide analysis of multi- and extensively drug-resistant <i>Mycobacterium tuberculosis</i> . <i>Nature Genetics</i> , 2018, 50, 307-316.	21.4	271
7	Methylation in <i>Mycobacterium tuberculosis</i> is lineage specific with associated mutations present globally. <i>Scientific Reports</i> , 2018, 8, 160.	3.3	31
8	Use of whole genome sequencing in surveillance of drug resistant tuberculosis. <i>Expert Review of Anti-Infective Therapy</i> , 2018, 16, 433-442.	4.4	22
9	Tuberculosis: advances and challenges in development of new diagnostics and biomarkers. <i>Lancet Infectious Diseases</i> , The, 2018, 18, e199-e210.	9.1	244
10	Integrating standardized whole genome sequence analysis with a global <i>Mycobacterium tuberculosis</i> antibiotic resistance knowledgebase. <i>Scientific Reports</i> , 2018, 8, 15382.	3.3	75
11	Identifying mixed <i>Mycobacterium tuberculosis</i> infections from whole genome sequence data. <i>BMC Genomics</i> , 2018, 19, 613.	2.8	57
12	The epidemiology, pathogenesis, transmission, diagnosis, and management of multidrug-resistant, extensively drug-resistant, and incurable tuberculosis. <i>Lancet Respiratory Medicine</i> , the, 2017, 5, 291-360.	10.7	459
13	Effect of new tuberculosis diagnostic technologies on community-based intensified case finding: a multicentre randomised controlled trial. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 441-450.	9.1	71
14	Removing the bottleneck in whole genome sequencing of <i>Mycobacterium tuberculosis</i> for rapid drug resistance analysis: a call to action. <i>International Journal of Infectious Diseases</i> , 2017, 56, 130-135.	3.3	49
15	Single nucleotide polymorphisms in efflux pumps genes in extensively drug resistant <i>Mycobacterium tuberculosis</i> isolates from Pakistan. <i>Tuberculosis</i> , 2017, 107, 20-30.	1.9	24
16	A standardised method for interpreting the association between mutations and phenotypic drug resistance in <i>Mycobacterium tuberculosis</i> . <i>European Respiratory Journal</i> , 2017, 50, 1701354.	6.7	273
17	A multiple genome analysis of <i>Mycobacterium tuberculosis</i> reveals specific novel genes and mutations associated with pyrazinamide resistance. <i>BMC Genomics</i> , 2017, 18, 769.	2.8	26
18	Outcomes, infectiousness, and transmission dynamics of patients with extensively drug-resistant tuberculosis and home-discharged patients with programmatically incurable tuberculosis: a prospective cohort study. <i>Lancet Respiratory Medicine</i> , the, 2017, 5, 269-281.	10.7	106

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19	The variability and reproducibility of whole genome sequencing technology for detecting resistance to anti-tuberculous drugs. <i>Genome Medicine</i> , 2016, 8, 132.	8.2	44
20	Alternate efflux pump mechanism may contribute to drug resistance in extensively drug-resistant isolates of <i>Mycobacterium tuberculosis</i> . <i>International Journal of Mycobacteriology</i> , 2016, 5, S97-S98.	0.6	6
21	<i>Mycobacterium tuberculosis</i> whole genome sequencing and protein structure modelling provides insights into anti-tuberculosis drug resistance. <i>BMC Medicine</i> , 2016, 14, 31.	5.5	102
22	Recombination in <i>pe/ppe</i> genes contributes to genetic variation in <i>Mycobacterium tuberculosis</i> lineages. <i>BMC Genomics</i> , 2016, 17, 151.	2.8	62
23	The emergence and spread of incurable tuberculosis in South Africa. <i>International Journal of Mycobacteriology</i> , 2016, 5, S68.	0.6	1
24	Turkish and Japanese <i>Mycobacterium tuberculosis</i> sublineages share a remote common ancestor. <i>Infection, Genetics and Evolution</i> , 2016, 45, 461-473.	2.3	8
25	Regulatory In Vitro Diagnostics Landscape in Africa: Update on Regional Activities. <i>Clinical Infectious Diseases</i> , 2015, 61, S135-S140.	5.8	28
26	Lifestyle, attitudes and needs of uncured XDR TB patients living in the communities of South Africa: a qualitative study. <i>Tropical Medicine and International Health</i> , 2015, 20, 1155-1161.	2.3	10
27	Diagnostics for Developing Countries. <i>Diagnostics</i> , 2015, 5, 200-209.	2.6	77
28	PhyTB: Phylogenetic tree visualisation and sample positioning for <i>M. tuberculosis</i> . <i>BMC Bioinformatics</i> , 2015, 16, 155.	2.6	23
29	Rapid determination of anti-tuberculosis drug resistance from whole-genome sequences. <i>Genome Medicine</i> , 2015, 7, 51.	8.2	323
30	Whole genome sequencing-based characterization of extensively drug resistant (XDR) strains of <i>Mycobacterium tuberculosis</i> from Pakistan. <i>International Journal of Mycobacteriology</i> , 2015, 4, 11-12.	0.6	1
31	A proportion of mutations fixed in the genomes of in vitro selected isogenic drug-resistant <i>Mycobacterium tuberculosis</i> mutants can be detected as minority variants in the parent culture. <i>FEMS Microbiology Letters</i> , 2015, 362, 1-7.	1.8	5
32	The draft genome of <i>Mycobacterium aurum</i> , a potential model organism for investigating drugs against <i>Mycobacterium tuberculosis</i> and <i>Mycobacterium leprae</i> . <i>International Journal of Mycobacteriology</i> , 2015, 4, 207-216.	0.6	19
33	Recurrence due to Relapse or Reinfection With <i>Mycobacterium tuberculosis</i> : A Whole-Genome Sequencing Approach in a Large, Population-Based Cohort With a High HIV Infection Prevalence and Active Follow-up. <i>Journal of Infectious Diseases</i> , 2015, 211, 1154-1163.	4.0	149
34	Development of sample clean up methods for the analysis of <i>Mycobacterium tuberculosis</i> 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.	2.3	5
35	Characterization of genomic variations in SNPs of PE_PGRS genes reveals deletions and insertions in extensively drug resistant (XDR) <i>M. tuberculosis</i> strains from Pakistan. <i>International Journal of Mycobacteriology</i> , 2015, 4, 73-79.	0.6	3
36	New tuberculosis diagnostics and rollout. <i>International Journal of Infectious Diseases</i> , 2015, 32, 81-86.	3.3	46

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37	Impact of the Xpert MTB/RIF diagnostic test for tuberculosis in countries with a high burden of disease. <i>Current Opinion in Pulmonary Medicine</i> , 2015, 21, 304-308.	2.6	20
38	Perspectives on Advances in Tuberculosis Diagnostics, Drugs, and Vaccines. <i>Clinical Infectious Diseases</i> , 2015, 61, S102-S118.	5.8	74
39	Whole Genome Sequencing Based Characterization of Extensively Drug-Resistant Mycobacterium tuberculosis Isolates from Pakistan. <i>PLoS ONE</i> , 2015, 10, e0117771.	2.5	59
40	Whole Genome Sequencing Shows a Low Proportion of Tuberculosis Disease Is Attributable to Known Close Contacts in Rural Malawi. <i>PLoS ONE</i> , 2015, 10, e0132840.	2.5	84
41	Treatment Outcomes of New Tuberculosis Patients Hospitalized in Kampala, Uganda: A Prospective Cohort Study. <i>PLoS ONE</i> , 2014, 9, e90614.	2.5	24
42	Rapid Detection of Mycobacterium tuberculosis by Recombinase Polymerase Amplification. <i>PLoS ONE</i> , 2014, 9, e103091.	2.5	125
43	Improving access to new diagnostics through harmonised regulation: priorities for action. <i>African Journal of Laboratory Medicine</i> , 2014, 3, 123.	0.6	36
44	Regulation of medical diagnostics and medical devices in the East African community partner states. <i>BMC Health Services Research</i> , 2014, 14, 524.	2.2	50
45	A robust SNP barcode for typing Mycobacterium tuberculosis complex strains. <i>Nature Communications</i> , 2014, 5, 4812.	12.8	531
46	Unraveling Mycobacterium tuberculosis genomic diversity and evolution in Lisbon, Portugal, a highly drug resistant setting. <i>BMC Genomics</i> , 2014, 15, 991.	2.8	52
47	Emerging technologies in point-of-care molecular diagnostics for resource-limited settings. <i>Expert Review of Molecular Diagnostics</i> , 2014, 14, 525-534.	3.1	52
48	PolyTB: A genomic variation map for Mycobacterium tuberculosis. <i>Tuberculosis</i> , 2014, 94, 346-354.	1.9	79
49	Sociodemographic basis of tuberculosis knowledge in Bolivia [Correspondence]. <i>International Journal of Tuberculosis and Lung Disease</i> , 2013, 17, 1245-1246.	1.2	1
50	Drug-resistant tuberculosis: time for visionary political leadership. <i>Lancet Infectious Diseases</i> , The, 2013, 13, 529-539.	9.1	243
51	Advances in tuberculosis diagnostics: the Xpert MTB/RIF assay and future prospects for a point-of-care test. <i>Lancet Infectious Diseases</i> , The, 2013, 13, 349-361.	9.1	385
52	Development and optimization of a gas chromatography/mass spectrometry method for the analysis of thermochemolytic degradation products of phthiocerol dimycocerosate waxes found in <i>Mycobacterium tuberculosis</i> . <i>Rapid Communications in Mass Spectrometry</i> , 2013, 27, 2374-2382.	1.5	14
53	Elucidating Emergence and Transmission of Multidrug-Resistant Tuberculosis in Treatment Experienced Patients by Whole Genome Sequencing. <i>PLoS ONE</i> , 2013, 8, e83012.	2.5	75
54	SpolPred: rapid and accurate prediction of <i>Mycobacterium tuberculosis</i> spoligotypes from short genomic sequences. <i>Bioinformatics</i> , 2012, 28, 2991-2993.	4.1	80

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55	Tuberculosis Diagnostics and Biomarkers: Needs, Challenges, Recent Advances, and Opportunities. <i>Journal of Infectious Diseases</i> , 2012, 205, S147-S158.	4.0	154
56	Detection of <i>Mycobacterium tuberculosis</i> in Sputum by Gas Chromatography-Mass Spectrometry of Methyl Mycocerosates Released by Thermochemolysis. <i>PLoS ONE</i> , 2012, 7, e32836.	2.5	24
57	Drug-Resistant Tuberculosis—Current Dilemmas, Unanswered Questions, Challenges, and Priority Needs. <i>Journal of Infectious Diseases</i> , 2012, 205, S228-S240.	4.0	140
58	Production of volatile organic compounds by mycobacteria. <i>FEMS Microbiology Letters</i> , 2012, 328, 150-156.	1.8	36
59	Propagation of Respiratory Aerosols by the Vuvuzela. <i>PLoS ONE</i> , 2011, 6, e20086.	2.5	30
60	Achieving STOP TB Partnership goals: perspectives on development of new diagnostics, drugs and vaccines for tuberculosis. <i>Tropical Medicine and International Health</i> , 2011, 16, 819-827.	2.3	18
61	Towards a point-of-care test for active tuberculosis: obstacles and opportunities. <i>Nature Reviews Microbiology</i> , 2011, 9, 204-213.	28.6	178
62	Tuberculosis in Sudan: a study of <i>Mycobacterium tuberculosis</i> strain genotype and susceptibility to anti-tuberculosis drugs. <i>BMC Infectious Diseases</i> , 2011, 11, 219.	2.9	64
63	The analysis of para-cresol production and tolerance in <i>Clostridium difficile</i> O27 and O12 strains. <i>BMC Microbiology</i> , 2011, 11, 86.	3.3	105
64	Screening of immigrants in the UK for latent tuberculosis. <i>Expert Review of Respiratory Medicine</i> , 2011, 5, 483-486.	2.5	2
65	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.	8.4	49
66	Field test of a novel detection device for <i>Mycobacterium tuberculosis</i> antigen in cough. <i>BMC Infectious Diseases</i> , 2010, 10, 161.	2.9	37
67	Changes in <i>Mycobacterium tuberculosis</i> Genotype Families Over 20 Years in a Population-Based Study in Northern Malawi. <i>PLoS ONE</i> , 2010, 5, e12259.	2.5	28
68	Association of Schistosomiasis with False-Positive HIV Test Results in an African Adolescent Population. <i>Journal of Clinical Microbiology</i> , 2010, 48, 1570-1577.	3.9	58
69	Molecular Detection of Mixed Infections of <i>Mycobacterium tuberculosis</i> Strains in Sputum Samples from Patients in Karonga District, Malawi. <i>Journal of Clinical Microbiology</i> , 2010, 48, 4512-4518.	3.9	57
70	Simplicio: Testes rápidos para o rastreio preliminar da tuberculose. <i>Revista Portuguesa De Pneumologia</i> , 2010, 16, S49-S55.	0.7	1
71	Comparison of rapid tests for detection of rifampicin-resistant <i>Mycobacterium tuberculosis</i> in Kampala, Uganda. <i>BMC Infectious Diseases</i> , 2009, 9, 139.	2.9	12
72	ScreenTape as a tool for the rapid differentiation of <i>Mycobacterium tuberculosis</i> isolates. <i>Journal of Medical Microbiology</i> , 2009, 58, 1266-1268.	1.8	1

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73	Multidrug-resistant tuberculosis. <i>BMC Infectious Diseases</i> , 2008, 8, 10.	2.9	109
74	Rate and Amplification of Drug Resistance among Previously Treated Patients with Tuberculosis in Kampala, Uganda. <i>Clinical Infectious Diseases</i> , 2008, 47, 1126-1134.	5.8	63
75	Colorimetric Phage-Based Assay for Detection of Rifampin-Resistant <i>Mycobacterium tuberculosis</i> . <i>Journal of Clinical Microbiology</i> , 2007, 45, 1330-1332.	3.9	17
76	Low-cost rapid detection of rifampicin resistant tuberculosis using bacteriophage in Kampala, Uganda. <i>Annals of Clinical Microbiology and Antimicrobials</i> , 2007, 6, 1.	3.8	39
77	Evaluation of phage assay for rapid phenotypic detection of rifampicin resistance in <i>Mycobacterium tuberculosis</i> . <i>Annals of Clinical Microbiology and Antimicrobials</i> , 2006, 5, 11.	3.8	12
78	In-House Phage Amplification Assay Is a Sound Alternative for Detecting Rifampin-Resistant <i>Mycobacterium tuberculosis</i> in Low-Resource Settings. <i>Antimicrobial Agents and Chemotherapy</i> , 2005, 49, 425-427.	3.2	30
79	Development of a Bacteriophage Phage Replication Assay for Diagnosis of Pulmonary Tuberculosis. <i>Journal of Clinical Microbiology</i> , 2004, 42, 2115-2120.	3.9	53
80	Micro-Well Phage Replication Assay for Screening <i>Mycobacteria</i> for Resistance to Rifampin and Streptomycin. , 2001, 48, 21-30.		3
81	Phage Replication Technology for Diagnosis and Drug Susceptibility Testing. , 2001, 54, 145-154.		2
82	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.	2.1	0
83	Evaluation of a new rapid bacteriophage-based method for the drug susceptibility testing of <i>Mycobacterium tuberculosis</i> . <i>Nature Medicine</i> , 1997, 3, 465-468.	30.7	137