

# Stefan Niemann

## List of PR Articles by Year in descending order

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244

PR articles

19,889

PR citations

5950

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7480

136

g-index

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14591

citing authors

#	ARTICLE	IF	PR CITATIONS
1	Molecular determinants of multidrug-resistant tuberculosis in Sierra Leone. <i>Microbiology Spectrum</i> , 2024, 12, .	3.7	2
2	Differential rates of <i>Mycobacterium tuberculosis</i> transmission associate with hostâ€“pathogen sympatry. <i>Nature Microbiology</i> , 2024, 9, 2113-2127.	17.0	18
3	Phylogenomic and genomic analysis reveals unique and shared genetic signatures of <i>Mycobacterium kansasii</i> complex species. <i>Microbial Genomics</i> , 2024, 10, .	2.0	1
4	Wollamide Cyclic Hexapeptides Synergize with Established and New Tuberculosis Antibiotics in Targeting <i>Mycobacterium tuberculosis</i> . <i>Microbiology Spectrum</i> , 2023, 11, .	3.7	2
5	Transmission Dynamics of a <i>Mycobacterium tuberculosis</i> Complex Outbreak in an Indigenous Population in the Colombian Amazon Region. <i>Microbiology Spectrum</i> , 2023, 11, .	3.7	3
6	<i>In vitro</i> activity of new combinations of $\beta$ -lactam and $\beta$ -lactamase inhibitors against the <i>Mycobacterium tuberculosis</i> complex. <i>Microbiology Spectrum</i> , 2023, 11, .	3.7	4
7	Emergence of bedaquiline resistance in a high tuberculosis burden country. <i>European Respiratory Journal</i> , 2022, 59, 2100621.	8.7	96
8	Whole genome sequencing-based classification of human-related <i>Haemophilus</i> species and detection of antimicrobial resistance genes. <i>Genome Medicine</i> , 2022, 14, .	9.8	10
9	Sub-Lineage Specific Phenolic Glycolipid Patterns in the <i>Mycobacterium tuberculosis</i> Complex Lineage 1. <i>Frontiers in Microbiology</i> , 2022, 13, .	3.9	10
10	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	57
11	Molecular Epidemiology of <i>Mycobacterium tuberculosis</i> Complex Strains in Urban and Slum Settings of Nairobi, Kenya. <i>Genes</i> , 2022, 13, 475.	2.6	7
12	The 2021 WHO catalogue of <i>Mycobacterium tuberculosis</i> complex mutations associated with drug resistance: a genotypic analysis. <i>Lancet Microbe</i> , The, 2022, 3, e265-e273.	12.6	256
13	Whole genome sequencing-based drug resistance predictions of multidrug-resistant <i>Mycobacterium tuberculosis</i> isolates from Tanzania. <i>JAC-Antimicrobial Resistance</i> , 2022, 4, .	1.9	8
14	One-year surveillance of SARS-CoV-2 transmission of the ELISA cohort: A model for population-based monitoring of infection risk. <i>Science Advances</i> , 2022, 8, .	11.2	23
15	Rapid molecular diagnostics of tuberculosis resistance by targeted stool sequencing. <i>Genome Medicine</i> , 2022, 14, .	9.8	52
16	Origin and Global Expansion of <i>Mycobacterium tuberculosis</i> Complex Lineage 3. <i>Genes</i> , 2022, 13, 990.	2.6	30
17	High fluoroquinolone resistance proportions among multidrug-resistant tuberculosis driven by dominant L2 <i>Mycobacterium tuberculosis</i> clones in the Mumbai Metropolitan Region. <i>Genome Medicine</i> , 2022, 14, .	9.8	40
18	Whole-Genome Sequencing for Resistance Prediction and Transmission Analysis of <i>Mycobacterium tuberculosis</i> Complex Strains from Namibia. <i>Microbiology Spectrum</i> , 2022, 10, .	3.7	6

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19	Case-Finding Strategies for Drug-Resistant Tuberculosis: Protocol for a Scoping Review. JMIR Research Protocols, 2022, 11, e40009.	1.3	3
20	Use of a whole genome sequencing-based approach for <i>Mycobacterium tuberculosis</i> surveillance in Europe in 2017–2019: an ECDC pilot study. European Respiratory Journal, 2021, 57, 2002272.	8.7	48
21	Deep amplicon sequencing for culture-free prediction of susceptibility or resistance to 13 anti-tuberculous drugs. European Respiratory Journal, 2021, 57, 2002338.	8.7	92
22	Improving tuberculosis surveillance by detecting international transmission using publicly available whole genome sequencing data. Eurosurveillance, 2021, 26, .	5.0	10
23	Survival of hypoxia-induced dormancy is not a common feature of all strains of the <i>Mycobacterium tuberculosis</i> complex. Scientific Reports, 2021, 11, .	3.5	15
24	Phylogenomics of <i>Mycobacterium africanum</i> reveals a new lineage and a complex evolutionary history. Microbial Genomics, 2021, 7, .	2.0	115
25	Design of Multidrug-Resistant Tuberculosis Treatment Regimens Based on DNA Sequencing. Clinical Infectious Diseases, 2021, 73, 1194-1202.	5.4	36
26	Evaluation of the Roche cobas MTB and MTB-RIF/INH Assays in Samples from Germany and Sierra Leone. Journal of Clinical Microbiology, 2021, 59, .	4.1	13
27	Secretome characterization of clinical isolates from the <i>Mycobacterium abscessus</i> complex provides insight into antigenic differences. BMC Genomics, 2021, 22, .	3.3	2
28	Perspectives for systems biology in the management of tuberculosis. European Respiratory Review, 2021, 30, 200377.	8.8	20
29	Microevolution of <i>Mycobacterium tuberculosis</i> Subpopulations and Heteroresistance in a Patient Receiving 27 Years of Tuberculosis Treatment in Germany. Antimicrobial Agents and Chemotherapy, 2021, 65, .	4.2	7
30	Implementation of whole genome sequencing for tuberculosis diagnostics in a low-middle income, high MDR-TB burden country. Scientific Reports, 2021, 11, .	3.5	31
31	Is the new WHO definition of extensively drug-resistant tuberculosis easy to apply in practice?. European Respiratory Journal, 2021, 58, 2100959.	8.7	12
32	<i>Mycobacterium tuberculosis</i> 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, .	2.0	22
33	The global outbreak of <i>Mycobacterium chimaera</i> infections in cardiac surgery—a systematic review of whole-genome sequencing studies and joint analysis. Clinical Microbiology and Infection, 2021, 27, 1613-1620.	5.6	24
34	A multi-phenotype genome-wide association study of clades causing tuberculosis in a Ghanaian- and South African cohort. Genomics, 2021, 113, 1802-1815.	2.8	11
35	WNT6/ACC2-induced storage of triacylglycerols in macrophages is exploited by <i>Mycobacterium tuberculosis</i> . Journal of Clinical Investigation, 2021, 131, .	9.0	34
36	Transmission patterns of rifampicin resistant <i>Mycobacterium tuberculosis</i> complex strains in Cameroon: a genomic epidemiological study. BMC Infectious Diseases, 2021, 21, .	2.8	7

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37	Role of Epistasis in Amikacin, Kanamycin, Bedaquiline, and Clofazimine Resistance in Mycobacterium tuberculosis Complex. Antimicrobial Agents and Chemotherapy, 2021, 65, .	4.2	59
38	Population structure, biogeography and transmissibility of Mycobacterium tuberculosis. Nature Communications, 2021, 12, .	13.9	126
39	Evaluation of whole-genome sequence data analysis approaches for short- and long-read sequencing of Mycobacterium tuberculosis. Microbial Genomics, 2021, 7, .	2.0	17
40	Two Pandemics, One Challenge—Leveraging Molecular Test Capacity of Tuberculosis Laboratories for Rapid COVID-19 Case-Finding. Emerging Infectious Diseases, 2020, 26, 2549-2554.	3.9	18
41	MDR M. tuberculosis outbreak clone in Eswatini missed by Xpert has elevated bedaquiline resistance dated to the pre-treatment era. Genome Medicine, 2020, 12, .	9.8	71
42	Perspective for Precision Medicine for Tuberculosis. Frontiers in Immunology, 2020, 11, .	5.1	59
43	Antimicrobial Susceptibility and Phylogenetic Relations in a German Cohort Infected with Mycobacterium abscessus. Journal of Clinical Microbiology, 2020, 58, .	4.1	23
44	Phenotypic and Transcriptomic Analyses of Seven Clinical Stenotrophomonas maltophilia Isolates Identify a Small Set of Shared and Commonly Regulated Genes Involved in the Biofilm Lifestyle. Applied and Environmental Microbiology, 2020, 86, .	3.5	19
45	Evolutionary Approaches to Combat Antibiotic Resistance: Opportunities and Challenges for Precision Medicine. Frontiers in Immunology, 2020, 11, .	5.1	68
46	Population Structure of Mycobacterium bovis in Germany: a Long-Term Study Using Whole-Genome Sequencing Combined with Conventional Molecular Typing Methods. Journal of Clinical Microbiology, 2020, 58, .	4.1	15
47	Detection of low-frequency resistance-mediating SNPs in next-generation sequencing data of Mycobacterium tuberculosis complex strains with binoSNP. Scientific Reports, 2020, 10, .	3.5	17
48	Phylogenetically informative mutations in genes implicated in antibiotic resistance in Mycobacterium tuberculosis complex. Genome Medicine, 2020, 12, .	9.8	78
49	Comparative analysis of phenotypic and genotypic antibiotic susceptibility patterns in Mycobacterium avium complex. International Journal of Infectious Diseases, 2020, 93, 320-328.	2.2	31
50	GenomeMap: Within-Species Genome-Wide dN/dS Estimation from over 10,000 Genomes. Molecular Biology and Evolution, 2020, 37, 2450-2460.	4.7	47
51	<i>Mycobacterium tuberculosis</i> Complex Lineage 3 as Causative Agent of Pulmonary Tuberculosis, Eastern Sudan. Emerging Infectious Diseases, 2020, 26, 427-436.	3.9	23
52	Multidrug- and Extensively Drug-Resistant <i>Mycobacterium tuberculosis</i> Beijing Clades, Ukraine, 2015. Emerging Infectious Diseases, 2020, 26, 481-490.	3.9	31
53	A landscape of genomic alterations at the root of a near-untreatable tuberculosis epidemic. BMC Medicine, 2020, 18, .	7.5	28
54	The phylogenetic landscape and nosocomial spread of the multidrug-resistant opportunist Stenotrophomonas maltophilia. Nature Communications, 2020, 11, .	13.9	115

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55	A publicly accessible database for <i>Clostridioides difficile</i> genome sequences supports tracing of transmission chains and epidemics. <i>Microbial Genomics</i> , 2020, 6, .	2.0	32
56	Insertion and deletion evolution reflects antibiotics selection pressure in a <i>Mycobacterium tuberculosis</i> outbreak. <i>PLoS Pathogens</i> , 2020, 16, e1008357.	4.5	32
57	The role of IS6110 in micro- and macroevolution of <i>Mycobacterium tuberculosis</i> lineage 2. <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106559.	3.0	10
58	Population structure of drug-resistant <i>Mycobacterium tuberculosis</i> in Central Asia. <i>BMC Infectious Diseases</i> , 2019, 19, .	2.8	19
59	The Lancet Respiratory Medicine Commission: 2019 update: epidemiology, pathogenesis, transmission, diagnosis, and management of multidrug-resistant and incurable tuberculosis. <i>Lancet Respiratory Medicine</i> , 2019, 7, 820-826.	24.1	105
60	Emergence of Low-level Delamanid and Bedaquiline Resistance During Extremely Drug-resistant Tuberculosis Treatment. <i>Clinical Infectious Diseases</i> , 2019, 69, 1229-1231.	5.4	63
61	Whole genome sequencing of <i>Mycobacterium tuberculosis</i> : current standards and open issues. <i>Nature Reviews Microbiology</i> , 2019, 17, 533-545.	86.4	372
62	Revised Interpretation of the Hain Lifescience GenoType MTBC To Differentiate <i>Mycobacterium canettii</i> and Members of the <i>Mycobacterium tuberculosis</i> Complex. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	4.2	25
63	DeepAMR for predicting co-occurrent resistance of <i>Mycobacterium tuberculosis</i> . <i>Bioinformatics</i> , 2019, 35, 3240-3249.	4.7	59
64	Reference set of <i>Mycobacterium tuberculosis</i> clinical strains: A tool for research and product development. <i>PLoS ONE</i> , 2019, 14, e0214088.	2.4	92
65	Molecular drug susceptibility testing and strain typing of tuberculosis by DNA hybridization. <i>PLoS ONE</i> , 2019, 14, e0212064.	2.4	5
66	SNP-IT Tool for Identifying Subspecies and Associated Lineages of <i>Mycobacterium tuberculosis</i> Complex. <i>Emerging Infectious Diseases</i> , 2019, 25, 482-488.	3.9	78
67	Longitudinal Outbreak of Multidrug-Resistant Tuberculosis in a Hospital Setting, Serbia. <i>Emerging Infectious Diseases</i> , 2019, 25, 555-558.	3.9	10
68	Same meat, different gravy: ignore the new names of mycobacteria. <i>European Respiratory Journal</i> , 2019, 54, 1900795.	8.7	76
69	Rapid microarray-based assay for detection of pyrazinamide resistant <i>Mycobacterium tuberculosis</i> . <i>Diagnostic Microbiology and Infectious Disease</i> , 2019, 94, 147-154.	1.7	8
70	Genetic Diversity of Multi- and Extensively Drug-Resistant <i>Mycobacterium tuberculosis</i> Isolates in the Capital of Iran, Revealed by Whole-Genome Sequencing. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	4.1	35
71	A Diagnostic Algorithm To Investigate Pyrazinamide and Ethambutol Resistance in Rifampin-Resistant <i>Mycobacterium tuberculosis</i> Isolates in a Low-Incidence Setting. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	4.2	23
72	Antibiotic resistance prediction for <i>Mycobacterium tuberculosis</i> from genome sequence data with Mykrobe. <i>Wellcome Open Research</i> , 2019, 4, 191.	1.0	174

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73	Towards standardisation: comparison of five whole genome sequencing (WGS) analysis pipelines for detection of epidemiologically linked tuberculosis cases. <i>Eurosurveillance</i> , 2019, 24, .	5.0	60
74	In vivo virulence of <i>Mycobacterium tuberculosis</i> depends on a single homologue of the LytR-CpsA-Psr proteins. <i>Scientific Reports</i> , 2018, 8, .	3.5	15
75	Risk of tuberculosis transmission among healthcare workers. <i>ERJ Open Research</i> , 2018, 4, 00161-2017.	2.6	15
76	A cluster of multidrug-resistant <i>Mycobacterium tuberculosis</i> among patients arriving in Europe from the Horn of Africa: a molecular epidemiological study. <i>Lancet Infectious Diseases</i> , The, 2018, 18, 431-440.	15.7	143
77	Genetic sequencing for surveillance of drug resistance in tuberculosis in highly endemic countries: a multi-country population-based surveillance study. <i>Lancet Infectious Diseases</i> , The, 2018, 18, 675-683.	15.7	139
78	New Approaches and Therapeutic Options for <i>Mycobacterium tuberculosis</i> in a Dormant State. <i>Clinical Microbiology Reviews</i> , 2018, 31, .	17.5	66
79	Rapid Microarray-Based Detection of Rifampin, Isoniazid, and Fluoroquinolone Resistance in <i>Mycobacterium tuberculosis</i> by Use of a Single Cartridge. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	4.1	10
80	What Is Resistance? Impact of Phenotypic versus Molecular Drug Resistance Testing on Therapy for Multi- and Extensively Drug-Resistant Tuberculosis. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	4.2	98
81	The Genetic Transformation of <i>Chlamydia pneumoniae</i> . <i>MSphere</i> , 2018, 3, .	3.1	31
82	Drug-resistance profiling and transmission dynamics of multidrug-resistant <em></em></i> <i>Mycobacterium tuberculosis</i> </i> in Saudi Arabia revealed by whole genome sequencing. <i>Infection and Drug Resistance</i> , 2018, Volume 11, 2219-2229.	2.7	18
83	Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing. <i>New England Journal of Medicine</i> , 2018, 379, 1403-1415.	44.0	496
84	Outbreak of multidrug-resistant tuberculosis in South Africa undetected by WHO-endorsed commercial tests: an observational study. <i>Lancet Infectious Diseases</i> , The, 2018, 18, 1350-1359.	15.7	145
85	Integrating standardized whole genome sequence analysis with a global <i>Mycobacterium tuberculosis</i> antibiotic resistance knowledgebase. <i>Scientific Reports</i> , 2018, 8, .	3.5	91
86	Pathogen-based precision medicine for drug-resistant tuberculosis. <i>PLoS Pathogens</i> , 2018, 14, e1007297.	4.5	49
87	The relationship between transmission time and clustering methods in <i>Mycobacterium tuberculosis</i> epidemiology. <i>EBioMedicine</i> , 2018, 37, 410-416.	10.0	124
88	Molecular epidemiology and drug resistance patterns of <i>Mycobacterium tuberculosis</i> complex isolates from university students and the local community in Eastern Ethiopia. <i>PLoS ONE</i> , 2018, 13, e0198054.	2.4	13
89	Whole genome sequencing of <i></i> <i>Mycobacterium tuberculosis</i> </i>. <i>European Respiratory Journal</i> , 2018, 52, 1801163.	8.7	50
90	<i>Mycobacterium bovis</i> Persistence in Two Different Captive Wild Animal Populations in Germany: a Longitudinal Molecular Epidemiological Study Revealing Pathogen Transmission by Whole-Genome Sequencing. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	4.1	14

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91	Comparative genomics of Mycobacterium africanum Lineage 5 and Lineage 6 from Ghana suggests distinct ecological niches. Scientific Reports, 2018, 8, .	3.5	45
92	Smear Microscopy for Diagnosis of Pulmonary Tuberculosis in Eastern Sudan. Tuberculosis Research and Treatment, 2018, 2018, 1-8.	0.9	9
93	Analysis of Phylogenetic Variation of Stenotrophomonas maltophilia Reveals Human-Specific Branches. Frontiers in Microbiology, 2018, 9, .	3.9	43
94	Aortic Endograft Infection with Mycobacterium chimaera and Granulicatella adiacens, Switzerland, 2014. Emerging Infectious Diseases, 2018, 24, 1700-1704.	3.9	3
95	Harmonized Genome Wide Typing of Tubercle Bacilli Using a Web-Based Gene-By-Gene Nomenclature System. EBioMedicine, 2018, 34, 131-138.	10.0	52
96	Mycobacterium abscessus, a taxonomic puzzle. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 467-469.	1.7	23
97	Mycobacterial infections in carcasses of ruminants slaughtered at the two slaughterhouses of Kassala, Sudan. Revue D'Elevage Et De Medecine Veterinaire Des Pays Tropicaux, 2018, 70, 131-136.	0.6	2
98	High Interlaboratory Reproducibility and Accuracy of Next-Generation-Sequencing-Based Bacterial Genotyping in a Ring Trial. Journal of Clinical Microbiology, 2017, 55, 908-913.	4.1	88
99	<i>Some Synonymous and Nonsynonymous Mutations in Mycobacterium tuberculosis Lead to Systematic False-Positive Fluoroquinolone Resistance Results with the Hain GenoType MTBDR</i> <i>gyrA</i> <i>sl</i> Assays, Antimicrobial Agents and Chemotherapy, 2017, 61, .	4.2	35
100	Multiplex detection of extensively drug resistant tuberculosis using binary deoxyribozyme sensors. Biosensors and Bioelectronics, 2017, 94, 176-183.	9.7	32
101	Mycobacterium tuberculosis resistance prediction and lineage classification from genome sequencing: comparison of automated analysis tools. Scientific Reports, 2017, 7, .	3.5	93
102	The epidemiology, pathogenesis, transmission, diagnosis, and management of multidrug-resistant, extensively drug-resistant, and incurable tuberculosis. Lancet Respiratory Medicine, the, 2017, 5, 291-360.	24.1	555
103	Extent of transmission captured by contact tracing in a tuberculosis high endemic setting. European Respiratory Journal, 2017, 49, 1601851.	8.7	7
104	Novel rapid PCR for the detection of Ile491Phe rpoB mutation of Mycobacterium tuberculosis , a rifampicin-resistance-conferring mutation undetected by commercial assays. Clinical Microbiology and Infection, 2017, 23, 267.e5-267.e7.	5.6	42
105	Role of Alanine Racemase Mutations in Mycobacterium tuberculosis <scp>d</scp> -Cycloserine Resistance. Antimicrobial Agents and Chemotherapy, 2017, 61, .	4.2	35
106	Global outbreak of severe Mycobacterium chimaera disease after cardiac surgery: a molecular epidemiological study. Lancet Infectious Diseases, The, 2017, 17, 1033-1041.	15.7	240
107	Whole genome sequencing for M/XDR tuberculosis surveillance and for resistance testing. Clinical Microbiology and Infection, 2017, 23, 161-166.	5.6	77
108	A standardised method for interpreting the association between mutations and phenotypic drug resistance in Mycobacterium tuberculosis. European Respiratory Journal, 2017, 50, 1701354.	8.7	321

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109	Integration of molecular typing results into tuberculosis surveillance in Germany – A pilot study. PLoS ONE, 2017, 12, e0188356.	2.4	5
110	New <i>Mycobacterium tuberculosis</i> Complex Sublineage, Brazzaville, Congo. Emerging Infectious Diseases, 2017, 23, 423-429.	3.9	40
111	Gesamtgenomsequenzierung der Tuberkulose. Pneumologie, 2017, 15, 35-42.	0.2	0
112	An application of competitive reporter monitored amplification (CMA) for rapid detection of single nucleotide polymorphisms (SNPs). PLoS ONE, 2017, 12, e0183561.	2.4	2
113	A joint cross-border investigation of a cluster of multidrug-resistant tuberculosis in Austria, Romania and Germany in 2014 using classic, genotyping and whole genome sequencing methods: lessons learnt. Eurosurveillance, 2017, 22, .	5.0	29
114	Drug susceptibility profiles of pulmonary <i>Mycobacterium tuberculosis</i> isolates from patients in informal urban settlements in Nairobi, Kenya. BMC Infectious Diseases, 2016, 16, .	2.8	13
115	High Sequence Variability of the ppE18 Gene of Clinical <i>Mycobacterium tuberculosis</i> Complex Strains Potentially Impacts Effectivity of Vaccine Candidate M72/AS01E. PLoS ONE, 2016, 11, e0152200.	2.4	28
116	In reply. International Journal of Tuberculosis and Lung Disease, 2016, 20, 424-424.	1.3	0
117	Population-based resistance of <i>Mycobacterium tuberculosis</i> isolates to pyrazinamide and fluoroquinolones: results from a multicountry surveillance project. Lancet Infectious Diseases, The, 2016, 16, 1185-1192.	15.7	171
118	Delamanid susceptibility testing of <i>Mycobacterium tuberculosis</i> using the resazurin microtitre assay and the BACTEC <sup>®</sup> MGIT <sup>™</sup> 960 system. Journal of Antimicrobial Chemotherapy, 2016, 71, 1532-1539.	3.2	77
119	Tuberculosis Treatment Outcome and Drug Resistance in Lambaré, Gabon: A Prospective Cohort Study. American Journal of Tropical Medicine and Hygiene, 2016, 95, 472-480.	0.0	23
120	A snapshot of the predominant single nucleotide polymorphism cluster groups of <i>Mycobacterium tuberculosis</i> clinical isolates in Delhi, India. Tuberculosis, 2016, 100, 72-81.	2.0	5
121	Impact of Genetic Diversity on the Biology of <i>Mycobacterium tuberculosis</i> Complex Strains. Microbiology Spectrum, 2016, 4, .	3.7	28
122	Tracing <i>Mycobacterium tuberculosis</i> transmission by whole genome sequencing in a high incidence setting: a retrospective population-based study in East Greenland. Scientific Reports, 2016, 6, .	3.5	57
123	<i>Mycobacterium tuberculosis</i> lineage 4 comprises globally distributed and geographically restricted sublineages. Nature Genetics, 2016, 48, 1535-1543.	25.9	419
124	Drug resistance and population structure of <i>M.tuberculosis</i> isolates from prisons and communities in Ethiopia. BMC Infectious Diseases, 2016, 16, .	2.8	25
125	Rapid, comprehensive, and affordable mycobacterial diagnosis with whole-genome sequencing: a prospective study. Lancet Respiratory Medicine, the, 2016, 4, 49-58.	24.1	321
126	Whole genome sequencing of <i>Mycobacterium tuberculosis</i> for detection of recent transmission and tracing outbreaks: A systematic review. Tuberculosis, 2016, 98, 77-85.	2.0	133

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127	Clinical implications of molecular drug resistance testing for <i>Mycobacterium tuberculosis</i> : a TBNET/RESIST-TB consensus statement. <i>International Journal of Tuberculosis and Lung Disease</i> , 2016, 20, 24-42.	1.3	131
128	Emended description of <i>Mycobacterium abscessus</i> , <i>Mycobacterium abscessus</i> subsp. <i>abscessus</i> and <i>Mycobacterium abscessus</i> subsp. <i>bolletii</i> and designation of <i>Mycobacterium abscessus</i> subsp. <i>massiliense</i> comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 4471-4479.	1.7	224
129	Rapid antibiotic-resistance predictions from genome sequence data for <i>Staphylococcus aureus</i> and <i>Mycobacterium tuberculosis</i> . <i>Nature Communications</i> , 2015, 6, .	13.9	540
130	Evolutionary history and global spread of the <i>Mycobacterium tuberculosis</i> Beijing lineage. <i>Nature Genetics</i> , 2015, 47, 242-249.	25.9	535
131	Whole-genome sequencing for prediction of <i>Mycobacterium tuberculosis</i> drug susceptibility and resistance: a retrospective cohort study. <i>Lancet Infectious Diseases</i> , The, 2015, 15, 1193-1202.	15.7	633
132	Integration of Published Information Into a Resistance-Associated Mutation Database for <i>Mycobacterium tuberculosis</i> . <i>Journal of Infectious Diseases</i> , 2015, 211, S50-S57.	3.9	35
133	Predominant <i>Mycobacterium tuberculosis</i> Families and High Rates of Recent Transmission among New Cases Are Not Associated with Primary Multidrug Resistance in Lima, Peru. <i>Journal of Clinical Microbiology</i> , 2015, 53, 1854-1863.	4.1	26
134	PhyResSE: a Web Tool Delineating <i>Mycobacterium tuberculosis</i> Antibiotic Resistance and Lineage from Whole-Genome Sequencing Data. <i>Journal of Clinical Microbiology</i> , 2015, 53, 1908-1914.	4.1	295
135	Ascertaining in vivo virulence of <i>Mycobacterium tuberculosis</i> lineages in patients in Mbeya, Tanzania. <i>International Journal of Tuberculosis and Lung Disease</i> , 2015, 19, 70-73.	1.3	2
136	Nosocomial transmission of multidrug-resistant tuberculosis. <i>International Journal of Tuberculosis and Lung Disease</i> , 2015, 19, 1520-1523.	1.3	32
137	Tuberculous Lymphadenitis in Ethiopia Predominantly Caused by Strains Belonging to the Delhi/CAS Lineage and Newly Identified Ethiopian Clades of the <i>Mycobacterium tuberculosis</i> Complex. <i>PLoS ONE</i> , 2015, 10, e0137865.	2.4	24
138	Tracing the Spread of <i>Clostridium difficile</i> Ribotype 027 in Germany Based on Bacterial Genome Sequences. <i>PLoS ONE</i> , 2015, 10, e0139811.	2.4	41
139	<i>Mycobacterium tuberculosis</i> Pyrazinamide Resistance Determinants: a Multicenter Study. <i>MBio</i> , 2014, 5, .	4.5	135
140	Whole-Genome Sequencing for Risk Assessment of Long-term Shiga Toxin-producing <i>Escherichia coli</i> . <i>Emerging Infectious Diseases</i> , 2014, 20, 732-733.	3.9	6
141	Phylogenetic polymorphisms in antibiotic resistance genes of the <i>Mycobacterium tuberculosis</i> complex. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 1205-1210.	3.2	80
142	Proposal of a Consensus Set of Hypervariable Mycobacterial Interspersed Repetitive-Variable-Number Tandem-Repeat Loci for Subtyping of <i>Mycobacterium tuberculosis</i> Beijing Isolates. <i>Journal of Clinical Microbiology</i> , 2014, 52, 164-172.	4.1	84
143	Fortschritte in der molekularen Epidemiologie der Tuberkulose. <i>Pneumologie</i> , 2014, 11, 21-27.	0.2	1
144	Diversity and Evolution of <i>Mycobacterium tuberculosis</i> : Moving to Whole-Genome-Based Approaches. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2014, 4, a021188-a021188.	6.7	67

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145	Genetic diversity within Mycobacterium tuberculosis complex impacts on the accuracy of genotypic pyrazinamide drug-susceptibility assay. <i>Tuberculosis</i> , 2014, 94, 451-453.	2.0	13
146	Whole-Genome-Based Mycobacterium tuberculosis Surveillance: a Standardized, Portable, and Expandable Approach. <i>Journal of Clinical Microbiology</i> , 2014, 52, 2479-2486.	4.1	192
147	Molecular epidemiology and transmission dynamics of Mycobacterium tuberculosis in Northwest Ethiopia: new phylogenetic lineages found in Northwest Ethiopia. <i>BMC Infectious Diseases</i> , 2013, 13, .	2.8	95
148	Out-of-Africa migration and Neolithic coexpansion of Mycobacterium tuberculosis with modern humans. <i>Nature Genetics</i> , 2013, 45, 1176-1182.	25.9	1,022
149	Mycobacterium canettii is intrinsically resistant to both pyrazinamide and pyrazinoic acid. <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 1439-1440.	3.2	44
150	Novel Mycobacterium tuberculosis Complex Isolate from a Wild Chimpanzee. <i>Emerging Infectious Diseases</i> , 2013, 19, 969-976.	3.9	112
151	Whole Genome Sequencing versus Traditional Genotyping for Investigation of a Mycobacterium tuberculosis Outbreak: A Longitudinal Molecular Epidemiological Study. <i>PLoS Medicine</i> , 2013, 10, e1001387.	8.1	464
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