

Stefan Niemann

List of Publications by Year in descending order

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262
papers

24,038
citations

8732

75
h-index

9553

142
g-index

292
all docs

292
docs citations

292
times ranked

13336
citing authors

#	ARTICLE	IF	CITATIONS
1	Emergence of bedaquiline resistance in a high tuberculosis burden country. <i>European Respiratory Journal</i> , 2022, 59, 2100621.	3.1	48
2	Whole genome sequencing-based classification of human-related <i>Haemophilus</i> species and detection of antimicrobial resistance genes. <i>Genome Medicine</i> , 2022, 14, 13.	3.6	6
3	Sub-Lineage Specific Phenolic Glycolipid Patterns in the <i>Mycobacterium tuberculosis</i> Complex Lineage 1. <i>Frontiers in Microbiology</i> , 2022, 13, 832054.	1.5	3
4	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.	1.3	34
5	Molecular Epidemiology of <i>Mycobacterium tuberculosis</i> Complex Strains in Urban and Slum Settings of Nairobi, Kenya. <i>Genes</i> , 2022, 13, 475.	1.0	2
6	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.	3.4	114
7	Whole genome sequencing-based drug resistance predictions of multidrug-resistant <i>Mycobacterium tuberculosis</i> isolates from Tanzania. <i>JAC-Antimicrobial Resistance</i> , 2022, 4, dlac042.	0.9	2
8	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, eabm5016.	4.7	14
9	Updating the approaches to define susceptibility and resistance to anti-tuberculosis agents: implications for diagnosis and treatment. <i>European Respiratory Journal</i> , 2022, 59, 2200166.	3.1	15
10	Rapid molecular diagnostics of tuberculosis resistance by targeted stool sequencing. <i>Genome Medicine</i> , 2022, 14, 52.	3.6	14
11	Origin and Global Expansion of <i>Mycobacterium tuberculosis</i> Complex Lineage 3. <i>Genes</i> , 2022, 13, 990.	1.0	13
12	Use of a Whole Genome Sequencing-based approach for <i>Mycobacterium tuberculosis</i> surveillance in Europe in 2017–2019: an ECDC pilot study. <i>European Respiratory Journal</i> , 2021, 57, 2002272.	3.1	27
13	Rapid genomic first- and second-line drug resistance prediction from clinical <i>Mycobacterium tuberculosis</i> specimens using Deeplex-MycTB. <i>European Respiratory Journal</i> , 2021, 57, 2001796.	3.1	47
14	Deep amplicon sequencing for culture-free prediction of susceptibility or resistance to 13 anti-tuberculous drugs. <i>European Respiratory Journal</i> , 2021, 57, 2002338.	3.1	58
15	Improving tuberculosis surveillance by detecting international transmission using publicly available whole genome sequencing data. <i>Eurosurveillance</i> , 2021, 26, .	3.9	9
16	Survival of hypoxia-induced dormancy is not a common feature of all strains of the <i>Mycobacterium tuberculosis</i> complex. <i>Scientific Reports</i> , 2021, 11, 2628.	1.6	6
17	Phylogenomics of <i>Mycobacterium africanum</i> reveals a new lineage and a complex evolutionary history. <i>Microbial Genomics</i> , 2021, 7, .	1.0	71
18	Design of Multidrug-Resistant Tuberculosis Treatment Regimens Based on DNA Sequencing. <i>Clinical Infectious Diseases</i> , 2021, 73, 1194-1202.	2.9	21

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19	Evaluation of the Roche cobas MTB and MTB-RIF/INH Assays in Samples from Germany and Sierra Leone. <i>Journal of Clinical Microbiology</i> , 2021, 59, .	1.8	5
20	Secretome characterization of clinical isolates from the <i>Mycobacterium abscessus</i> complex provides insight into antigenic differences. <i>BMC Genomics</i> , 2021, 22, 385.	1.2	2
21	Perspectives for systems biology in the management of tuberculosis. <i>European Respiratory Review</i> , 2021, 30, 200377.	3.0	13
22	Microevolution of <i>Mycobacterium tuberculosis</i> Subpopulations and Heteroresistance in a Patient Receiving 27 Years of Tuberculosis Treatment in Germany. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0252020.	1.4	4
23	Implementation of whole genome sequencing for tuberculosis diagnostics in a low-middle income, high MDR-TB burden country. <i>Scientific Reports</i> , 2021, 11, 15333.	1.6	13
24	Is the new WHO definition of extensively drug-resistant tuberculosis easy to apply in practice?. <i>European Respiratory Journal</i> , 2021, 58, 2100959.	3.1	5
25	<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. <i>Microbial Genomics</i> , 2021, 7, .	1.0	9
26	The global outbreak of <i>Mycobacterium chimaera</i> infections in cardiac surgery—a systematic review of whole-genome sequencing studies and joint analysis. <i>Clinical Microbiology and Infection</i> , 2021, 27, 1613-1620.	2.8	14
27	High potency of sequential therapy with only β -lactam antibiotics. <i>ELife</i> , 2021, 10, .	2.8	29
28	A multi-phenotype genome-wide association study of clades causing tuberculosis in a Ghanaian- and South African cohort. <i>Genomics</i> , 2021, 113, 1802-1815.	1.3	8
29	WNT6/ACC2-induced storage of triacylglycerols in macrophages is exploited by <i>Mycobacterium tuberculosis</i> . <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	17
30	Transmission patterns of rifampicin resistant <i>Mycobacterium tuberculosis</i> complex strains in Cameroon: a genomic epidemiological study. <i>BMC Infectious Diseases</i> , 2021, 21, 891.	1.3	3
31	Role of Epistasis in Amikacin, Kanamycin, Bedaquiline, and Clofazimine Resistance in <i>Mycobacterium tuberculosis</i> Complex. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0116421.	1.4	35
32	Population structure, biogeography and transmissibility of <i>Mycobacterium tuberculosis</i> . <i>Nature Communications</i> , 2021, 12, 6099.	5.8	59
33	Evaluation of whole-genome sequence data analysis approaches for short- and long-read sequencing of <i>Mycobacterium tuberculosis</i> . <i>Microbial Genomics</i> , 2021, 7, .	1.0	13
34	Two Pandemics, One Challenge—Leveraging Molecular Test Capacity of Tuberculosis Laboratories for Rapid COVID-19 Case-Finding. <i>Emerging Infectious Diseases</i> , 2020, 26, 2549-2554.	2.0	14
35	MDR <i>M. tuberculosis</i> outbreak clone in Eswatini missed by Xpert has elevated bedaquiline resistance dated to the pre-treatment era. <i>Genome Medicine</i> , 2020, 12, 104.	3.6	50
36	Perspective for Precision Medicine for Tuberculosis. <i>Frontiers in Immunology</i> , 2020, 11, 566608.	2.2	35

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37	Antimicrobial Susceptibility and Phylogenetic Relations in a German Cohort Infected with <i>Mycobacterium abscessus</i> . <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	18
38	Phenotypic and Transcriptomic Analyses of Seven Clinical <i>Stenotrophomonas maltophilia</i> Isolates Identify a Small Set of Shared and Commonly Regulated Genes Involved in the Biofilm Lifestyle. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	12
39	Evolutionary Approaches to Combat Antibiotic Resistance: Opportunities and Challenges for Precision Medicine. <i>Frontiers in Immunology</i> , 2020, 11, 1938.	2.2	35
40	Population Structure of <i>Mycobacterium bovis</i> in Germany: a Long-Term Study Using Whole-Genome Sequencing Combined with Conventional Molecular Typing Methods. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	10
41	Detection of low-frequency resistance-mediating SNPs in next-generation sequencing data of <i>Mycobacterium tuberculosis</i> complex strains with binoSNP. <i>Scientific Reports</i> , 2020, 10, 7874.	1.6	14
42	Phylogenetically informative mutations in genes implicated in antibiotic resistance in <i>Mycobacterium tuberculosis</i> complex. <i>Genome Medicine</i> , 2020, 12, 27.	3.6	58
43	Comparative analysis of phenotypic and genotypic antibiotic susceptibility patterns in <i>Mycobacterium avium</i> complex. <i>International Journal of Infectious Diseases</i> , 2020, 93, 320-328.	1.5	19
44	GenomeMap: Within-Species Genome-Wide dN/dS Estimation from over 10,000 Genomes. <i>Molecular Biology and Evolution</i> , 2020, 37, 2450-2460.	3.5	25
45	<i>Mycobacterium tuberculosis</i> Complex Lineage 3 as Causative Agent of Pulmonary Tuberculosis, Eastern Sudan. <i>Emerging Infectious Diseases</i> , 2020, 26, 427-436.	2.0	14
46	Multidrug- and Extensively Drug-Resistant <i>Mycobacterium tuberculosis</i> Beijing Clades, Ukraine, 2015. <i>Emerging Infectious Diseases</i> , 2020, 26, 481-490.	2.0	23
47	Bedaquiline-Resistant Tuberculosis: Dark Clouds on the Horizon. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 201, 1564-1568.	2.5	59
48	A landscape of genomic alterations at the root of a near-untreatable tuberculosis epidemic. <i>BMC Medicine</i> , 2020, 18, 24.	2.3	19
49	The phylogenetic landscape and nosocomial spread of the multidrug-resistant opportunist <i>Stenotrophomonas maltophilia</i> . <i>Nature Communications</i> , 2020, 11, 2044.	5.8	76
50	A publicly accessible database for <i>Clostridioides difficile</i> genome sequences supports tracing of transmission chains and epidemics. <i>Microbial Genomics</i> , 2020, 6, .	1.0	22
51	Insertion and deletion evolution reflects antibiotics selection pressure in a <i>Mycobacterium tuberculosis</i> outbreak. <i>PLoS Pathogens</i> , 2020, 16, e1008357.	2.1	22
52	The role of IS6110 in micro- and macroevolution of <i>Mycobacterium tuberculosis</i> lineage 2. <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106559.	1.2	9
53	Population structure of drug-resistant <i>Mycobacterium tuberculosis</i> in Central Asia. <i>BMC Infectious Diseases</i> , 2019, 19, 908.	1.3	13
54	Accuracy of whole-genome sequencing to determine recent tuberculosis transmission: an 11-year population-based study in Hamburg, Germany. <i>European Respiratory Journal</i> , 2019, 54, 1901154.	3.1	21

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55	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.	5.2	92
56	Emergence of Low-level Delamanid and Bedaquiline Resistance During Extremely Drug-resistant Tuberculosis Treatment. <i>Clinical Infectious Diseases</i> , 2019, 69, 1229-1231.	2.9	55
57	Whole genome sequencing of <i>Mycobacterium tuberculosis</i> : current standards and open issues. <i>Nature Reviews Microbiology</i> , 2019, 17, 533-545.	13.6	237
58	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, .	1.4	20
59	Isoniazid Resistance in <i>Mycobacterium tuberculosis</i> Is a Heterogeneous Phenotype Composed of Overlapping MIC Distributions with Different Underlying Resistance Mechanisms. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	32
60	DeepAMR for predicting co-occurrent resistance of <i>Mycobacterium tuberculosis</i> . <i>Bioinformatics</i> , 2019, 35, 3240-3249.	1.8	38
61	New World Health Organization Treatment Recommendations for Multidrug-Resistant Tuberculosis: Are We Well Enough Prepared?. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2019, 200, 514-515.	2.5	10
62	Reference set of <i>Mycobacterium tuberculosis</i> clinical strains: A tool for research and product development. <i>PLoS ONE</i> , 2019, 14, e0214088.	1.1	56
63	Molecular drug susceptibility testing and strain typing of tuberculosis by DNA hybridization. <i>PLoS ONE</i> , 2019, 14, e0212064.	1.1	4
64	SNP-IT Tool for Identifying Subspecies and Associated Lineages of <i>Mycobacterium tuberculosis</i> Complex. <i>Emerging Infectious Diseases</i> , 2019, 25, 482-488.	2.0	64
65	Longitudinal Outbreak of Multidrug-Resistant Tuberculosis in a Hospital Setting, Serbia. <i>Emerging Infectious Diseases</i> , 2019, 25, 555-558.	2.0	8
66	Same meat, different gravy: ignore the new names of mycobacteria. <i>European Respiratory Journal</i> , 2019, 54, 1900795.	3.1	54
67	Rapid microarray-based assay for detection of pyrazinamide resistant <i>Mycobacterium tuberculosis</i> . <i>Diagnostic Microbiology and Infectious Disease</i> , 2019, 94, 147-154.	0.8	5
68	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, .	1.8	29
69	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, .	1.4	22
70	TB sequel: incidence, pathogenesis and risk factors of long-term medical and social sequelae of pulmonary TB – a study protocol. <i>BMC Pulmonary Medicine</i> , 2019, 19, 4.	0.8	45
71	No Evidence for Acquired Mutations Associated with Cytochrome <i>bc₁</i> Inhibitor Resistance in 13,559 Clinical <i>Mycobacterium tuberculosis</i> Complex Isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	7
72	Antibiotic resistance prediction for <i>Mycobacterium tuberculosis</i> from genome sequence data with Mykrobe. <i>Wellcome Open Research</i> , 2019, 4, 191.	0.9	103

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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, .	3.9	42
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, 3936.	1.6	10
75	Risk of tuberculosis transmission among healthcare workers. <i>ERJ Open Research</i> , 2018, 4, 00161-2017.	1.1	13
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.	4.6	121
77	EUSeqMyTB to set standards and build capacity for whole genome sequencing for tuberculosis in the EU. <i>Lancet Infectious Diseases</i> , The, 2018, 18, 377.	4.6	25
78	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.	4.6	119
79	New Approaches and Therapeutic Options for <i>Mycobacterium tuberculosis</i> in a Dormant State. <i>Clinical Microbiology Reviews</i> , 2018, 31, .	5.7	55
80	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, .	1.8	10
81	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, .	1.4	83
82	MTBseq: a comprehensive pipeline for whole genome sequence analysis of <i>Mycobacterium tuberculosis</i> complex isolates. <i>PeerJ</i> , 2018, 6, e5895.	0.9	148
83	The Genetic Transformation of <i>Chlamydia pneumoniae</i> . <i>MSphere</i> , 2018, 3, .	1.3	23
84	Drug-resistance profiling and transmission dynamics of multidrug-resistant <i>Mycobacterium tuberculosis</i> in Saudi Arabia revealed by whole genome sequencing. <i>Infection and Drug Resistance</i> , 2018, Volume 11, 2219-2229.	1.1	17
85	Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing. <i>New England Journal of Medicine</i> , 2018, 379, 1403-1415.	13.9	405
86	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.	4.6	118
87	Integrating standardized whole genome sequence analysis with a global <i>Mycobacterium tuberculosis</i> antibiotic resistance knowledgebase. <i>Scientific Reports</i> , 2018, 8, 15382.	1.6	75
88	Pathogen-based precision medicine for drug-resistant tuberculosis. <i>PLoS Pathogens</i> , 2018, 14, e1007297.	2.1	43
89	The relationship between transmission time and clustering methods in <i>Mycobacterium tuberculosis</i> epidemiology. <i>EBioMedicine</i> , 2018, 37, 410-416.	2.7	106
90	Fast update of undetected <i>Mycobacterium chimaera</i> infections to reveal unsuspected cases. <i>Journal of Hospital Infection</i> , 2018, 100, 451-455.	1.4	8

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91	Molecular epidemiology and drug resistance patterns of Mycobacterium tuberculosis complex isolates from university students and the local community in Eastern Ethiopia. PLoS ONE, 2018, 13, e0198054.	1.1	11
92	Whole genome sequencing of <i>Mycobacterium tuberculosis</i> . European Respiratory Journal, 2018, 52, 1801163.	3.1	35
93	Mycobacterium bovis Persistence in Two Different Captive Wild Animal Populations in Germany: a Longitudinal Molecular Epidemiological Study Revealing Pathogen Transmission by Whole-Genome Sequencing. Journal of Clinical Microbiology, 2018, 56, .	1.8	12
94	Comparative genomics of Mycobacterium africanum Lineage 5 and Lineage 6 from Ghana suggests distinct ecological niches. Scientific Reports, 2018, 8, 11269.	1.6	34
95	Reply to Dookie et al., "Whole-Genome Sequencing To Guide the Selection of Treatment for Drug-Resistant Tuberculosis". Antimicrobial Agents and Chemotherapy, 2018, 62, .	1.4	1
96	Smear Microscopy for Diagnosis of Pulmonary Tuberculosis in Eastern Sudan. Tuberculosis Research and Treatment, 2018, 2018, 1-8.	0.2	7
97	Analysis of Phylogenetic Variation of Stenotrophomonas maltophilia Reveals Human-Specific Branches. Frontiers in Microbiology, 2018, 9, 806.	1.5	39
98	Aortic Endograft Infection with Mycobacterium chimaera and Granulicatella adiacens, Switzerland, 2014. Emerging Infectious Diseases, 2018, 24, 1700-1704.	2.0	2
99	Harmonized Genome Wide Typing of Tubercle Bacilli Using a Web-Based Gene-By-Gene Nomenclature System. EBioMedicine, 2018, 34, 131-138.	2.7	42
100	Mycobacterium abscessus, a taxonomic puzzle. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 467-469.	0.8	21
101	Compensatory evolution drives multidrug-resistant tuberculosis in Central Asia. ELife, 2018, 7, .	2.8	93
102	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.	0.2	2
103	High Interlaboratory Reproducibility and Accuracy of Next-Generation-Sequencing-Based Bacterial Genotyping in a Ring Trial. Journal of Clinical Microbiology, 2017, 55, 908-913.	1.8	75
104	Some Synonymous and Nonsynonymous <i>gyrA</i> Mutations in Mycobacterium tuberculosis Lead to Systematic False-Positive Fluoroquinolone Resistance Results with the Hain GenoType MTBDR Assays. Antimicrobial Agents and Chemotherapy, 2017, 61, .	1.4	29
105	Multiplex detection of extensively drug resistant tuberculosis using binary deoxyribozyme sensors. Biosensors and Bioelectronics, 2017, 94, 176-183.	5.3	29
106	Mycobacterium tuberculosis resistance prediction and lineage classification from genome sequencing: comparison of automated analysis tools. Scientific Reports, 2017, 7, 46327.	1.6	82
107	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
108	Extent of transmission captured by contact tracing in a tuberculosis high endemic setting. European Respiratory Journal, 2017, 49, 1601851.	3.1	5

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109	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.	2.8	36
110	Role of Alanine Racemase Mutations in Mycobacterium tuberculosis <scp>d</scp> -Cycloserine Resistance. Antimicrobial Agents and Chemotherapy, 2017, 61, .	1.4	24
111	Aiming for zero tuberculosis transmission in low-burden countries. Lancet Respiratory Medicine,the, 2017, 5, 846-848.	5.2	13
112	Global outbreak of severe Mycobacterium chimaera disease after cardiac surgery: a molecular epidemiological study. Lancet Infectious Diseases, The, 2017, 17, 1033-1041.	4.6	198
113	<i>Mycobacterium abscessus</i> in patients with cystic fibrosis: low impact of inter-human transmission in Italy. European Respiratory Journal, 2017, 50, 1602525.	3.1	63
114	The Evolution of Strain Typing in the Mycobacterium tuberculosis Complex. Advances in Experimental Medicine and Biology, 2017, 1019, 43-78.	0.8	43
115	Whole genome sequencing for M/XDR tuberculosis surveillance and for resistance testing. Clinical Microbiology and Infection, 2017, 23, 161-166.	2.8	61
116	A standardised method for interpreting the association between mutations and phenotypic drug resistance in<i>Mycobacterium tuberculosis</i>. European Respiratory Journal, 2017, 50, 1701354.	3.1	273
117	Impact of Genetic Diversity on the Biology ofMycobacterium tuberculosisComplex Strains. , 2017, , 475-493.		0
118	Integration of molecular typing results into tuberculosis surveillance in Germanyâ€”A pilot study. PLoS ONE, 2017, 12, e0188356.	1.1	5
119	New<i>Mycobacterium tuberculosis</i> Complex Sublineage, Brazzaville, Congo. Emerging Infectious Diseases, 2017, 23, 423-429.	2.0	35
120	An application of competitive reporter monitored amplification (CMA) for rapid detection of single nucleotide polymorphisms (SNPs). PLoS ONE, 2017, 12, e0183561.	1.1	2
121	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, .	3.9	26
122	Drug susceptibility profiles of pulmonary Mycobacterium tuberculosis isolates from patients in informal urban settlements in Nairobi, Kenya. BMC Infectious Diseases, 2016, 16, 583.	1.3	7
123	High Sequence Variability of the ppE18 Gene of Clinical Mycobacterium tuberculosis Complex Strains Potentially Impacts Effectivity of Vaccine Candidate M72/AS01E. PLoS ONE, 2016, 11, e0152200.	1.1	22
124	In reply. International Journal of Tuberculosis and Lung Disease, 2016, 20, 424-424.	0.6	0
125	Population-based resistance of Mycobacterium tuberculosis isolates to pyrazinamide and fluoroquinolones: results from a multicountry surveillance project. Lancet Infectious Diseases, The, 2016, 16, 1185-1192.	4.6	151
126	Delamanid susceptibility testing of<i>Mycobacterium tuberculosis</i> using the resazurin microtitre assay and the BACTECâ„¢,¢ MGITâ„¢,¢ 960 system. Journal of Antimicrobial Chemotherapy, 2016, 71, 1532-1539.	1.3	68

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127	Tuberculosis Treatment Outcome and Drug Resistance in Lambaré, Gabon: A Prospective Cohort Study. <i>American Journal of Tropical Medicine and Hygiene</i> , 2016, 95, 472-480.	0.6	19
128	A snapshot of the predominant single nucleotide polymorphism cluster groups of <i>Mycobacterium tuberculosis</i> clinical isolates in Delhi, India. <i>Tuberculosis</i> , 2016, 100, 72-81.	0.8	5
129	Impact of Genetic Diversity on the Biology of <i>Mycobacterium tuberculosis</i> Complex Strains. <i>Microbiology Spectrum</i> , 2016, 4, .	1.2	26
130	Tracing <i>Mycobacterium tuberculosis</i> transmission by whole genome sequencing in a high incidence setting: a retrospective population-based study in East Greenland. <i>Scientific Reports</i> , 2016, 6, 33180.	1.6	51
131	Reply: Call for Regular Susceptibility Testing of Bedaquiline and Delamanid. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2016, 194, 1171-1172.	2.5	5
132	<i>Mycobacterium tuberculosis</i> lineage 4 comprises globally distributed and geographically restricted sublineages. <i>Nature Genetics</i> , 2016, 48, 1535-1543.	9.4	326
133	Drug resistance and population structure of <i>M.tuberculosis</i> isolates from prisons and communities in Ethiopia. <i>BMC Infectious Diseases</i> , 2016, 16, 687.	1.3	22
134	Rapid, comprehensive, and affordable mycobacterial diagnosis with whole-genome sequencing: a prospective study. <i>Lancet Respiratory Medicine</i> , 2016, 4, 49-58.	5.2	282
135	Delamanid and Bedaquiline Resistance in Ancestral Beijing Genotype Causing Extensively Drug-Resistant Tuberculosis in a Tibetan Refugee. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2016, 193, 337-340.	2.5	125
136	Whole genome sequencing of <i>Mycobacterium tuberculosis</i> for detection of recent transmission and tracing outbreaks: A systematic review. <i>Tuberculosis</i> , 2016, 98, 77-85.	0.8	108
137	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.	0.6	123
138	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.	0.8	190
139	Rapid antibiotic-resistance predictions from genome sequence data for <i>Staphylococcus aureus</i> and <i>Mycobacterium tuberculosis</i> . <i>Nature Communications</i> , 2015, 6, 10063.	5.8	479
140	Drug-resistance mechanisms and tuberculosis drugs. <i>Lancet</i> , 2015, 385, 305-307.	6.3	22
141	Evolutionary history and global spread of the <i>Mycobacterium tuberculosis</i> Beijing lineage. <i>Nature Genetics</i> , 2015, 47, 242-249.	9.4	466
142	Detection of Drug-Resistant Tuberculosis by Xpert MTB/RIF in Swaziland. <i>New England Journal of Medicine</i> , 2015, 372, 1181-1182.	13.9	146
143	Direct DNA Extraction from <i>Mycobacterium tuberculosis</i> Frozen Stocks as a Reculture-Independent Approach to Whole-Genome Sequencing. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2716-2719.	1.8	16
144	Whole-genome sequencing for prediction of <i>Mycobacterium tuberculosis</i> drug susceptibility and resistance: a retrospective cohort study. <i>Lancet Infectious Diseases</i> , 2015, 15, 1193-1202.	4.6	553

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145	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.	1.9	32
146	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.	1.8	22
147	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.	1.8	257
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