

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	Proposal for Standardization of Optimized Mycobacterial Interspersed Repetitive Unit-Variable-Number Tandem Repeat Typing of Mycobacterium tuberculosis. <i>Journal of Clinical Microbiology</i> , 2006, 44, 4498-4510.	1.8	1,181
2	Mycobacterium tuberculosis complex genetic diversity: mining the fourth international spoligotyping database (SpolDB4) for classification, population genetics and epidemiology. <i>BMC Microbiology</i> , 2006, 6, 23.	1.3	900
3	Out-of-Africa migration and Neolithic coexpansion of Mycobacterium tuberculosis with modern humans. <i>Nature Genetics</i> , 2013, 45, 1176-1182.	9.4	900
4	Variable host-pathogen compatibility in Mycobacterium tuberculosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 2869-2873.	3.3	897
5	Human T cell epitopes of Mycobacterium tuberculosis are evolutionarily hyperconserved. <i>Nature Genetics</i> , 2010, 42, 498-503.	9.4	642
6	Whole-genome sequencing for prediction of Mycobacterium tuberculosis drug susceptibility and resistance: a retrospective cohort study. <i>Lancet Infectious Diseases</i> , The, 2015, 15, 1193-1202.	4.6	553
7	High Functional Diversity in Mycobacterium tuberculosis Driven by Genetic Drift and Human Demography. <i>PLoS Biology</i> , 2008, 6, e311.	2.6	507
8	Pre-Columbian mycobacterial genomes reveal seals as a source of New World human tuberculosis. <i>Nature</i> , 2014, 514, 494-497.	13.7	506
9	Rapid antibiotic-resistance predictions from genome sequence data for Staphylococcus aureus and Mycobacterium tuberculosis. <i>Nature Communications</i> , 2015, 6, 10063.	5.8	479
10	Whole-genome sequencing of rifampicin-resistant Mycobacterium tuberculosis strains identifies compensatory mutations in RNA polymerase genes. <i>Nature Genetics</i> , 2012, 44, 106-110.	9.4	475
11	Evolutionary history and global spread of the Mycobacterium tuberculosis Beijing lineage. <i>Nature Genetics</i> , 2015, 47, 242-249.	9.4	466
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.	5.2	459
13	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.	3.9	425
14	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
15	Origin, Spread and Demography of the Mycobacterium tuberculosis Complex. <i>PLoS Pathogens</i> , 2008, 4, e1000160.	2.1	378
16	Genotyping of Genetically Monomorphic Bacteria: DNA Sequencing in Mycobacterium tuberculosis Highlights the Limitations of Current Methodologies. <i>PLoS ONE</i> , 2009, 4, e7815.	1.1	377
17	Evaluation and Strategy for Use of MIRU-VNTR, a Multifunctional Database for Online Analysis of Genotyping Data and Phylogenetic Identification of Mycobacterium tuberculosis Complex Isolates. <i>Journal of Clinical Microbiology</i> , 2008, 46, 2692-2699.	1.8	366
18	Predictive Value of a Whole Blood IFN- γ Assay for the Development of Active Tuberculosis Disease after Recent Infection with Mycobacterium tuberculosis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2008, 177, 1164-1170.	2.5	347

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19	Mycobacterium tuberculosis lineage 4 comprises globally distributed and geographically restricted sublineages. <i>Nature Genetics</i> , 2016, 48, 1535-1543.	9.4	326
20	MIRU-VNTRplus: a web tool for polyphasic genotyping of Mycobacterium tuberculosis complex bacteria. <i>Nucleic Acids Research</i> , 2010, 38, W326-W331.	6.5	287
21	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
22	Negative and Positive Predictive Value of a Whole-Blood Interferon- γ Release Assay for Developing Active Tuberculosis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2011, 183, 88-95.	2.5	275
23	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.	3.1	273
24	PhyResSE: a Web Tool Delineating Mycobacterium tuberculosis Antibiotic Resistance and Lineage from Whole-Genome Sequencing Data. <i>Journal of Clinical Microbiology</i> , 2015, 53, 1908-1914.	1.8	257
25	Whole genome sequencing of Mycobacterium tuberculosis: current standards and open issues. <i>Nature Reviews Microbiology</i> , 2019, 17, 533-545.	13.6	237
26	Functional Genetic Diversity among Mycobacterium tuberculosis Complex Clinical Isolates: Delineation of Conserved Core and Lineage-Specific Transcriptomes during Intracellular Survival. <i>PLoS Pathogens</i> , 2010, 6, e1000988.	2.1	228
27	Frequency of rpoB Mutations Inside and Outside the Cluster I Region in Rifampin-Resistant Clinical Mycobacterium tuberculosis Isolates. <i>Journal of Clinical Microbiology</i> , 2001, 39, 107-110.	1.8	204
28	Assessment of an Optimized Mycobacterial Interspersed Repetitive- Unit-Variable-Number Tandem-Repeat Typing System Combined with Spoligotyping for Population-Based Molecular Epidemiology Studies of Tuberculosis. <i>Journal of Clinical Microbiology</i> , 2007, 45, 691-697.	1.8	198
29	Global outbreak of severe Mycobacterium chimaera disease after cardiac surgery: a molecular epidemiological study. <i>Lancet Infectious Diseases</i> , 2017, 17, 1033-1041.	4.6	198
30	Definition of the Beijing/W Lineage of Mycobacterium tuberculosis on the Basis of Genetic Markers. <i>Journal of Clinical Microbiology</i> , 2004, 42, 4040-4049.	1.8	197
31	Use of the Genotype MTBDR Assay for Rapid Detection of Rifampin and Isoniazid Resistance in Mycobacterium tuberculosis Complex Isolates. <i>Journal of Clinical Microbiology</i> , 2005, 43, 3699-3703.	1.8	195
32	Autophagy Gene Variant IRGM Δ 261T Contributes to Protection from Tuberculosis Caused by Mycobacterium tuberculosis but Not by M. africanum Strains. <i>PLoS Pathogens</i> , 2009, 5, e1000577.	2.1	193
33	Emended description of Mycobacterium abscessus, Mycobacterium abscessus subsp. abscessus and Mycobacterium abscessus subsp. bolletii and designation of Mycobacterium abscessus subsp. massiliense comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 4471-4479.	0.8	190
34	Whole-Genome-Based Mycobacterium tuberculosis Surveillance: a Standardized, Portable, and Expandable Approach. <i>Journal of Clinical Microbiology</i> , 2014, 52, 2479-2486.	1.8	175
35	Mycobacterium tuberculosis Wears What It Eats. <i>Cell Host and Microbe</i> , 2010, 8, 68-76.	5.1	166
36	Bacterial Artificial Chromosome-Based Comparative Genomic Analysis Identifies Mycobacterium microti as a Natural ESAT-6 Deletion Mutant. <i>Infection and Immunity</i> , 2002, 70, 5568-5578.	1.0	152

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37	Population-based resistance of <i>Mycobacterium tuberculosis</i> isolates to pyrazinamide and fluoroquinolones: results from a multicountry surveillance project. <i>Lancet Infectious Diseases</i> , The, 2016, 16, 1185-1192.	4.6	151
38	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
39	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
40	RIDOM: Comprehensive and public sequence database for identification of <i>Mycobacterium</i> species. <i>BMC Infectious Diseases</i> , 2003, 3, 26.	1.3	141
41	Differentiation of Clinical <i>Mycobacterium tuberculosis</i> Complex Isolates by <i>gyrB</i> DNA Sequence Polymorphism Analysis. <i>Journal of Clinical Microbiology</i> , 2000, 38, 3231-3234.	1.8	141
42	Clade-Specific Virulence Patterns of <i>Mycobacterium tuberculosis</i> Complex Strains in Human Primary Macrophages and Aerogenically Infected Mice. <i>MBio</i> , 2013, 4, .	1.8	136
43	High Resolution Discrimination of Clinical <i>Mycobacterium tuberculosis</i> Complex Strains Based on Single Nucleotide Polymorphisms. <i>PLoS ONE</i> , 2012, 7, e39855.	1.1	129
44	Genomic Diversity among Drug Sensitive and Multidrug Resistant Isolates of <i>Mycobacterium tuberculosis</i> with Identical DNA Fingerprints. <i>PLoS ONE</i> , 2009, 4, e7407.	1.1	128
45	<i>Mycobacterium tuberculosis</i> Pyrazinamide Resistance Determinants: a Multicenter Study. <i>MBio</i> , 2014, 5, e01819-14.	1.8	125
46	Delamanid and Bedaquiline Resistance in <i>Mycobacterium tuberculosis</i> 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
47	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
48	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
49	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
50	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
51	Whole Genome Sequencing Reveals Complex Evolution Patterns of Multidrug-Resistant <i>Mycobacterium tuberculosis</i> Beijing Strains in Patients. <i>PLoS ONE</i> , 2013, 8, e82551.	1.1	117
52	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
53	<i>Mycobacterium bovis</i> subsp. <i>caprae</i> Caused One-Third of Human <i>M. bovis</i> -Associated Tuberculosis Cases Reported in Germany between 1999 and 2001. <i>Journal of Clinical Microbiology</i> , 2003, 41, 3070-3077.	1.8	108
54	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

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55	Differentiation among Members of the <i>Mycobacterium tuberculosis</i> Complex by Molecular and Biochemical Features: Evidence for Two Pyrazinamide-Susceptible Subtypes of <i>M. bovis</i> . <i>Journal of Clinical Microbiology</i> , 2000, 38, 152-157.	1.8	108
56	European 1: A globally important clonal complex of <i>Mycobacterium bovis</i> . <i>Infection, Genetics and Evolution</i> , 2011, 11, 1340-1351.	1.0	107
57	The relationship between transmission time and clustering methods in <i>Mycobacterium tuberculosis</i> epidemiology. <i>EBioMedicine</i> , 2018, 37, 410-416.	2.7	106
58	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
59	Genomic Analysis Distinguishes <i>Mycobacterium africanum</i> . <i>Journal of Clinical Microbiology</i> , 2004, 42, 3594-3599.	1.8	102
60	<i>Mycobacterium tuberculosis</i> Beijing Lineage Favors the Spread of Multidrug-Resistant Tuberculosis in the Republic of Georgia. <i>Journal of Clinical Microbiology</i> , 2010, 48, 3544-3550.	1.8	102
61	Tuberculosis Recurrence and Mortality after Successful Treatment: Impact of Drug Resistance. <i>PLoS Medicine</i> , 2006, 3, e384.	3.9	100
62	Novel <i>Mycobacterium tuberculosis</i> Complex Isolate from a Wild Chimpanzee. <i>Emerging Infectious Diseases</i> , 2013, 19, 969-976.	2.0	100
63	Epidemiology of Tuberculosis in Hamburg, Germany: Long-Term Population-Based Analysis Applying Classical and Molecular Epidemiological Techniques. <i>Journal of Clinical Microbiology</i> , 2002, 40, 532-539.	1.8	99
64	Evaluation of Genotype MTBC Assay for Differentiation of Clinical <i>Mycobacterium tuberculosis</i> Complex Isolates. <i>Journal of Clinical Microbiology</i> , 2003, 41, 2672-2675.	1.8	97
65	The Beijing genotype and drug resistant tuberculosis in the Aral Sea region of Central Asia. <i>Respiratory Research</i> , 2005, 6, 134.	1.4	96
66	Compensatory evolution drives multidrug-resistant tuberculosis in Central Asia. <i>ELife</i> , 2018, 7, .	2.8	93
67	Molecular Characterization of Rifampin- and Isoniazid-Resistant <i>Mycobacterium tuberculosis</i> Strains Isolated in Poland. <i>Journal of Clinical Microbiology</i> , 2004, 42, 2425-2431.	1.8	92
68	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
69	ALOX5 variants associated with susceptibility to human pulmonary tuberculosis. <i>Human Molecular Genetics</i> , 2007, 17, 1052-1060.	1.4	91
70	Sequence Analyses of Just Four Genes To Detect Extensively Drug-Resistant <i>Mycobacterium tuberculosis</i> Strains in Multidrug-Resistant Tuberculosis Patients Undergoing Treatment. <i>Antimicrobial Agents and Chemotherapy</i> , 2009, 53, 3353-3356.	1.4	88
71	Molecular Epidemiology of Tuberculosis among Immigrants in Hamburg, Germany. <i>Journal of Clinical Microbiology</i> , 2004, 42, 2952-2960.	1.8	86
72	Molecular epidemiology and transmission dynamics of <i>Mycobacterium tuberculosis</i> in Northwest Ethiopia: new phylogenetic lineages found in Northwest Ethiopia. <i>BMC Infectious Diseases</i> , 2013, 13, 131.	1.3	86

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73	<i>rplC</i> T460C Identified as a Dominant Mutation in Linezolid-Resistant Mycobacterium tuberculosis Strains. Antimicrobial Agents and Chemotherapy, 2012, 56, 2743-2745.	1.4	83
74	What Is Resistance? Impact of Phenotypic versus Molecular Drug Resistance Testing on Therapy for Multi- and Extensively Drug-Resistant Tuberculosis. Antimicrobial Agents and Chemotherapy, 2018, 62, .	1.4	83
75	Mycobacterium tuberculosis resistance prediction and lineage classification from genome sequencing: comparison of automated analysis tools. Scientific Reports, 2017, 7, 46327.	1.6	82
76	Stability of Mycobacterium tuberculosis IS 6110 Restriction Fragment Length Polymorphism Patterns and Spoligotypes Determined by Analyzing Serial Isolates from Patients with Drug-Resistant Tuberculosis. Journal of Clinical Microbiology, 1999, 37, 409-412.	1.8	82
77	Proposal of a Consensus Set of Hypervariable Mycobacterial Interspersed Repetitive-Unit Variable-Number Tandem-Repeat Loci for Subtyping of Mycobacterium tuberculosis Beijing Isolates. Journal of Clinical Microbiology, 2014, 52, 164-172.	1.8	81
78	Characterization of Mycobacterium caprae Isolates from Europe by Mycobacterial Interspersed Repetitive Unit Genotyping. Journal of Clinical Microbiology, 2005, 43, 4984-4992.	1.8	80
79	Significance of Mutations in embB Codon 306 for Prediction of Ethambutol Resistance in Clinical Mycobacterium tuberculosis Isolates. Antimicrobial Agents and Chemotherapy, 2006, 50, 1900-1902.	1.4	80
80	embCAB sequence variation among ethambutol-resistant Mycobacterium tuberculosis isolates without embB306 mutation. Journal of Antimicrobial Chemotherapy, 2010, 65, 1359-1367.	1.3	76
81	Phylogenetic polymorphisms in antibiotic resistance genes of the Mycobacterium tuberculosis complex. Journal of Antimicrobial Chemotherapy, 2014, 69, 1205-1210.	1.3	76
82	The phylogenetic landscape and nosocomial spread of the multidrug-resistant opportunist Stenotrophomonas maltophilia. Nature Communications, 2020, 11, 2044.	5.8	76
83	Sequence analysis for detection of first-line drug resistance in Mycobacterium tuberculosis strains from a high-incidence setting. BMC Microbiology, 2012, 12, 90.	1.3	75
84	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
85	Integrating standardized whole genome sequence analysis with a global Mycobacterium tuberculosis antibiotic resistance knowledgebase. Scientific Reports, 2018, 8, 15382.	1.6	75
86	Identification of Mycobacterium kansasii by Using a DNA Probe (AccuProbe) and Molecular Techniques. Journal of Clinical Microbiology, 1999, 37, 964-970.	1.8	75
87	Phylogenomics of Mycobacterium africanum reveals a new lineage and a complex evolutionary history. Microbial Genomics, 2021, 7, .	1.0	71
88	Risk of Acquired Drug Resistance during Short-Course Directly Observed Treatment of Tuberculosis in an Area with High Levels of Drug Resistance. Clinical Infectious Diseases, 2007, 44, 1421-1427.	2.9	68
89	Delamanid susceptibility testing of Mycobacterium tuberculosis using the resazurin microtitre assay and the BACTEC MGIT 960 system. Journal of Antimicrobial Chemotherapy, 2016, 71, 1532-1539.	1.3	68
90	Variant G57E of Mannose Binding Lectin Associated with Protection against Tuberculosis Caused by Mycobacterium africanum but not by M. tuberculosis. PLoS ONE, 2011, 6, e20908.	1.1	67

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91	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
92	<i>Mycobacterium abscessus</i> in patients with cystic fibrosis: low impact of inter-human transmission in Italy. <i>European Respiratory Journal</i> , 2017, 50, 1602525.	3.1	63
93	Whole genome sequencing for M/XDR tuberculosis surveillance and for resistance testing. <i>Clinical Microbiology and Infection</i> , 2017, 23, 161-166.	2.8	61
94	Impact of <i>fgd1</i> and <i>ddn</i> Diversity in <i>Mycobacterium tuberculosis</i> Complex on <i>In Vitro</i> Susceptibility to PA-824. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 5718-5722.	1.4	60
95	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.	2.9	59
96	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
97	Population structure, biogeography and transmissibility of <i>Mycobacterium tuberculosis</i> . <i>Nature Communications</i> , 2021, 12, 6099.	5.8	59
98	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
99	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
100	Emergence of Extensive Drug Resistance during Treatment for Multidrug-Resistant Tuberculosis. <i>New England Journal of Medicine</i> , 2008, 359, 2398-2400.	13.9	57
101	Two Cases of <i>Mycobacterium microti</i> -Derived Tuberculosis in HIV-Negative Immunocompetent Patients. <i>Emerging Infectious Diseases</i> , 2000, 6, 539-542.	2.0	57
102	Disequilibrium in Distribution of Resistance Mutations among <i>Mycobacterium tuberculosis</i> Beijing and Non-Beijing Strains Isolated from Patients in Germany. <i>Antimicrobial Agents and Chemotherapy</i> , 2005, 49, 1229-1231.	1.4	56
103	High genetic diversity among <i>Mycobacterium tuberculosis</i> complex strains from Sierra Leone. <i>BMC Microbiology</i> , 2008, 8, 103.	1.3	56
104	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
105	Importance of the Genetic Diversity within the <i>Mycobacterium tuberculosis</i> Complex for the Development of Novel Antibiotics and Diagnostic Tests of Drug Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 6080-6087.	1.4	55
106	New Approaches and Therapeutic Options for <i>Mycobacterium tuberculosis</i> in a Dormant State. <i>Clinical Microbiology Reviews</i> , 2018, 31, .	5.7	55
107	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
108	IL10 Haplotype Associated with Tuberculin Skin Test Response but Not with Pulmonary TB. <i>PLoS ONE</i> , 2009, 4, e5420.	1.1	55

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109	Same meat, different gravy: ignore the new names of mycobacteria. <i>European Respiratory Journal</i> , 2019, 54, 1900795.	3.1	54
110	Biochemical and genetic evidence for the transfer of <i>Mycobacterium tuberculosis</i> subsp. <i>caprae</i> Aranaz et al. 1999 to the species <i>Mycobacterium bovis</i> Karlson and Lessel 1970 (approved lists 1980) as <i>Mycobacterium bovis</i> subsp. <i>caprae</i> comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2002, 52, 433-436.	0.8	53
111	Transmission dynamics of pulmonary tuberculosis between autochthonous and immigrant sub-populations. <i>BMC Infectious Diseases</i> , 2009, 9, 197.	1.3	52
112	Occupational risk of tuberculosis transmission in a low incidence area. <i>Respiratory Research</i> , 2005, 6, 35.	1.4	51
113	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
114	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
115	Double infection with a Resistant and a Multidrug-Resistant Strain of <i>Mycobacterium tuberculosis</i> . <i>Emerging Infectious Diseases</i> , 2000, 6, 548-551.	2.0	50
116	Evaluation of <i>Mycobacterium tuberculosis</i> Typing Methods in a 4-Year Study in Schleswig-Holstein, Northern Germany. <i>Journal of Clinical Microbiology</i> , 2011, 49, 4173-4178.	1.8	49
117	Emergence of bedaquiline resistance in a high tuberculosis burden country. <i>European Respiratory Journal</i> , 2022, 59, 2100621.	3.1	48
118	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
119	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
120	The Evolution of Strain Typing in the <i>Mycobacterium tuberculosis</i> Complex. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1019, 43-78.	0.8	43
121	Pathogen-based precision medicine for drug-resistant tuberculosis. <i>PLoS Pathogens</i> , 2018, 14, e1007297.	2.1	43
122	<i>Mycobacterium canettii</i> is intrinsically resistant to both pyrazinamide and pyrazinoic acid. <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 1439-1440.	1.3	42
123	Harmonized Genome Wide Typing of Tubercle Bacilli Using a Web-Based Gene-By-Gene Nomenclature System. <i>EBioMedicine</i> , 2018, 34, 131-138.	2.7	42
124	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
125	Lab-on-Chip-Based Platform for Fast Molecular Diagnosis of Multidrug-Resistant Tuberculosis. <i>Journal of Clinical Microbiology</i> , 2015, 53, 3876-3880.	1.8	41
126	Tracing the Spread of <i>Clostridium difficile</i> Ribotype 027 in Germany Based on Bacterial Genome Sequences. <i>PLoS ONE</i> , 2015, 10, e0139811.	1.1	40

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127	Drug resistance-conferring mutations in <i>Mycobacterium tuberculosis</i> from Madang, Papua New Guinea. <i>BMC Microbiology</i> , 2012, 12, 191.	1.3	39
128	Analysis of Phylogenetic Variation of <i>Stenotrophomonas maltophilia</i> Reveals Human-Specific Branches. <i>Frontiers in Microbiology</i> , 2018, 9, 806.	1.5	39
129	A Pyrosequencing assay for rapid recognition of SNPs in <i>Mycobacterium tuberculosis</i> embB306 region. <i>Journal of Microbiological Methods</i> , 2005, 62, 113-120.	0.7	38
130	Pulmonary tuberculosis: Virulence of <i>Mycobacterium africanum</i> and relevance in HIV co-infection. <i>Tuberculosis</i> , 2008, 88, 482-489.	0.8	38
131	Characteristics of drug-resistant tuberculosis in Abkhazia (Georgia), a high-prevalence area in Eastern Europe. <i>Tuberculosis</i> , 2009, 89, 317-324.	0.8	38
132	A Novel Multiplex Real-Time PCR for the Identification of <i>Mycobacteria</i> Associated with Zoonotic Tuberculosis. <i>PLoS ONE</i> , 2011, 6, e23481.	1.1	38
133	DeepAMR for predicting co-occurrent resistance of <i>Mycobacterium tuberculosis</i> . <i>Bioinformatics</i> , 2019, 35, 3240-3249.	1.8	38
134	Stability of IS 6110 Restriction Fragment Length Polymorphism Patterns of <i>Mycobacterium tuberculosis</i> Strains in Actual Chains of Transmission. <i>Journal of Clinical Microbiology</i> , 2000, 38, 2563-2567.	1.8	38
135	Rapid Detection of <i>Mycobacterium tuberculosis</i> Beijing Genotype Strains by Real-Time PCR. <i>Journal of Clinical Microbiology</i> , 2006, 44, 302-306.	1.8	37
136	<i>Mycobacterium tuberculosis</i> embB Codon 306 Mutations Confer Moderately Increased Resistance to Ethambutol In Vitro and In Vivo. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 2891-2896.	1.4	36
137	Novel rapid PCR for the detection of Ile491Phe rpoB mutation of <i>Mycobacterium tuberculosis</i> , a rifampicin-resistance-conferring mutation undetected by commercial assays. <i>Clinical Microbiology and Infection</i> , 2017, 23, 267.e5-267.e7.	2.8	36
138	New <i>Mycobacterium tuberculosis</i> Complex Sublineage, Brazzaville, Congo. <i>Emerging Infectious Diseases</i> , 2017, 23, 423-429.	2.0	35
139	Whole genome sequencing of <i>Mycobacterium tuberculosis</i> . <i>European Respiratory Journal</i> , 2018, 52, 1801163.	3.1	35
140	Perspective for Precision Medicine for Tuberculosis. <i>Frontiers in Immunology</i> , 2020, 11, 566608.	2.2	35
141	Evolutionary Approaches to Combat Antibiotic Resistance: Opportunities and Challenges for Precision Medicine. <i>Frontiers in Immunology</i> , 2020, 11, 1938.	2.2	35
142	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
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