Philip Supply

List of Publications by Year
in descending order

127 papers	12,684 citations	30070 54 h-index	25787 108 g-index
132 all docs	132 docs citations	132 times ranked	6948 citing authors

#	Article	IF	Citations
1	Proposal for Standardization of Optimized Mycobacterial Interspersed Repetitive Unit-Variable-Number Tandem Repeat Typing of Mycobacterium tuberculosis. Journal of Clinical Microbiology, 2006, 44, 4498-4510.	3.9	1,181
2	Automated High-Throughput Genotyping for Study of Global Epidemiology of Mycobacterium tuberculosis Based on Mycobacterial Interspersed Repetitive Units. Journal of Clinical Microbiology, 2001, 39, 3563-3571.	3.9	559
3	Whole-genome sequencing for prediction of Mycobacterium tuberculosis drug susceptibility and resistance: a retrospective cohort study. Lancet Infectious Diseases, The, 2015, 15, 1193-1202.	9.1	553
4	Ancient Origin and Gene Mosaicism of the Progenitor of Mycobacterium tuberculosis. PLoS Pathogens, 2005, 1, e5.	4.7	469
5	Evolutionary history and global spread of the Mycobacterium tuberculosis Beijing lineage. Nature Genetics, 2015, 47, 242-249.	21.4	466
6	Variable human minisatelliteâ€like regions in the Mycobacterium tuberculosis genome. Molecular Microbiology, 2000, 36, 762-771.	2.5	461
7	Whole Genome Sequencing versus Traditional Genotyping for Investigation of a Mycobacterium tuberculosis Outbreak: A Longitudinal Molecular Epidemiological Study. PLoS Medicine, 2013, 10, e1001387.	8.4	425
8	Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing. New England Journal of Medicine, 2018, 379, 1403-1415.	27.0	405
9	High-resolution minisatellite-based typing as a portable approach to global analysis of Mycobacterium tuberculosis molecular epidemiology. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 1901-1906.	7.1	393
10	Origin, Spread and Demography of the Mycobacterium tuberculosis Complex. PLoS Pathogens, 2008, 4, e1000160.	4.7	378
11	Evaluation and Strategy for Use of MIRU-VNTRplus, a Multifunctional Database for Online Analysis of Genotyping Data and Phylogenetic Identification ofMycobacterium tuberculosisComplex Isolates. Journal of Clinical Microbiology, 2008, 46, 2692-2699.	3.9	366
12	Mycobacterium tuberculosis lineage 4 comprises globally distributed and geographically restricted sublineages. Nature Genetics, 2016, 48, 1535-1543.	21.4	326
13	MIRU-VNTRplus: a web tool for polyphasic genotyping of Mycobacterium tuberculosis complex bacteria. Nucleic Acids Research, 2010, 38, W326-W331.	14.5	287
14	Rapid, comprehensive, and affordable mycobacterial diagnosis with whole-genome sequencing: a prospective study. Lancet Respiratory Medicine,the, 2016, 4, 49-58.	10.7	282
15	Genomic analysis of smooth tubercle bacilli provides insights into ancestry and pathoadaptation of Mycobacterium tuberculosis. Nature Genetics, 2013, 45, 172-179.	21.4	264
16	Whole genome sequencing of Mycobacterium tuberculosis: current standards and open issues. Nature Reviews Microbiology, 2019, 17, 533-545.	28.6	237
17	Genotyping of the Mycobacterium tuberculosis complex using MIRUs: association with VNTR and spoligotyping for molecular epidemiology and evolutionary genetics. Infection, Genetics and Evolution, 2003, 3, 125-133.	2.3	208
18	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. Journal of Clinical Microbiology, 2007, 45, 691-697.	3.9	198

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19	Identification of novel intergenic repetitive units in a mycobacterial twoâ€component system operon. Molecular Microbiology, 1997, 26, 991-1003.	2.5	197
20	New Variable-Number Tandem-Repeat Markers for TypingMycobacterium aviumsubsp.paratuberculosisandM. aviumStrains: Comparison with IS900and IS1245Restriction Fragment Length Polymorphism Typing. Journal of Clinical Microbiology, 2007, 45, 2404-2410.	3.9	188
21	Linkage disequilibrium between minisatellite loci supports clonal evolution of Mycobacterium tuberculosis in a high tuberculosis incidence area. Molecular Microbiology, 2003, 47, 529-538.	2.5	171
22	Three-Year Population-Based Evaluation of Standardized Mycobacterial Interspersed Repetitive-Unit-Variable-Number Tandem-Repeat Typing ofMycobacterium tuberculosis. Journal of Clinical Microbiology, 2008, 46, 1398-1406.	3.9	142
23	A sister lineage of the Mycobacterium tuberculosis complex discovered in the African Great Lakes region. Nature Communications, 2020, 11, 2917.	12.8	136
24	Mixed infection and clonal representativeness of a single sputum sample in tuberculosis patients from a penitentiary hospital in Georgia. Respiratory Research, 2006, 7, 99.	3.6	135
25	Evaluation of the Epidemiological Relevance of Variable-Number Tandem-Repeat Genotyping of Mycobacterium bovis and Comparison of the Method with IS6110 Restriction Fragment Length Polymorphism Analysis and Spoligotyping. Journal of Clinical Microbiology, 2006, 44, 1951-1962.	3.9	121
26	Outbreak of multidrug-resistant tuberculosis in South Africa undetected by WHO-endorsed commercial tests: an observational study. Lancet Infectious Diseases, The, 2018, 18, 1350-1359.	9.1	118
27	The 2021 WHO catalogue of Mycobacterium tuberculosis complex mutations associated with drug resistance: a genotypic analysis. Lancet Microbe, The, 2022, 3, e265-e273.	7.3	114
28	Predominance of Ancestral Lineages ofMycobacterium tuberculosisin India. Emerging Infectious Diseases, 2006, 12, 1367-1374.	4.3	106
29	Stability of Variable-Number Tandem Repeats of Mycobacterial Interspersed Repetitive Units from 12 Loci in Serial Isolates of Mycobacterium tuberculosis. Journal of Clinical Microbiology, 2002, 40, 4561-4566.	3.9	105
30	Key experimental evidence of chromosomal DNA transfer among selected tuberculosis-causing mycobacteria. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 9876-9881.	7.1	103
31	Antibiotic resistance prediction for Mycobacterium tuberculosis from genome sequence data with Mykrobe. Wellcome Open Research, 2019, 4, 191.	1.8	103
32	Genotypic and Phenotypic Heterogeneity among Mycobacterium tuberculosis Isolates from Pulmonary Tuberculosis Patients. Journal of Clinical Microbiology, 2004, 42, 5528-5536.	3.9	100
33	Impact of HIV Infection on the Recurrence of Tuberculosis in South India. Journal of Infectious Diseases, 2010, 201, 691-703.	4.0	99
34	Compensatory evolution drives multidrug-resistant tuberculosis in Central Asia. ELife, 2018, 7, .	6.0	93
35	Discriminatory Power and Reproducibility of Novel DNA Typing Methods for Mycobacterium tuberculosis Complex Strains. Journal of Clinical Microbiology, 2005, 43, 5628-5638.	3.9	89
36	Transient Requirement of the PrrA-PrrB Two-Component System for Early Intracellular Multiplication of Mycobacterium tuberculosis. Infection and Immunity, 2002, 70, 2256-2263.	2.2	87

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37	Molecular Typing of Mycobacterium tuberculosis by Mycobacterial Interspersed Repetitive Unit-Variable-Number Tandem Repeat Analysis, a More Accurate Method for Identifying Epidemiological Links between Patients with Tuberculosis. Journal of Clinical Microbiology, 2005, 43, 4473-4479.	3.9	85
38	Functional Complementation of a Null Mutation of the Yeast Saccharomyces cerevisiae Plasma Membrane H+-ATPase by a Plant H+-ATPase Gene. Journal of Biological Chemistry, 1995, 270, 23828-23837.	3.4	84
39	Determination of Genotypic Diversity ofMycobacterium aviumSubspecies from Human and Animal Origins by Mycobacterial Interspersed Repetitive-Unit-Variable-Number Tandem-Repeat and IS1311Restriction Fragment Length Polymorphism Typing Methods. Journal of Clinical Microbiology, 2010, 48, 1026-1034.	3.9	83
40	Use of Mycobacterial Interspersed Repetitive Unit-Variable-Number Tandem Repeat Typing To Examine Genetic Diversity of Mycobacterium tuberculosis in Singapore. Journal of Clinical Microbiology, 2004, 42, 1986-1993.	3.9	81
41	Proposal of a Consensus Set of Hypervariable Mycobacterial Interspersed Repetitive-Unitâ€“Variable-Number Tandem-Repeat Loci for Subtyping of Mycobacterium tuberculosis Beijing Isolates. Journal of Clinical Microbiology, 2014, 52, 164-172.	3.9	81
42	pks5-recombination-mediated surface remodelling in Mycobacterium tuberculosis emergence. Nature Microbiology, 2016, 1, 15019.	13.3	81
43	Utility of Fast Mycobacterial Interspersed Repetitive Unit–Variable Number Tandem Repeat Genotyping in Clinical Mycobacteriological Analysis. Clinical Infectious Diseases, 2004, 39, 783-789.	5.8	78
44	A glimpse into the past and predictions for the future: the molecular evolution of the tuberculosis agent. Molecular Microbiology, 2014, 93, 835-852.	2.5	76
45	Comparative genomics of the dairy isolate Streptococcus macedonicus ACA-DC 198 against related members of the Streptococcus bovis/Streptococcus equinus complex. BMC Genomics, 2014, 15, 272.	2.8	74
46	Genetic Diversity of Mycobacterium tuberculosis Isolates from a Tertiary Care Tuberculosis Hospital in South Korea. Journal of Clinical Microbiology, 2010, 48, 387-394.	3.9	73
47	First Molecular Epidemiology Study of Mycobacterium tuberculosis in Burkina Faso. Journal of Clinical Microbiology, 2007, 45, 921-927.	3.9	71
48	Use of Variable-Number Tandem-Repeat Typing To Differentiate Mycobacterium tuberculosis Beijing Family Isolates from Hong Kong and Comparison with IS 6110 Restriction Fragment Length Polymorphism Typing and Spoligotyping. Journal of Clinical Microbiology, 2005, 43, 314-320.	3.9	69
49	Multilocus Variable-Number Tandem Repeat Typing of Mycobacterium ulcerans. Journal of Clinical Microbiology, 2005, 43, 1546-1551.	3.9	66
50	Microevolution of Mycobacterium tuberculosis in a Tuberculosis Patient. Journal of Clinical Microbiology, 2010, 48, 3813-3816.	3.9	65
51	Molecular characterization of the mycobacterial SenX3â€“RegX3 two-component system: evidence for autoregulation. Microbiology (United Kingdom), 2000, 146, 3091-3098.	1.8	62
52	Specific Differentiation between Mycobacterium bovis BCG and Virulent Strains of the Mycobacterium tuberculosis Complex. Journal of Clinical Microbiology, 1998, 36, 2471-2476.	3.9	60
53	Diversity and Evolution of Mycobacterium tuberculosis: Moving to Whole-Genome-Based Approaches. Cold Spring Harbor Perspectives in Medicine, 2014, 4, a021188-a021188.	6.2	59
54	Deep amplicon sequencing for culture-free prediction of susceptibility or resistance to 13 anti-tuberculous drugs. European Respiratory Journal, 2021, 57, 2002338.	6.7	58

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55	Identification of a New DNA Region Specific for Members of Mycobacterium tuberculosis Complex. Journal of Clinical Microbiology, 1998, 36, 937-943.	3.9	57
56	Combined Multilocus Short-Sequence-Repeat and Mycobacterial Interspersed Repetitive Unit-Variable-Number Tandem-Repeat Typing of Mycobacterium avium subsp. paratuberculosis Isolates. Journal of Clinical Microbiology, 2008, 46, 4091-4094.	3.9	56
57	Inter- and Intra-subtype genotypic differences that differentiate Mycobacterium avium subspecies paratuberculosis strains. BMC Microbiology, 2012, 12, 264.	3.3	53
58	The Forest behind the Tree: Phylogenetic Exploration of a Dominant Mycobacterium tuberculosis Strain Lineage from a High Tuberculosis Burden Country. PLoS ONE, 2011, 6, e18256.	2.5	49
59	First Worldwide Proficiency Study on Variable-Number Tandem-Repeat Typing of Mycobacterium tuberculosis Complex Strains. Journal of Clinical Microbiology, 2012, 50, 662-669.	3.9	48
60	Comparative Study of IS 6110 Restriction Fragment Length Polymorphism and Variable-Number Tandem-Repeat Typing of Mycobacterium tuberculosis Isolates in the Netherlands, Based on a 5-Year Nationwide Survey. Journal of Clinical Microbiology, 2013, 51, 1193-1198.	3.9	48
61	Rapid genomic first- and second-line drug resistance prediction from clinical Mycobacterium tuberculosis specimens using Deeplex-MycTB. European Respiratory Journal, 2021, 57, 2001796.	6.7	47
62	Immunogenicity of recombinant BCG producing the GRA1 antigen from Toxoplasma gondii. Vaccine, 1999, 17, 705-714.	3.8	43
63	The Evolution of Strain Typing in the Mycobacterium tuberculosis Complex. Advances in Experimental Medicine and Biology, 2017, 1019, 43-78.	1.6	43
64	Clonal Expansion of a Globally Disseminated Lineage of Mycobacterium tuberculosis with Low IS 6110 Copy Numbers. Journal of Clinical Microbiology, 2004, 42, 5774-5782.	3.9	42
65	Importance of identifying Mycobacterium bovis as a causative agent of human tuberculosis. European Respiratory Journal, 2010, 35, 692-694.	6.7	42
66	Niche specialization and spread of Staphylococcus capitis involved in neonatal sepsis. Nature Microbiology, 2020, 5, 735-745.	13.3	40
67	Acquisition through Horizontal Gene Transfer of Plasmid pSMA198 by Streptococcus macedonicus ACA-DC 198 Points towards the Dairy Origin of the Species. PLoS ONE, 2015, 10, e0116337.	2.5	39
68	Thein vivo activation ofSaccharomyces cerevisiae plasma membrane H+-ATPase by ethanol depends on the expression of thePMA1 gene, but not of thePMA2 gene. Yeast, 1994, 10, 1439-1446.	1.7	38
69	Intracellular autoregulation of the Mycobacterium tuberculosis PrrA response regulator. Microbiology (United Kingdom), 2004, 150, 241-246.	1.8	38
70	Characterization of Ancestral Mycobacterium tuberculosis by Multiple Genetic Markers and Proposal of Genotyping Strategy. Journal of Clinical Microbiology, 2004, 42, 5058-5064.	3.9	37
71	Mycobacterial Pathogenomics and Evolution. Microbiology Spectrum, 2014, 2, MGM2-0025-2013.	3.0	36
72	How Well Do Routine Molecular Diagnostics Detect Rifampin Heteroresistance in Mycobacterium tuberculosis?. Journal of Clinical Microbiology, 2019, 57, .	3.9	36

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73	Prevalence and drivers of false-positive rifampicin-resistant Xpert MTB/RIF results: a prospective observational study in Rwanda. Lancet Microbe, The, 2020, 1, e74-e83.	7.3	35
74	One year nationwide evaluation of 24-locus MIRU-VNTR genotyping on Slovenian Mycobacterium tuberculosis isolates. Respiratory Medicine, 2011, 105, S67-S73.	2.9	32
75	Horizontal acquisition of a hypoxia-responsive molybdenum cofactor biosynthesis pathway contributed to Mycobacterium tuberculosis pathoadaptation. PLoS Pathogens, 2017, 13, e1006752.	4.7	32
76	Evaluation of 24-locus MIRU-VNTR in extrapulmonary specimens: Study from a tertiary centre in Mumbai. Tuberculosis, 2012, 92, 264-272.	1.9	31
77	Pan-genome multilocus sequence typing and outbreak-specific reference-based single nucleotide polymorphism analysis to resolve two concurrent Staphylococcus aureus outbreaks in neonatal services. Clinical Microbiology and Infection, 2016, 22, 520-526.	6.0	29
78	Culture and Next-generation sequencing-based drug susceptibility testing unveil high levels of drug-resistant-TB in Djibouti: results from the first national survey. Scientific Reports, 2017, 7, 17672.	3.3	28
79	Complete Genome Sequence of the Dairy Isolate Streptococcus macedonicus ACA-DC 198. Journal of Bacteriology, 2012, 194, 1838-1839.	2.2	27
80	From Multidrug- to Extensively Drug-Resistant Tuberculosis: Upward Trends as Seen from a 15-Year Nationwide Study. PLoS ONE, 2013, 8, e63128.	2.5	26
81	Impact of Genetic Diversity on the Biology of Mycobacterium tuberculosis Complex Strains. Microbiology Spectrum, 2016, 4, .	3.0	26
82	Admixed Phylogenetic Distribution of Drug Resistant Mycobacterium tuberculosis in Saudi Arabia. PLoS ONE, 2013, 8, e55598.	2.5	26
83	Amino Acid Replacements at Seven Different Histidines in the Yeast Plasma Membrane H+â^'ATPase Reveal Critical Positions at His285 and His701â€. Biochemistry, 1996, 35, 883-890.	2.5	25
84	Molecular Typing of Mycobacterium Tuberculosis Complex by 24-Locus Based MIRU-VNTR Typing in Conjunction with Spoligotyping to Assess Genetic Diversity of Strains Circulating in Morocco. PLoS ONE, 2015, 10, e0135695.	2.5	25
85	The Biology and Epidemiology of Mycobacterium canettii. Advances in Experimental Medicine and Biology, 2017, 1019, 27-41.	1.6	25
86	GenomegaMap: Within-Species Genome-Wide dN/dS Estimation from over 10,000 Genomes. Molecular Biology and Evolution, 2020, 37, 2450-2460.	8.9	25
87	Review: Subcellular traffic of the plasma membrane H+-ATPase in Saccharomyces cerevisiae. Yeast, 1996, 12, 907-916.	1.7	24
88	MAC-INMV-SSR: a web application dedicated to genotyping members of Mycobacterium avium complex (MAC) including Mycobacterium avium subsp. paratuberculosis strains. Infection, Genetics and Evolution, 2020, 77, 104075.	2.3	24
89	Tuberculosis Transmission among Immigrants and Autochthonous Populations of the Eastern Province of Saudi Arabia. PLoS ONE, 2013, 8, e77635.	2.5	23
90	Second worldwide proficiency study on variable number of tandem repeats typing of <I>Mycobacterium tuberculosis</I> complex. International Journal of Tuberculosis and Lung Disease, 2014, 18, 594-600.	1.2	23

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91	Genetic Diversity and Population Structure of Mycobacterium tuberculosis in Casablanca, a Moroccan City with High Incidence of Tuberculosis. Journal of Clinical Microbiology, 2004, 42, 461-466.	3.9	22
92	International Spread of MDR TB from Tugela Ferry, South Africa. Emerging Infectious Diseases, 2011, 17, 2035-7.	4.3	22
93	Clustering of Tuberculosis Cases Based on Variable-Number Tandem-Repeat Typing in Relation to the Population Structure of Mycobacterium tuberculosis in the Netherlands. Journal of Clinical Microbiology, 2013, 51, 2427-2431.	3.9	22
94	Standardised PCR-based molecular epidemiology of tuberculosis. European Respiratory Journal, 2008, 31, 1077-1084.	6.7	21
95	Accuracy of whole-genome sequencing to determine recent tuberculosis transmission: an 11-year population-based study in Hamburg, Germany. European Respiratory Journal, 2019, 54, 1901154.	6.7	21
96	An Outpatient Clinic as a Potential Site of Transmission for an Outbreak of New Delhi Metallo-Î²-Lactamaseâ€“producing Klebsiella pneumoniae Sequence Type 716: A Study Using Whole-genome Sequencing. Clinical Infectious Diseases, 2019, 68, 993-1000.	5.8	21
97	Characterization of a novel variant of Mycobacterium chimaera. Journal of Medical Microbiology, 2012, 61, 1234-1239.	1.8	20
98	Strain-specific estimation of epidemic success provides insights into the transmission dynamics of tuberculosis. Scientific Reports, 2017, 7, 45326.	3.3	19
99	â€œA Re-Evaluation of M. prototuberculosisâ€• Continuing the Debate. PLoS Pathogens, 2006, 2, e95.	4.7	18
100	Evaluation of Mycobacterial Interspersed Repetitive-Unit-Variable-Number Tandem-Repeat Genotyping as Performed in Laboratories in Canada, France, and the United States. Journal of Clinical Microbiology, 2012, 50, 1830-1831.	3.9	18
101	Prospective Genotyping of Mycobacterium tuberculosis from Fresh Clinical Samples. PLoS ONE, 2014, 9, e109547.	2.5	17
102	Online tools for polyphasic analysis of Mycobacterium tuberculosis complex genotyping data: Now and next. Infection, Genetics and Evolution, 2012, 12, 748-754.	2.3	16
103	Drug-Resistant Tuberculosis, Lebanon, 2016 â€“ 2017. Emerging Infectious Diseases, 2019, 25, 564-568.	4.3	15
104	Parallel in vivo experimental evolution reveals that increased stress resistance was key for the emergence of persistent tuberculosis bacilli. Nature Microbiology, 2021, 6, 1082-1093.	13.3	15
105	Origin and Global Expansion of Mycobacterium tuberculosis Complex Lineage 3. Genes, 2022, 13, 990.	2.4	13
106	Novel transport ATPases in yeast. Biochimica Et Biophysica Acta - Bioenergetics, 1990, 1018, 200-202.	1.0	11
107	A new series of mycobacterial expression vectors for the development of live recombinant vaccines. Gene, 1996, 176, 149-154.	2.2	11
108	On the mutation rates of spoligotypes and variable numbers of tandem repeat loci of Mycobacterium tuberculosis. Infection, Genetics and Evolution, 2011, 11, 251-252.	2.3	11

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109	Patient nostril microbial flora: individual-dependency and diversity precluding prediction of Staphylococcus aureus acquisition. Clinical Microbiology and Infection, 2014, 20, 70-78.	6.0	11
110	Analysis of Mycobacterium tuberculosis genetic lineages circulating in Riga and Riga region, Latvia, isolated between 2008 and 2012. Infection, Genetics and Evolution, 2020, 78, 104126.	2.3	11
111	Changing patterns of human migrations shaped the global population structure of Mycobacterium tuberculosis in France. Scientific Reports, 2018, 8, 5855.	3.3	10
112	Occurrence and Nature of Double Alleles in Variable-Number Tandem-Repeat Patterns of More than 8,000 Mycobacterium tuberculosis Complex Isolates in The Netherlands. Journal of Clinical Microbiology, 2018, 56, .	3.9	9
113	Zoonotic tuberculosis in humans assessed by next-generation sequencing: an 18-month nationwide study in Lebanon. European Respiratory Journal, 2020, 55, 1900513.	6.7	9
114	Investigating drug resistance of Mycobacterium leprae in the Comoros: an observational deep-sequencing study. Lancet Microbe, The, 2022, 3, e693-e700.	7.3	9
115	Rapidly progressing tuberculosis outbreak in a very low risk group. European Respiratory Journal, 2014, 43, 903-906.	6.7	8
116	Functional analysis of chimerical plasma membrane H+-ATPases fromSaccharomyces cerevisiaeandSchizosaccharomyces pombe. Molecular Microbiology, 1997, 25, 261-273.	2.5	6
117	Accurate Whole-Genome Sequencing-Based Epidemiological Surveillance of Mycobacterium Tuberculosis. Methods in Microbiology, 2015, 42, 359-394.	0.8	6
118	Case Report: Dynamics of Acquired Fluoroquinolone Resistance under Standardized Short-Course Treatment of Multidrug-Resistant Tuberculosis. American Journal of Tropical Medicine and Hygiene, 2020, 103, 1443-1446.	1.4	6
119	Against All Odds: Molecular Confirmation of an Implausible Case of Bone Tuberculosis. Clinical Infectious Diseases, 2006, 42, e86-e88.	5.8	4
120	On the mutation rates of spoligotypes and variable numbers of tandem repeat loci of Mycobacterium tuberculosis: Continued-When tuning matters. Infection, Genetics and Evolution, 2011, 11, 1191.	2.3	4
121	Optimization of Standard 24-Locus Variable-Number Tandem-Repeat Typing of Mycobacterium tuberculosis Isolates: a Multicenter Perspective: TABLE 1. Journal of Clinical Microbiology, 2014, 52, 3518-3519.	3.9	4
122	Set-up and validation of mycobacterial interspersed repetitive unit-variable number of tandem repeat (MIRU-VNTR) analysis of Mycobacterium tuberculosis using BioNumerics software. PLoS ONE, 2018, 13, e0205336.	2.5	3
123	Precision tuberculosis control by genome sequencing: Benefit and challenges of a new standard. EBioMedicine, 2018, 36, 14-15.	6.1	3
124	Mycobacterial Pathogenomics and Evolution. , 0, , 27-47.		3
125	A glimpse into the past and predictions for the future: the molecular evolution of the tuberculosis agent. Molecular Microbiology, 2014, 94, 742-742.	2.5	0
126	Impact of Genetic Diversity on the Biology ofMycobacterium tuberculosisComplex Strains. , 2017, , 475-493.		0

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127	Multidrug-resistant tuberculosis outbreak in South Africa â€“ Authors' reply. Lancet Infectious Diseases, The, 2019, 19, 135-136.	9.1	0