

Philip Supply

List of Publications by Year in descending order

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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	The 2021 WHO catalogue of Mycobacterium tuberculosis complex mutations associated with drug resistance: a genotypic analysis. <i>Lancet Microbe</i> , The, 2022, 3, e265-e273.	7.3	114
2	Origin and Global Expansion of Mycobacterium tuberculosis Complex Lineage 3. <i>Genes</i> , 2022, 13, 990.	2.4	13
3	Investigating drug resistance of Mycobacterium leprae in the Comoros: an observational deep-sequencing study. <i>Lancet Microbe</i> , The, 2022, 3, e693-e700.	7.3	9
4	Rapid genomic first- and second-line drug resistance prediction from clinical Mycobacterium tuberculosis specimens using Deeplex-MycTB. <i>European Respiratory Journal</i> , 2021, 57, 2001796.	6.7	47
5	Deep amplicon sequencing for culture-free prediction of susceptibility or resistance to 13 anti-tuberculous drugs. <i>European Respiratory Journal</i> , 2021, 57, 2002338.	6.7	58
6	Parallel in vivo experimental evolution reveals that increased stress resistance was key for the emergence of persistent tuberculosis bacilli. <i>Nature Microbiology</i> , 2021, 6, 1082-1093.	13.3	15
7	MAC-INMV-SSR: a web application dedicated to genotyping members of Mycobacterium avium complex (MAC) including Mycobacterium avium subsp. paratuberculosis strains. <i>Infection, Genetics and Evolution</i> , 2020, 77, 104075.	2.3	24
8	Zoonotic tuberculosis in humans assessed by next-generation sequencing: an 18-month nationwide study in Lebanon. <i>European Respiratory Journal</i> , 2020, 55, 1900513.	6.7	9
9	Analysis of Mycobacterium tuberculosis genetic lineages circulating in Riga and Riga region, Latvia, isolated between 2008 and 2012. <i>Infection, Genetics and Evolution</i> , 2020, 78, 104126.	2.3	11
10	Prevalence and drivers of false-positive rifampicin-resistant Xpert MTB/RIF results: a prospective observational study in Rwanda. <i>Lancet Microbe</i> , The, 2020, 1, e74-e83.	7.3	35
11	A sister lineage of the Mycobacterium tuberculosis complex discovered in the African Great Lakes region. <i>Nature Communications</i> , 2020, 11, 2917.	12.8	136
12	GenomeMap: Within-Species Genome-Wide dN/dS Estimation from over 10,000 Genomes. <i>Molecular Biology and Evolution</i> , 2020, 37, 2450-2460.	8.9	25
13	Niche specialization and spread of Staphylococcus capitis involved in neonatal sepsis. <i>Nature Microbiology</i> , 2020, 5, 735-745.	13.3	40
14	Case Report: Dynamics of Acquired Fluoroquinolone Resistance under Standardized Short-Course Treatment of Multidrug-Resistant Tuberculosis. <i>American Journal of Tropical Medicine and Hygiene</i> , 2020, 103, 1443-1446.	1.4	6
15	How Well Do Routine Molecular Diagnostics Detect Rifampin Heteroresistance in Mycobacterium tuberculosis?. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	36
16	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.	6.7	21
17	Whole genome sequencing of Mycobacterium tuberculosis: current standards and open issues. <i>Nature Reviews Microbiology</i> , 2019, 17, 533-545.	28.6	237
18	Drug-Resistant Tuberculosis, Lebanon, 2016 – 2017. <i>Emerging Infectious Diseases</i> , 2019, 25, 564-568.	4.3	15

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19	An Outpatient Clinic as a Potential Site of Transmission for an Outbreak of New Delhi Metallo- β -Lactamase-producing <i>Klebsiella pneumoniae</i> Sequence Type 716: A Study Using Whole-genome Sequencing. <i>Clinical Infectious Diseases</i> , 2019, 68, 993-1000.	5.8	21
20	Multidrug-resistant tuberculosis outbreak in South Africa – Authors' reply. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 135-136.	9.1	0
21	Antibiotic resistance prediction for <i>Mycobacterium tuberculosis</i> from genome sequence data with Mykrobe. <i>Wellcome Open Research</i> , 2019, 4, 191.	1.8	103
22	Occurrence and Nature of Double Alleles in Variable-Number Tandem-Repeat Patterns of More than 8,000 <i>Mycobacterium tuberculosis</i> Complex Isolates in The Netherlands. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	9
23	Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing. <i>New England Journal of Medicine</i> , 2018, 379, 1403-1415.	27.0	405
24	Set-up and validation of mycobacterial interspersed repetitive unit-variable number of tandem repeat (MIRU-VNTR) analysis of <i>Mycobacterium tuberculosis</i> using BioNumerics software. <i>PLoS ONE</i> , 2018, 13, e0205336.	2.5	3
25	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.	9.1	118
26	Precision tuberculosis control by genome sequencing: Benefit and challenges of a new standard. <i>EBioMedicine</i> , 2018, 36, 14-15.	6.1	3
27	Changing patterns of human migrations shaped the global population structure of <i>Mycobacterium tuberculosis</i> in France. <i>Scientific Reports</i> , 2018, 8, 5855.	3.3	10
28	Compensatory evolution drives multidrug-resistant tuberculosis in Central Asia. <i>ELife</i> , 2018, 7, .	6.0	93
29	Strain-specific estimation of epidemic success provides insights into the transmission dynamics of tuberculosis. <i>Scientific Reports</i> , 2017, 7, 45326.	3.3	19
30	The Biology and Epidemiology of <i>Mycobacterium canettii</i> . <i>Advances in Experimental Medicine and Biology</i> , 2017, 1019, 27-41.	1.6	25
31	The Evolution of Strain Typing in the <i>Mycobacterium tuberculosis</i> Complex. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1019, 43-78.	1.6	43
32	Culture and Next-generation sequencing-based drug susceptibility testing unveil high levels of drug-resistant-TB in Djibouti: results from the first national survey. <i>Scientific Reports</i> , 2017, 7, 17672.	3.3	28
33	Impact of Genetic Diversity on the Biology of <i>Mycobacterium tuberculosis</i> Complex Strains. , 2017, , 475-493.		0
34	Horizontal acquisition of a hypoxia-responsive molybdenum cofactor biosynthesis pathway contributed to <i>Mycobacterium tuberculosis</i> pathoadaptation. <i>PLoS Pathogens</i> , 2017, 13, e1006752.	4.7	32
35	Key experimental evidence of chromosomal DNA transfer among selected tuberculosis-causing mycobacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9876-9881.	7.1	103
36	Impact of Genetic Diversity on the Biology of <i>Mycobacterium tuberculosis</i> Complex Strains. <i>Microbiology Spectrum</i> , 2016, 4, .	3.0	26

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37	pks5-recombination-mediated surface remodelling in Mycobacterium tuberculosis emergence. Nature Microbiology, 2016, 1, 15019.	13.3	81
38	Mycobacterium tuberculosis lineage 4 comprises globally distributed and geographically restricted sublineages. Nature Genetics, 2016, 48, 1535-1543.	21.4	326
39	Rapid, comprehensive, and affordable mycobacterial diagnosis with whole-genome sequencing: a prospective study. Lancet Respiratory Medicine, the, 2016, 4, 49-58.	10.7	282
40	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
41	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
42	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
43	Evolutionary history and global spread of the Mycobacterium tuberculosis Beijing lineage. Nature Genetics, 2015, 47, 242-249.	21.4	466
44	Accurate Whole-Genome Sequencing-Based Epidemiological Surveillance of Mycobacterium Tuberculosis. Methods in Microbiology, 2015, 42, 359-394.	0.8	6
45	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
46	Prospective Genotyping of Mycobacterium tuberculosis from Fresh Clinical Samples. PLoS ONE, 2014, 9, e109547.	2.5	17
47	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
48	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
49	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
50	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.	3.9	81
51	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
52	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
53	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
54	Rapidly progressing tuberculosis outbreak in a very low risk group. European Respiratory Journal, 2014, 43, 903-906.	6.7	8

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55	Mycobacterial Pathogenomics and Evolution. <i>Microbiology Spectrum</i> , 2014, 2, MGM2-0025-2013.	3.0	36
56	Second worldwide proficiency study on variable number of tandem repeats typing of <i>Mycobacterium tuberculosis</i> complex. <i>International Journal of Tuberculosis and Lung Disease</i> , 2014, 18, 594-600.	1.2	23
57	Genomic analysis of smooth tubercle bacilli provides insights into ancestry and pathoadaptation of <i>Mycobacterium tuberculosis</i> . <i>Nature Genetics</i> , 2013, 45, 172-179.	21.4	264
58	Whole Genome Sequencing versus Traditional Genotyping for Investigation of a <i>Mycobacterium tuberculosis</i> Outbreak: A Longitudinal Molecular Epidemiological Study. <i>PLoS Medicine</i> , 2013, 10, e1001387.	8.4	425
59	Comparative Study of IS 6110 Restriction Fragment Length Polymorphism and Variable-Number Tandem-Repeat Typing of <i>Mycobacterium tuberculosis</i> Isolates in the Netherlands, Based on a 5-Year Nationwide Survey. <i>Journal of Clinical Microbiology</i> , 2013, 51, 1193-1198.	3.9	48
60	Clustering of Tuberculosis Cases Based on Variable-Number Tandem-Repeat Typing in Relation to the Population Structure of <i>Mycobacterium tuberculosis</i> in the Netherlands. <i>Journal of Clinical Microbiology</i> , 2013, 51, 2427-2431.	3.9	22
61	From Multidrug- to Extensively Drug-Resistant Tuberculosis: Upward Trends as Seen from a 15-Year Nationwide Study. <i>PLoS ONE</i> , 2013, 8, e63128.	2.5	26
62	Tuberculosis Transmission among Immigrants and Autochthonous Populations of the Eastern Province of Saudi Arabia. <i>PLoS ONE</i> , 2013, 8, e77635.	2.5	23
63	Admixed Phylogenetic Distribution of Drug Resistant <i>Mycobacterium tuberculosis</i> in Saudi Arabia. <i>PLoS ONE</i> , 2013, 8, e55598.	2.5	26
64	Evaluation of Mycobacterial Interspersed Repetitive-Unit-Variable-Number Tandem-Repeat Genotyping as Performed in Laboratories in Canada, France, and the United States. <i>Journal of Clinical Microbiology</i> , 2012, 50, 1830-1831.	3.9	18
65	Complete Genome Sequence of the Dairy Isolate <i>Streptococcus macedonicus</i> ACA-DC 198. <i>Journal of Bacteriology</i> , 2012, 194, 1838-1839.	2.2	27
66	First Worldwide Proficiency Study on Variable-Number Tandem-Repeat Typing of <i>Mycobacterium tuberculosis</i> Complex Strains. <i>Journal of Clinical Microbiology</i> , 2012, 50, 662-669.	3.9	48
67	Characterization of a novel variant of <i>Mycobacterium chimaera</i> . <i>Journal of Medical Microbiology</i> , 2012, 61, 1234-1239.	1.8	20
68	Inter- and Intra-subtype genotypic differences that differentiate <i>Mycobacterium avium</i> subspecies paratuberculosis strains. <i>BMC Microbiology</i> , 2012, 12, 264.	3.3	53
69	Online tools for polyphasic analysis of <i>Mycobacterium tuberculosis</i> complex genotyping data: Now and next. <i>Infection, Genetics and Evolution</i> , 2012, 12, 748-754.	2.3	16
70	Evaluation of 24-locus MIRU-VNTR in extrapulmonary specimens: Study from a tertiary centre in Mumbai. <i>Tuberculosis</i> , 2012, 92, 264-272.	1.9	31
71	One year nationwide evaluation of 24-locus MIRU-VNTR genotyping on Slovenian <i>Mycobacterium tuberculosis</i> isolates. <i>Respiratory Medicine</i> , 2011, 105, S67-S73.	2.9	32
72	International Spread of MDR TB from Tugela Ferry, South Africa. <i>Emerging Infectious Diseases</i> , 2011, 17, 2035-7.	4.3	22

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73	On the mutation rates of spoligotypes and variable numbers of tandem repeat loci of <i>Mycobacterium tuberculosis</i> . <i>Infection, Genetics and Evolution</i> , 2011, 11, 251-252.	2.3	11
74	On the mutation rates of spoligotypes and variable numbers of tandem repeat loci of <i>Mycobacterium tuberculosis</i> : Continued-When tuning matters. <i>Infection, Genetics and Evolution</i> , 2011, 11, 1191.	2.3	4
75	The Forest behind the Tree: Phylogenetic Exploration of a Dominant <i>Mycobacterium tuberculosis</i> Strain Lineage from a High Tuberculosis Burden Country. <i>PLoS ONE</i> , 2011, 6, e18256.	2.5	49
76	Importance of identifying <i>Mycobacterium bovis</i> as a causative agent of human tuberculosis. <i>European Respiratory Journal</i> , 2010, 35, 692-694.	6.7	42
77	Impact of HIV Infection on the Recurrence of Tuberculosis in South India. <i>Journal of Infectious Diseases</i> , 2010, 201, 691-703.	4.0	99
78	Microevolution of <i>Mycobacterium tuberculosis</i> in a Tuberculosis Patient. <i>Journal of Clinical Microbiology</i> , 2010, 48, 3813-3816.	3.9	65
79	Genetic Diversity of <i>Mycobacterium tuberculosis</i> Isolates from a Tertiary Care Tuberculosis Hospital in South Korea. <i>Journal of Clinical Microbiology</i> , 2010, 48, 387-394.	3.9	73
80	MIRU-VNTRplus: a web tool for polyphasic genotyping of <i>Mycobacterium tuberculosis</i> complex bacteria. <i>Nucleic Acids Research</i> , 2010, 38, W326-W331.	14.5	287
81	Determination of Genotypic Diversity of <i>Mycobacterium avium</i> Subspecies from Human and Animal Origins by <i>Mycobacterial Interspersed Repetitive-Unit-Variable-Number Tandem-Repeat and IS1311</i> Restriction Fragment Length Polymorphism Typing Methods. <i>Journal of Clinical Microbiology</i> , 2010, 48, 1026-1034.	3.9	83
82	Origin, Spread and Demography of the <i>Mycobacterium tuberculosis</i> Complex. <i>PLoS Pathogens</i> , 2008, 4, e1000160.	4.7	378
83	Combined Multilocus Short-Sequence-Repeat and <i>Mycobacterial Interspersed Repetitive Unit-Variable-Number Tandem-Repeat</i> Typing of <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> Isolates. <i>Journal of Clinical Microbiology</i> , 2008, 46, 4091-4094.	3.9	56
84	Standardised PCR-based molecular epidemiology of tuberculosis. <i>European Respiratory Journal</i> , 2008, 31, 1077-1084.	6.7	21
85	Evaluation and Strategy for Use of MIRU-VNTRplus, a Multifunctional Database for Online Analysis of Genotyping Data and Phylogenetic Identification of <i>Mycobacterium tuberculosis</i> Complex Isolates. <i>Journal of Clinical Microbiology</i> , 2008, 46, 2692-2699.	3.9	366
86	Three-Year Population-Based Evaluation of Standardized <i>Mycobacterial Interspersed Repetitive-Unit-Variable-Number Tandem-Repeat</i> Typing of <i>Mycobacterium tuberculosis</i> . <i>Journal of Clinical Microbiology</i> , 2008, 46, 1398-1406.	3.9	142
87	New Variable-Number Tandem-Repeat Markers for Typing <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> and <i>M. avium</i> Strains: Comparison with <i>IS900</i> and <i>IS1245</i> Restriction Fragment Length Polymorphism Typing. <i>Journal of Clinical Microbiology</i> , 2007, 45, 2404-2410.	3.9	188
88	First Molecular Epidemiology Study of <i>Mycobacterium tuberculosis</i> in Burkina Faso. <i>Journal of Clinical Microbiology</i> , 2007, 45, 921-927.	3.9	71
89	Assessment of an Optimized <i>Mycobacterial Interspersed Repetitive- Unit-Variable-Number Tandem-Repeat</i> Typing System Combined with Spoligotyping for Population-Based Molecular Epidemiology Studies of Tuberculosis. <i>Journal of Clinical Microbiology</i> , 2007, 45, 691-697.	3.9	198
90	Mixed infection and clonal representativeness of a single sputum sample in tuberculosis patients from a penitentiary hospital in Georgia. <i>Respiratory Research</i> , 2006, 7, 99.	3.6	135

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91	Predominance of Ancestral Lineages of <i>Mycobacterium tuberculosis</i> in India. <i>Emerging Infectious Diseases</i> , 2006, 12, 1367-1374.	4.3	106
92	Re-Evaluation of <i>M. prototuberculosis</i> : Continuing the Debate. <i>PLoS Pathogens</i> , 2006, 2, e95.	4.7	18
93	Against All Odds: Molecular Confirmation of an Implausible Case of Bone Tuberculosis. <i>Clinical Infectious Diseases</i> , 2006, 42, e86-e88.	5.8	4
94	Proposal for Standardization of Optimized Mycobacterial Interspersed Repetitive Unit-Variable-Number Tandem Repeat Typing of <i>Mycobacterium tuberculosis</i> . <i>Journal of Clinical Microbiology</i> , 2006, 44, 4498-4510.	3.9	1,181
95	Evaluation of the Epidemiological Relevance of Variable-Number Tandem-Repeat Genotyping of <i>Mycobacterium bovis</i> and Comparison of the Method with IS6110 Restriction Fragment Length Polymorphism Analysis and Spoligotyping. <i>Journal of Clinical Microbiology</i> , 2006, 44, 1951-1962.	3.9	121
96	Ancient Origin and Gene Mosaicism of the Progenitor of <i>Mycobacterium tuberculosis</i> . <i>PLoS Pathogens</i> , 2005, 1, e5.	4.7	469
97	Use of Variable-Number Tandem-Repeat Typing To Differentiate <i>Mycobacterium tuberculosis</i> Beijing Family Isolates from Hong Kong and Comparison with IS 6110 Restriction Fragment Length Polymorphism Typing and Spoligotyping. <i>Journal of Clinical Microbiology</i> , 2005, 43, 314-320.	3.9	69
98	Discriminatory Power and Reproducibility of Novel DNA Typing Methods for <i>Mycobacterium tuberculosis</i> Complex Strains. <i>Journal of Clinical Microbiology</i> , 2005, 43, 5628-5638.	3.9	89
99	Multilocus Variable-Number Tandem Repeat Typing of <i>Mycobacterium ulcerans</i> . <i>Journal of Clinical Microbiology</i> , 2005, 43, 1546-1551.	3.9	66
100	Molecular Typing of <i>Mycobacterium tuberculosis</i> by Mycobacterial Interspersed Repetitive Unit-Variable-Number Tandem Repeat Analysis, a More Accurate Method for Identifying Epidemiological Links between Patients with Tuberculosis. <i>Journal of Clinical Microbiology</i> , 2005, 43, 4473-4479.	3.9	85
101	Characterization of Ancestral <i>Mycobacterium tuberculosis</i> by Multiple Genetic Markers and Proposal of Genotyping Strategy. <i>Journal of Clinical Microbiology</i> , 2004, 42, 5058-5064.	3.9	37
102	Clonal Expansion of a Globally Disseminated Lineage of <i>Mycobacterium tuberculosis</i> with Low IS 6110 Copy Numbers. <i>Journal of Clinical Microbiology</i> , 2004, 42, 5774-5782.	3.9	42
103	Utility of Fast Mycobacterial Interspersed Repetitive Unit-Variable Number Tandem Repeat Genotyping in Clinical Mycobacteriological Analysis. <i>Clinical Infectious Diseases</i> , 2004, 39, 783-789.	5.8	78
104	Use of Mycobacterial Interspersed Repetitive Unit-Variable-Number Tandem Repeat Typing To Examine Genetic Diversity of <i>Mycobacterium tuberculosis</i> in Singapore. <i>Journal of Clinical Microbiology</i> , 2004, 42, 1986-1993.	3.9	81
105	Genetic Diversity and Population Structure of <i>Mycobacterium tuberculosis</i> in Casablanca, a Moroccan City with High Incidence of Tuberculosis. <i>Journal of Clinical Microbiology</i> , 2004, 42, 461-466.	3.9	22
106	Genotypic and Phenotypic Heterogeneity among <i>Mycobacterium tuberculosis</i> Isolates from Pulmonary Tuberculosis Patients. <i>Journal of Clinical Microbiology</i> , 2004, 42, 5528-5536.	3.9	100
107	Intracellular autoregulation of the <i>Mycobacterium tuberculosis</i> PrrA response regulator. <i>Microbiology (United Kingdom)</i> , 2004, 150, 241-246.	1.8	38
108	Linkage disequilibrium between minisatellite loci supports clonal evolution of <i>Mycobacterium tuberculosis</i> in a high tuberculosis incidence area. <i>Molecular Microbiology</i> , 2003, 47, 529-538.	2.5	171

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109	Genotyping of the Mycobacterium tuberculosis complex using MIRUs: association with VNTR and spoligotyping for molecular epidemiology and evolutionary genetics. <i>Infection, Genetics and Evolution</i> , 2003, 3, 125-133.	2.3	208
110	Stability of Variable-Number Tandem Repeats of Mycobacterial Interspersed Repetitive Units from 12 Loci in Serial Isolates of Mycobacterium tuberculosis. <i>Journal of Clinical Microbiology</i> , 2002, 40, 4561-4566.	3.9	105
111	Transient Requirement of the PrrA-PrrB Two-Component System for Early Intracellular Multiplication of Mycobacterium tuberculosis. <i>Infection and Immunity</i> , 2002, 70, 2256-2263.	2.2	87
112	Automated High-Throughput Genotyping for Study of Global Epidemiology of Mycobacterium tuberculosis Based on Mycobacterial Interspersed Repetitive Units. <i>Journal of Clinical Microbiology</i> , 2001, 39, 3563-3571.	3.9	559
113	High-resolution minisatellite-based typing as a portable approach to global analysis of Mycobacterium tuberculosis molecular epidemiology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 1901-1906.	7.1	393
114	Variable human minisatellite-like regions in the Mycobacterium tuberculosis genome. <i>Molecular Microbiology</i> , 2000, 36, 762-771.	2.5	461
115	Molecular characterization of the mycobacterial SenX3-RegX3 two-component system: evidence for autoregulation. <i>Microbiology (United Kingdom)</i> , 2000, 146, 3091-3098.	1.8	62
116	Immunogenicity of recombinant BCG producing the GRA1 antigen from Toxoplasma gondii. <i>Vaccine</i> , 1999, 17, 705-714.	3.8	43
117	Identification of a New DNA Region Specific for Members of Mycobacterium tuberculosis Complex. <i>Journal of Clinical Microbiology</i> , 1998, 36, 937-943.	3.9	57
118	Specific Differentiation between Mycobacterium bovis BCG and Virulent Strains of the Mycobacterium tuberculosis Complex. <i>Journal of Clinical Microbiology</i> , 1998, 36, 2471-2476.	3.9	60
119	Functional analysis of chimerical plasma membrane H ⁺ -ATPases from Saccharomyces cerevisiae and Schizosaccharomyces pombe. <i>Molecular Microbiology</i> , 1997, 25, 261-273.	2.5	6
120	Identification of novel intergenic repetitive units in a mycobacterial two-component system operon. <i>Molecular Microbiology</i> , 1997, 26, 991-1003.	2.5	197
121	Amino Acid Replacements at Seven Different Histidines in the Yeast Plasma Membrane H ⁺ -ATPase Reveal Critical Positions at His285 and His701. <i>Biochemistry</i> , 1996, 35, 883-890.	2.5	25
122	A new series of mycobacterial expression vectors for the development of live recombinant vaccines. <i>Gene</i> , 1996, 176, 149-154.	2.2	11
123	Review: Subcellular traffic of the plasma membrane H ⁺ -ATPase in Saccharomyces cerevisiae. <i>Yeast</i> , 1996, 12, 907-916.	1.7	24
124	Functional Complementation of a Null Mutation of the Yeast Saccharomyces cerevisiae Plasma Membrane H ⁺ -ATPase by a Plant H ⁺ -ATPase Gene. <i>Journal of Biological Chemistry</i> , 1995, 270, 23828-23837.	3.4	84
125	The in vivo activation of Saccharomyces cerevisiae plasma membrane H ⁺ -ATPase by ethanol depends on the expression of the PMA1 gene, but not of the PMA2 gene. <i>Yeast</i> , 1994, 10, 1439-1446.	1.7	38
126	Novel transport ATPases in yeast. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 1990, 1018, 200-202.	1.0	11

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127	Mycobacterial Pathogenomics and Evolution. , 0, , 27-47.		3