

Nalin Rastogi

List of Publications by Year in descending order

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325
papers

13,920
citations

36303

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30922

102
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docs citations

349
times ranked

6709
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.	3.9	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.	3.3	900
3	The geographic diversity of nontuberculous mycobacteria isolated from pulmonary samples: an NTM-NET collaborative study. <i>European Respiratory Journal</i> , 2013, 42, 1604-1613.	6.7	683
4	Evolutionary history and global spread of the Mycobacterium tuberculosis Beijing lineage. <i>Nature Genetics</i> , 2015, 47, 242-249.	21.4	466
5	Global Phylogeny of Mycobacterium tuberculosis Based on Single Nucleotide Polymorphism (SNP) Analysis: Insights into Tuberculosis Evolution, Phylogenetic Accuracy of Other DNA Fingerprinting Systems, and Recommendations for a Minimal Standard SNP Set. <i>Journal of Bacteriology</i> , 2006, 188, 759-772.	2.2	381
6	SITVITWEB – A publicly available international multimarker database for studying Mycobacterium tuberculosis genetic diversity and molecular epidemiology. <i>Infection, Genetics and Evolution</i> , 2012, 12, 755-766.	2.3	380
7	Snapshot of Moving and Expanding Clones of <i>Mycobacterium tuberculosis</i> and Their Global Distribution Assessed by Spoligotyping in an International Study. <i>Journal of Clinical Microbiology</i> , 2003, 41, 1963-1970.	3.9	233
8	Characterization of <i>Mycobacterium tuberculosis</i> Complex DNAs from Egyptian Mummies by Spoligotyping. <i>Journal of Clinical Microbiology</i> , 2003, 41, 359-367.	3.9	224
9	Rapid identification of mycobacteria to species level by PCR-restriction fragment length polymorphism analysis of the hsp65 gene and proposition of an algorithm to differentiate 34 mycobacterial species. <i>Journal of Clinical Microbiology</i> , 1997, 35, 2969-2973.	3.9	213
10	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
11	Global Distribution of Mycobacterium tuberculosis Spoligotypes. <i>Emerging Infectious Diseases</i> , 2002, 8, 1347-1349.	4.3	180
12	In Vitro Activities of Fourteen Antimicrobial Agents Against Drug Susceptible and Resistant Clinical Isolates of Mycobacterium tuberculosis and Comparative Intracellular Activities Against the Virulent H37Rv Strain in Human Macrophages. <i>Current Microbiology</i> , 1996, 33, 167-175.	2.2	155
13	Genetic Biodiversity of <i>Mycobacterium tuberculosis</i> Complex Strains from Patients with Pulmonary Tuberculosis in Cameroon. <i>Journal of Clinical Microbiology</i> , 2003, 41, 2547-2553.	3.9	155
14	IS <i>1245</i> Restriction Fragment Length Polymorphism Typing of <i>Mycobacterium avium</i> Isolates: Proposal for Standardization. <i>Journal of Clinical Microbiology</i> , 1998, 36, 3051-3054.	3.9	135
15	Extracellular and intracellular activities of clarithromycin used alone and in association with ethambutol and rifampin against Mycobacterium avium complex. <i>Antimicrobial Agents and Chemotherapy</i> , 1991, 35, 462-470.	3.2	133
16	Methodological and Clinical Aspects of the Molecular Epidemiology of Mycobacterium tuberculosis and Other Mycobacteria. <i>Clinical Microbiology Reviews</i> , 2016, 29, 239-290.	13.6	131
17	Phylogenomic analysis of the species of the Mycobacterium tuberculosis complex demonstrates that Mycobacterium africanum, Mycobacterium bovis, Mycobacterium caprae, Mycobacterium microti and Mycobacterium pinnipedii are later heterotypic synonyms of Mycobacterium tuberculosis. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 324-332.	1.7	130
18	Spoligotype Database of Mycobacterium tuberculosis: Biogeographic Distribution of Shared Types and Epidemiologic and Phylogenetic Perspectives. <i>Emerging Infectious Diseases</i> , 2001, 7, 390-396.	4.3	130

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19	Spacer oligonucleotide typing of bacteria of the Mycobacterium tuberculosis complex: recommendations for standardised nomenclature. International Journal of Tuberculosis and Lung Disease, 2001, 5, 216-9.	1.2	129
20	Evolution and Diversity of Clonal Bacteria: The Paradigm of Mycobacterium tuberculosis. PLoS ONE, 2008, 3, e1538.	2.5	117
21	Predominant Tuberculosis Spoligotypes, Delhi, India. Emerging Infectious Diseases, 2004, 10, 1138-1142.	4.3	109
22	Mycobacterium tuberculosis Phylogeny Reconstruction Based on Combined Numerical Analysis with IS1081, IS6110, VNTR, and DR-Based Spoligotyping Suggests the Existence of Two New Phylogeographical Clades. Journal of Molecular Evolution, 2001, 53, 680-689.	1.8	108
23	Current Methods in the Molecular Typing of Mycobacterium tuberculosis and Other Mycobacteria. BioMed Research International, 2014, 2014, 1-21.	1.9	108
24	Spoligotype Signatures in the Mycobacterium tuberculosis Complex. Journal of Clinical Microbiology, 2007, 45, 237-240.	3.9	106
25	Macro-geographical specificities of the prevailing tuberculosis epidemic as seen through SITVIT2, an updated version of the Mycobacterium tuberculosis genotyping database. Infection, Genetics and Evolution, 2019, 72, 31-43.	2.3	100
26	Spoligotype Database of Mycobacterium tuberculosis: Biogeographic Distribution of Shared Types and Epidemiologic and Phylogenetic Perspectives. Emerging Infectious Diseases, 2001, 7, 390-396.	4.3	100
27	Secretion of cytokines by human macrophages upon infection by pathogenic and non-pathogenic mycobacteria. Microbial Pathogenesis, 2000, 28, 313-318.	2.9	95
28	Mechanisms of pathogenicity in mycobacteria. Biochimie, 1988, 70, 1101-1120.	2.6	91
29	Molecular Characterization of Ofloxacin-Resistant Mycobacterium tuberculosis Strains from Russia. Antimicrobial Agents and Chemotherapy, 2008, 52, 2937-2939.	3.2	89
30	TB-Lineage: An online tool for classification and analysis of strains of Mycobacterium tuberculosis complex. Infection, Genetics and Evolution, 2012, 12, 789-797.	2.3	87
31	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
32	Application of Sensitive and Specific Molecular Methods To Uncover Global Dissemination of the Major RD ^{Rio} Sublineage of the Latin American-Mediterranean Mycobacterium tuberculosis Spoligotype Family. Journal of Clinical Microbiology, 2008, 46, 1259-1267.	3.9	80
33	Recent observations concerning structure and function relationships in the mycobacterial cell envelope: elaboration of a model in terms of mycobacterial pathogenicity, virulence and drug-resistance. Research in Microbiology, 1991, 142, 464-476.	2.1	79
34	Triple-layered structure of mycobacterial cell wall: Evidence for the existence of a polysaccharide-rich outer layer in 18 mycobacterial species. Current Microbiology, 1986, 13, 237-242.	2.2	77
35	Burden of Unidentifiable Mycobacteria in a Reference Laboratory. Journal of Clinical Microbiology, 2001, 39, 4058-4065.	3.9	75
36	Synergistic activities of antituberculous drugs with cerulenin and trans-cinnamic acid against Mycobacterium tuberculosis. FEMS Immunology and Medical Microbiology, 1998, 21, 149-157.	2.7	74

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37	Epidemic Spread of Multidrug-Resistant Tuberculosis in Johannesburg, South Africa. <i>Journal of Clinical Microbiology</i> , 2013, 51, 1818-1825.	3.9	70
38	<i>Mycobacterium tuberculosis</i> Beijing Genotype in Russia: in Search of Informative Variable-Number Tandem-Repeat Loci. <i>Journal of Clinical Microbiology</i> , 2008, 46, 3576-3584.	3.9	69
39	Genetic Diversity of <i>Mycobacterium africanum</i> Clinical Isolates Based on IS 6110-Restriction Fragment Length Polymorphism Analysis, Spoligotyping, and Variable Number of Tandem DNA Repeats. <i>Journal of Clinical Microbiology</i> , 2001, 39, 57-65.	3.9	68
40	Selective <i>Mycobacterium avium</i> -induced production of nitric oxide by human monocyte-derived macrophages. <i>Journal of Leukocyte Biology</i> , 1994, 56, 36-40.	3.3	66
41	Distribution of Strain Families of <i>Mycobacterium tuberculosis</i> Causing Pulmonary and Extrapulmonary Disease in Hospitalized Children in Cape Town, South Africa. <i>Journal of Clinical Microbiology</i> , 2005, 43, 5779-5781.	3.9	64
42	Sequencing of the pncA Gene in Members of the <i>Mycobacterium tuberculosis</i> Complex Has Important Diagnostic Applications: Identification of a Species-Specific pncA Mutation in <i>Mycobacterium canettii</i> and the Reliable and Rapid Predictor of Pyrazinamide Resistance. <i>Journal of Clinical Microbiology</i> , 2007, 45, 595-599.	3.9	62
43	Genetic biodiversity of <i>Mycobacterium tuberculosis</i> isolates from patients with pulmonary tuberculosis in India. <i>Infection, Genetics and Evolution</i> , 2007, 7, 441-448.	2.3	62
44	High Rates of Clustering of Strains Causing Tuberculosis in Harare, Zimbabwe: a Molecular Epidemiological Study. <i>Journal of Clinical Microbiology</i> , 2004, 42, 4536-4544.	3.9	61
45	In vitro activities of levofloxacin used alone and in combination with first- and second-line antituberculous drugs against <i>Mycobacterium tuberculosis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 1996, 40, 1610-1616.	3.2	60
46	Tuberculosis in the Caribbean: Using Spacer Oligonucleotide Typing to Understand Strain Origin and Transmission. <i>Emerging Infectious Diseases</i> , 1999, 5, 404-411.	4.3	59
47	First Insight into the Population Structure of <i>Mycobacterium tuberculosis</i> in Saudi Arabia. <i>Journal of Clinical Microbiology</i> , 2007, 45, 2467-2473.	3.9	59
48	Intracellular growth of pathogenic mycobacteria in the continuous murine macrophage cell line J-774: Ultrastructure and drug-susceptibility studies. <i>Current Microbiology</i> , 1987, 16, 79-92.	2.2	56
49	Spoligotyping of <i>Mycobacterium tuberculosis</i> isolates from patients with pulmonary tuberculosis in Mumbai, India. <i>Research in Microbiology</i> , 2005, 156, 588-596.	2.1	56
50	Drug susceptibility testing in tuberculosis: A comparison of the proportion methods using Lowenstein-Jensen, middlebrook 7H10 and 7H11 agar media and a radiometric method. <i>Research in Microbiology</i> , 1989, 140, 405-417.	2.1	55
51	Penitentiary population of <i>Mycobacterium tuberculosis</i> in Kyrgyzstan: Exceptionally high prevalence of the Beijing genotype and its Russia-specific subtype. <i>Infection, Genetics and Evolution</i> , 2009, 9, 1400-1405.	2.3	54
52	Geospatial distribution of <i>Mycobacterium tuberculosis</i> genotypes in Africa. <i>PLoS ONE</i> , 2018, 13, e0200632.	2.5	54
53	Spoligotyping Followed by Double-Repetitive-Element PCR as Rapid Alternative to IS 6110 Fingerprinting for Epidemiological Studies of Tuberculosis. <i>Journal of Clinical Microbiology</i> , 1998, 36, 1122-1124.	3.9	54
54	Use of Spoligotyping and Large Sequence Polymorphisms To Study the Population Structure of the <i>Mycobacterium tuberculosis</i> Complex in a Cohort Study of Consecutive Smear-Positive Tuberculosis Cases in The Gambia. <i>Journal of Clinical Microbiology</i> , 2009, 47, 994-1001.	3.9	53

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55	Emergence during unsuccessful chemotherapy of multiple drug resistance in a strain of <i>Mycobacterium tuberculosis</i> . <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 1992, 11, 901-907.	2.9	52
56	PCR-Based Methodology for Detecting Multidrug-Resistant Strains of <i>Mycobacterium tuberculosis</i> Beijing Family Circulating in Russia. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2003, 22, 342-348.	2.9	52
57	Genotypic and Phenotypic Characterization of Drug-Resistant <i>Mycobacterium tuberculosis</i> Isolates from Rural Districts of the Western Cape Province of South Africa. <i>Journal of Clinical Microbiology</i> , 2004, 42, 891-894.	3.9	49
58	Spoligotypes of <i>Mycobacterium tuberculosis</i> complex isolates from patients residents of 11 states of Brazil. <i>Infection, Genetics and Evolution</i> , 2012, 12, 649-656.	2.3	49
59	Multilocus sequence typing scheme for the <i>Mycobacterium abscessus</i> complex. <i>Research in Microbiology</i> , 2014, 165, 82-90.	2.1	49
60	Molecular Typing of <i>Mycobacterium tuberculosis</i> Based on Variable Number of Tandem DNA Repeats Used Alone and in Association with Spoligotyping. <i>Journal of Clinical Microbiology</i> , 2000, 38, 2520-2524.	3.9	49
61	Methods used in the molecular epidemiology of tuberculosis. <i>Clinical Microbiology and Infection</i> , 2002, 8, 694-704.	6.0	48
62	Innovations in the molecular epidemiology of tuberculosis. <i>Enfermedades Infecciosas Y Microbiología Clínica</i> , 2011, 29, 8-13.	0.5	48
63	The Guinea-Bissau Family of <i>Mycobacterium tuberculosis</i> Complex Revisited. <i>PLoS ONE</i> , 2011, 6, e18601.	2.5	47
64	Tuberculosis – A global emergency: Tools and methods to monitor, understand, and control the epidemic with specific example of the Beijing lineage. <i>Tuberculosis</i> , 2015, 95, S177-S189.	1.9	47
65	Activity of rifapentine and its metabolite 25-O-desacetyl-rifapentine compared with rifampicin and rifabutin against <i>Mycobacterium tuberculosis</i> , <i>Mycobacterium africanum</i> , <i>Mycobacterium bovis</i> and <i>M. bovis</i> BCG. <i>Journal of Antimicrobial Chemotherapy</i> , 2000, 46, 565-570.	3.0	46
66	Population Structure among <i>Mycobacterium tuberculosis</i> Isolates from Pulmonary Tuberculosis Patients in Colombia. <i>PLoS ONE</i> , 2014, 9, e93848.	2.5	46
67	Evaluation of Amplicor MTB test as adjunct to smears and culture for direct detection of <i>Mycobacterium tuberculosis</i> in the French Caribbean. <i>Journal of Clinical Microbiology</i> , 1996, 34, 1065-1068.	3.9	46
68	Comparison of spoligotyping, mycobacterial interspersed repetitive units typing and IS6110-RFLP in a study of genotypic diversity of <i>Mycobacterium tuberculosis</i> in Delhi, North India. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2011, 106, 524-535.	1.6	43
69	Molecular epidemiology and genetic diversity of <i>Mycobacterium tuberculosis</i> complex in the Cross River State, Nigeria. <i>Infection, Genetics and Evolution</i> , 2012, 12, 671-677.	2.3	43
70	In Vitro Activities of the Ketolides Telithromycin (HMR 3647) and HMR 3004 Compared to Those of Clarithromycin against Slowly Growing Mycobacteria at pHs 6.8 and 7.4. <i>Antimicrobial Agents and Chemotherapy</i> , 2000, 44, 2848-2852.	3.2	42
71	Molecular diversity of <i>Mycobacterium tuberculosis</i> isolates from patients with pulmonary tuberculosis in Mozambique. <i>BMC Microbiology</i> , 2010, 10, 195.	3.3	42
72	A first insight on the population structure of <i>Mycobacterium tuberculosis</i> complex as studied by spoligotyping and MIRU-VNTRs in Bogotá, Colombia. <i>Infection, Genetics and Evolution</i> , 2012, 12, 657-663.	2.3	42

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73	Molecular Epidemiology of Mycobacterium tuberculosis in Western Sweden. Journal of Clinical Microbiology, 2004, 42, 3046-3051.	3.9	41
74	Long-Term Population-Based Genotyping Study of Mycobacterium tuberculosis Complex Isolates in the French Departments of the Americas. Journal of Clinical Microbiology, 2006, 44, 183-191.	3.9	41
75	First insight into Mycobacterium tuberculosis genetic diversity in Paraguay. BMC Microbiology, 2007, 7, 75.	3.3	41
76	Utility of New 24-Locus Variable-Number Tandem-Repeat Typing for Discriminating Mycobacterium tuberculosis Clinical Isolates Collected in Bulgaria. Journal of Clinical Microbiology, 2008, 46, 3005-3011.	3.9	41
77	Association of Mycobacterium tuberculosis complex isolates of BOVIS and Central Asian (CAS) genotypic lineages with extrapulmonary disease. Clinical Microbiology and Infection, 2009, 15, 538-543.	6.0	41
78	Impact of immigration on tuberculosis epidemiology in a low-incidence country. Clinical Microbiology and Infection, 2011, 17, 881-887.	6.0	41
79	Mapping of Mycobacterium tuberculosis Complex Genetic Diversity Profiles in Tanzania and Other African Countries. PLoS ONE, 2016, 11, e0154571.	2.5	41
80	Structure of the Cell Envelope of Mycobacterium avium. Zentralblatt Fur Bakteriologie, Mikrobiologie, Und Hygiene Series A, Medical Microbiology, Infectious Diseases, Virology, Parasitology, 1987, 264, 49-66.	0.5	40
81	Effect of pH on radiometric MICs of clarithromycin against 18 species of mycobacteria. Antimicrobial Agents and Chemotherapy, 1992, 36, 2841-2842.	3.2	40
82	Mode of action of antituberculous drugs and mechanisms of drug resistance in Mycobacterium tuberculosis. Research in Microbiology, 1993, 144, 133-143.	2.1	40
83	Integration of tuberculosis screening at an HIV voluntary counselling and testing centre in Haiti. Aids, 2001, 15, 1875-1879.	2.2	40
84	Strain Diversity of Mycobacterium tuberculosis Isolates from Pulmonary Tuberculosis Patients in Afar Pastoral Region of Ethiopia. BioMed Research International, 2014, 2014, 1-12.	1.9	40
85	Characterization of mutations in streptomycin-resistant Mycobacterium tuberculosis isolates in Sichuan, China and the association between Beijing-lineage and dual-mutation in gidB. Tuberculosis, 2016, 96, 102-106.	1.9	40
86	rpoB gene sequencing and spoligotyping of multidrug-resistant Mycobacterium tuberculosis isolates from India. Infection, Genetics and Evolution, 2006, 6, 474-483.	2.3	39
87	Insights into the evolutionary history of tubercle bacilli as disclosed by genetic rearrangements within a PE_PGRS duplicated gene pair. BMC Evolutionary Biology, 2006, 6, 107.	3.2	39
88	Molecular characterisation of Mycobacterium tuberculosis isolates in the First National Survey of Anti-tuberculosis Drug Resistance from Venezuela. BMC Microbiology, 2006, 6, 90.	3.3	39
89	Alterations in the outer wall architecture caused by the inhibition of mycoside C biosynthesis in Mycobacterium avium. Current Microbiology, 1988, 17, 61-68.	2.2	38
90	Evolutionary Relationships among Strains of Mycobacterium tuberculosis with Few Copies of IS 6110. Journal of Bacteriology, 2003, 185, 2555-2562.	2.2	38

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91	Genetic diversity and drug susceptibility profile of <i>Mycobacterium tuberculosis</i> isolated from different regions of India. <i>Journal of Infection</i> , 2015, 71, 207-219.	3.3	38
92	Comparative evaluation of PCR and commercial DNA probes for detection and identification to species level of <i>Mycobacterium avium</i> and <i>Mycobacterium intracellulare</i> . <i>Journal of Clinical Microbiology</i> , 1996, 34, 2756-2759.	3.9	38
93	Genetic Diversity of <i>Mycobacterium tuberculosis</i> in Peru and Exploration of Phylogenetic Associations with Drug Resistance. <i>PLoS ONE</i> , 2013, 8, e65873.	2.5	38
94	Spectrum of activity of levofloxacin against nontuberculous mycobacteria and its activity against the <i>Mycobacterium avium</i> complex in combination with ethambutol, rifampin, roxithromycin, amikacin, and clofazimine. <i>Antimicrobial Agents and Chemotherapy</i> , 1996, 40, 2483-2487.	3.2	37
95	Genetic Diversity of <i>Mycobacterium tuberculosis</i> in Sicily Based on Spoligotyping and Variable Number of Tandem DNA Repeats and Comparison with a Spoligotyping Database for Population-Based Analysis. <i>Journal of Clinical Microbiology</i> , 2001, 39, 1559-1565.	3.9	37
96	Molecular characterization of multiple-drug-resistant <i>Mycobacterium tuberculosis</i> isolates from northwestern Russia and analysis of rifampin resistance using RNA/RNA mismatch analysis as compared to the line probe assay and sequencing of the <i>rpoB</i> gene. <i>Research in Microbiology</i> , 2002, 153, 213-219.	2.1	37
97	Data mining of <i>Mycobacterium tuberculosis</i> complex genotyping results using mycobacterial interspersed repetitive units validates the clonal structure of spoligotyping-defined families. <i>Research in Microbiology</i> , 2004, 155, 647-654.	2.1	37
98	Genotyping of <i>Mycobacterium tuberculosis</i> clinical isolates in two cities of Turkey: description of a new family of genotypes that is phylogeographically specific for Asia Minor. <i>BMC Microbiology</i> , 2005, 5, 44.	3.3	37
99	Mixed Infections and Rifampin Heteroresistance among <i>Mycobacterium tuberculosis</i> Clinical Isolates. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2138-2147.	3.9	37
100	Detection of a Previously Unamplified Spacer within the DR Locus of <i>Mycobacterium tuberculosis</i> : Epidemiological Implications. <i>Journal of Clinical Microbiology</i> , 2000, 38, 1231-1234.	3.9	36
101	<i>Mycobacterium florentinum</i> sp. nov., isolated from humans. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2005, 55, 1101-1106.	1.7	35
102	Epidemiological and genetic markers, virulence factors and intracellular growth of <i>Mycobacterium avium</i> in AIDS. <i>Research in Microbiology</i> , 1992, 143, 423-430.	2.1	34
103	Rapid Differentiation of <i>Mycobacterium canettii</i> from Other <i>Mycobacterium tuberculosis</i> Complex Organisms by PCR-Restriction Analysis of the <i>hsp65</i> Gene. <i>Journal of Clinical Microbiology</i> , 2001, 39, 3705-3708.	3.9	34
104	Molecular characterization of <i>Mycobacterium avium</i> complex isolates giving discordant results in AccuProbe tests by PCR-restriction enzyme analysis, 16S rRNA gene sequencing, and DT1-DT6 PCR. <i>Journal of Clinical Microbiology</i> , 1997, 35, 2767-2772.	3.9	34
105	Intracellular growth of <i>Mycobacterium avium</i> in human macrophages is linked to the increased synthesis of prostaglandin E2 and inhibition of the phagosome-lysosome fusions. <i>FEMS Microbiology Letters</i> , 1992, 89, 273-280.	1.8	33
106	Unexpectedly High Proportion of Ancestral Manu Genotype <i>Mycobacterium tuberculosis</i> Strains Cultured from Tuberculosis Patients in Egypt. <i>Journal of Clinical Microbiology</i> , 2009, 47, 2794-2801.	3.9	33
107	Species-Specific Identification of <i>Mycobacterium leprae</i> by PCR-Restriction Fragment Length Polymorphism Analysis of the <i>hsp65</i> Gene. <i>Journal of Clinical Microbiology</i> , 1999, 37, 2016-2019.	3.9	33
108	Distribution of Spoligotyping Defined Genotypic Lineages among Drug-Resistant <i>Mycobacterium tuberculosis</i> Complex Clinical Isolates in Ankara, Turkey. <i>PLoS ONE</i> , 2012, 7, e30331.	2.5	33

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109	<i>Mycobacterium tuberculosis</i> Spoligotypes in Monterrey, Mexico. <i>Journal of Clinical Microbiology</i> , 2010, 48, 448-455.	3.9	32
110	Molecular fingerprinting of <i>Mycobacterium tuberculosis</i> on a Caribbean island with IS6110 and DRr probes. <i>Journal of Clinical Microbiology</i> , 1997, 35, 843-846.	3.9	32
111	Exposure of human peripheral blood mononuclear cells to total lipids and serovar-specific glycopeptidolipids from <i>Mycobacterium avium</i> serovars 4 and 8 results in inhibition of TH1-type responses. <i>Microbial Pathogenesis</i> , 2000, 29, 9-16.	2.9	31
112	A study of spoligotyping-defined <i>Mycobacterium tuberculosis</i> clades in relation to the origin of peopling and the demographic history in Madagascar. <i>Infection, Genetics and Evolution</i> , 2005, 5, 340-348.	2.3	30
113	Evaluation of Methods for Rapid Detection of Resistance to Isoniazid and Rifampin in <i>Mycobacterium tuberculosis</i> Isolates Collected in the Caribbean. <i>Journal of Clinical Microbiology</i> , 2008, 46, 3426-3428.	3.9	30
114	At Baltic crossroads: a molecular snapshot of <i>Mycobacterium tuberculosis</i> population diversity in Kaliningrad, Russia. <i>FEMS Immunology and Medical Microbiology</i> , 2009, 55, 13-22.	2.7	30
115	Spoligotype-Based Comparative Population Structure Analysis of Multidrug-Resistant and Isoniazid-Monoresistant <i>Mycobacterium tuberculosis</i> Complex Clinical Isolates in Poland. <i>Journal of Clinical Microbiology</i> , 2010, 48, 3899-3909.	3.9	30
116	<i>Mycobacterium tuberculosis</i> spoligotypes that may derive from mixed strain infections are revealed by a novel computational approach. <i>Infection, Genetics and Evolution</i> , 2012, 12, 798-806.	2.3	30
117	Genetic diversity among multidrug-resistant <i>Mycobacterium tuberculosis</i> strains in Mexico. <i>Infection, Genetics and Evolution</i> , 2013, 14, 434-443.	2.3	30
118	Treatment outcomes of multidrug-resistant tuberculosis patients in Gauteng, South Africa. <i>Infection</i> , 2014, 42, 405-413.	4.7	30
119	Strain Classification of <i>Mycobacterium tuberculosis</i> Isolates in Brazil Based on Genotypes Obtained by Spoligotyping, Mycobacterial Interspersed Repetitive Unit Typing and the Presence of Large Sequence and Single Nucleotide Polymorphism. <i>PLoS ONE</i> , 2014, 9, e107747.	2.5	30
120	Emergence of multiple-drug-resistant tuberculosis: fundamental and applied research aspects, global issues and current strategies. <i>Research in Microbiology</i> , 1993, 144, 103.	2.1	29
121	Evolutionary robust SNPs reveal the misclassification of <i>Mycobacterium tuberculosis</i> Beijing family strains into sublineages. <i>Infection, Genetics and Evolution</i> , 2013, 16, 174-177.	2.3	29
122	Do test tube-grown pathogenic mycobacteria possess a protective capsule?. <i>FEMS Microbiology Letters</i> , 1988, 56, 225-229.	1.8	28
123	French multicenter study involving eight test sites for radiometric determination of activities of 10 antimicrobial agents against <i>Mycobacterium avium</i> complex. <i>Antimicrobial Agents and Chemotherapy</i> , 1995, 39, 638-644.	3.2	28
124	Use of Spoligotyping To Study the Evolution of the Direct Repeat Locus by IS 6110 Transposition in <i>Mycobacterium tuberculosis</i> . <i>Journal of Clinical Microbiology</i> , 2001, 39, 1595-1599.	3.9	28
125	Multicenter evaluation of mycobacteria identification by PCR restriction enzyme analysis in laboratories from Latin America and the Caribbean. <i>Journal of Microbiological Methods</i> , 2005, 61, 193-199.	1.6	28
126	Three-Year Longitudinal Study of Genotypes of <i>Mycobacterium tuberculosis</i> Isolates in Tuscany, Italy. <i>Journal of Clinical Microbiology</i> , 2007, 45, 1851-1857.	3.9	28

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127	Real-Time PCR Assay for Rapid Detection of Epidemiologically and Clinically Significant Mycobacterium tuberculosis Beijing Genotype Isolates. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1691-1693.	3.9	28
128	A First Insight on the Population Structure of Mycobacterium tuberculosis Complex as Studied by Spoligotyping and MIRU-VNTRs in Santiago, Chile. <i>PLoS ONE</i> , 2015, 10, e0118007.	2.5	28
129	Characterization of Finnish Mycobacterium tuberculosis Isolates by Spoligotyping. <i>Journal of Clinical Microbiology</i> , 2003, 41, 1525-1528.	3.9	27
130	Molecular identification and characterization of Mycobacterium tuberculosis complex in ancient Egyptian mummies. <i>International Journal of Osteoarchaeology</i> , 2004, 14, 404-413.	1.2	27
131	Multidrug-resistant tuberculosis at an HIV testing center in Haiti. <i>Aids</i> , 2006, 20, 415-418.	2.2	27
132	Assessment of Mycobacterial Interspersed Repetitive Unit-QUB Markers To Further Discriminate the Beijing Genotype in a Population-Based Study of the Genetic Diversity of Mycobacterium tuberculosis Clinical Isolates from Okinawa, Ryukyu Islands, Japan. <i>Journal of Clinical Microbiology</i> , 2007, 45, 3606-3615.	3.9	27
133	Population-Based Molecular Epidemiological Study of Tuberculosis in Malatya, Turkey. <i>Journal of Clinical Microbiology</i> , 2007, 45, 4027-4035.	3.9	27
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