Igor Mokrousov

List of Publications by Year
in descending order

135 papers	6,322 citations	71102 41 h-index	71685 76 g-index
138 all docs	138 docs citations	138 times ranked	3743 citing authors

#	Article	IF	Citations
1	Impact of pathobiological diversity of Mycobacterium tuberculosis on clinical features and lethal outcome of tuberculosis. BMC Microbiology, 2022, 22, 50.	3.3	4
2	Transborder molecular analysis of drugâ€resistant tuberculosis in Mongolia and Eastern Siberia, Russia. Transboundary and Emerging Diseases, 2022, 69, .	3.0	9
3	Mycobacterium bovis and M. caprae in Bulgaria: insight into transmission and phylogeography gained through whole-genome sequencing. BMC Veterinary Research, 2022, 18, 148.	1.9	4
4	Synthesis, Characterization and Complex Evaluation of Antibacterial Activity and Cytotoxicity of New Arylmethylidene Ketones and Pyrimidines with Camphane Skeletons. ChemistrySelect, 2022, 7, .	1.5	0
5	Molecular snapshot of drug-resistant Mycobacterium tuberculosis strains from the Plateau State, Nigeria. PLoS ONE, 2022, 17, e0266837.	2.5	2
6	Probable longâ€term prevalence for a predominant Mycobacterium tuberculosis clone of a Beijing genotype in Colon, Panama. Transboundary and Emerging Diseases, 2021, 68, 2229-2238.	3.0	2
7	Spatiotemporal dynamics of drugâ€resistant Mycobacterium tuberculosis : Contrasting trends and implications for tuberculosis control in EU highâ€priority country. Transboundary and Emerging Diseases, 2021, 68, 896-906.	3.0	3
8	Ubiquitous and multifaceted: SIT53 spoligotype does not correlate with any particular family of Mycobacterium tuberculosis. Tuberculosis, 2021, 126, 102024.	1.9	4
9	Extremely lethal and hypervirulent Mycobacterium tuberculosis strain cluster emerging in Far East, Russia. Emerging Microbes and Infections, 2021, 10, 1691-1701.	6.5	6
10	Frequent acquisition of bedaquiline resistance by epidemic extensively drug-resistant Mycobacterium tuberculosis strains in Russia during long-term treatment. Clinical Microbiology and Infection, 2021, 27, 478-480.	6.0	13
11	Practical approach to detection and surveillance of emerging highly resistant Mycobacterium tuberculosis Beijing 1071-32-cluster. Scientific Reports, 2021, 11, 21392.	3.3	5
12	Peculiar features of the Mycobacterium tuberculosis population structure in Albania. Infection, Genetics and Evolution, 2020, 78, 104136.	2.3	4
13	Genetic Variation Putatively Associated with Mycobacterium tuberculosis Resistance to Perchlozone, a New Thiosemicarbazone: Clues from Whole Genome Sequencing and Implications for Treatment of Multidrug-Resistant Tuberculosis. Antibiotics, 2020, 9, 669.	3.7	3
14	First insight into the whole-genome sequence variations in Mycobacterium bovis BCG-1 (Russia) vaccine seed lots and their progeny clinical isolates from children with BCG-induced adverse events. BMC Genomics, 2020, 21, 567.	2.8	7
15	Genomic signatures of drug resistance in highly resistant Mycobacterium tuberculosis strains of the early ancient sublineage of Beijing genotype in Russia. International Journal of Antimicrobial Agents, 2020, 56, 106036.	2.5	8
16	Emergence of multidrug-resistant Mycobacterium tuberculosis of the Beijing lineage in Portugal and Guinea-Bissau: a snapshot of moving clones by whole-genome sequencing. Emerging Microbes and Infections, 2020, 9, 1342-1353.	6.5	14
17	Increased transmissibility of Russian successful strain Beijing B0/W148 of Mycobacterium tuberculosis: Indirect clues from history and demographics. Tuberculosis, 2020, 122, 101937.	1.9	15
18	Molecular characteristics of Mycobacterium tuberculosis in the â€œclosedâ€•Russian town with limited population migration. Infection, Genetics and Evolution, 2020, 79, 104174.	2.3	9

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19	Tuberculosis in Estonia: a major impact of Russian MDR Mycobacterium tuberculosis Beijing B0/W148-cluster. , 2020, , .		1
20	Genomic analysis of new pre-XDR/XDR cluster of Mycobacterium tuberculosis Beijing genotype emerging in Russia. , 2020, , .		1
21	The role of IS6110 in micro- and macroevolution of Mycobacterium tuberculosis lineage 2. Molecular Phylogenetics and Evolution, 2019, 139, 106559.	2.7	9
22	Acquisition of bedaquiline resistance by extensively drug-resistant Mycobacterium tuberculosis strain of Central Asian Outbreak clade. Clinical Microbiology and Infection, 2019, 25, 1295-1297.	6.0	14
23	Genetic relatedness of Mycobacterium avium subsp. hominissuis isolates from bathrooms of healthy volunteers, rivers, and soils in Japan with human clinical isolates from different geographical areas. Infection, Genetics and Evolution, 2019, 74, 103923.	2.3	15
24	Current topics of molecular mycobacteriology. Infection, Genetics and Evolution, 2019, 73, 132-138.	2.3	4
25	Simple Assay for Detection of the Central Asia Outbreak Clade of the Mycobacterium tuberculosis Beijing Genotype. Journal of Clinical Microbiology, 2019, 57, .	3.9	25
26	Special Issue on Molecular aspects of mycobacterial infections. Infection, Genetics and Evolution, 2019, 72, 1-3.	2.3	0
27	Mycobacterium tuberculosis RD-Rio Strain in Kazakhstan. Emerging Infectious Diseases, 2019, 25, 604-606.	4.3	3
28	System OMICs analysis of Mycobacterium tuberculosis Beijing B0/W148 cluster. Scientific Reports, 2019, 9, 19255.	3.3	7
29	Diphtheria. Nature Reviews Disease Primers, 2019, 5, 81.	30.5	117
30	Early ancient sublineages of Mycobacterium tuberculosis Beijing genotype: unexpected clues from phylogenomics of the pathogen and human history. Clinical Microbiology and Infection, 2019, 25, 1039.e1-1039.e6.	6.0	12
31	Mutations of Mycobacterium tuberculosis induced by anti-tuberculosis treatment result in metabolism changes and elevation of ethambutol resistance. Infection, Genetics and Evolution, 2019, 72, 151-158.	2.3	10
32	Clonal expansion across the seas as seen through CPLP-TB database: A joint effort in cataloguing Mycobacterium tuberculosis genetic diversity in Portuguese-speaking countries. Infection, Genetics and Evolution, 2019, 72, 44-58.	2.3	18
33	Emerging resistant clones of Mycobacterium tuberculosis in a spatiotemporal context. Journal of Antimicrobial Chemotherapy, 2018, 73, 325-331.	3.0	4
34	On sunspots, click science and molecular iconography. Tuberculosis, 2018, 110, 91-95.	1.9	8
35	Major genotype families and epidemic clones of Mycobacterium tuberculosis in Omsk region, Western Siberia, Russia, marked by a high burden of tuberculosis-HIV coinfection. Tuberculosis, 2018, 108, 163-168.	1.9	20
36	Rapid Assay for Detection of the Epidemiologically Important Central Asian/Russian Strain of the Mycobacterium tuberculosis Beijing Genotype. Journal of Clinical Microbiology, 2018, 56, .	3.9	25

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37	New epidemic cluster of pre-extensively drug resistant isolates of Mycobacterium tuberculosis Ural family emerging in Eastern Europe. BMC Genomics, 2018, 19, 762.	2.8	28
38	Whole-Genome Analysis ofMycobacterium tuberculosisfrom Patients with Tuberculous Spondylitis, Russia. Emerging Infectious Diseases, 2018, 24, 579-583.	4.3	9
39	Clinical and Drug Resistance Characteristics of New Pediatric Tuberculosis Cases in Northern China. Microbial Drug Resistance, 2018, 24, 1397-1403.	2.0	4
40	Molecular analysis of mutations in genes associated with multidrug-resistance in Mycobacterium tuberculosis isolates from patients with tuberculosis in Moscow region, Russia. , 2018, , .		0
41	Revisiting the Hunter Gaston discriminatory index: Note of caution and courses of change. Tuberculosis, 2017, 104, 20-23.	1.9	14
42	Positive epistasis of major low-cost drug resistance mutations rpoB 531-TTG and katG 315-ACC depends on the phylogenetic background of Mycobacterium tuberculosis strains. International Journal of Antimicrobial Agents, 2017, 49, 757-762.	2.5	16
43	FATE: the new partnership to Fight Against TB in Central and Eastern Europe. Lancet Infectious Diseases, The, 2017, 17, 363.	9.1	5
44	Emerging peak on the phylogeographic landscape of Mycobacterium tuberculosis in West Asia: Definitely smoke, likely fire. Molecular Phylogenetics and Evolution, 2017, 116, 202-212.	2.7	25
45	Evolutionary pathway analysis and unified classification of East Asian lineage of Mycobacterium tuberculosis. Scientific Reports, 2017, 7, 9227.	3.3	98
46	Multidrug-resistant/extensively drug-resistant tuberculosis in Greece: predominance of Mycobacterium tuberculosis genotypes endemic in the Former Soviet Union countries. Clinical Microbiology and Infection, 2017, 23, 1002-1004.	6.0	9
47	Population Structure and Local Adaptation of MAC Lung Disease Agent Mycobacterium avium subsp. hominissuis. Genome Biology and Evolution, 2017, 9, 2403-2417.	2.5	75
48	Next-Generation Sequencing ofMycobacterium tuberculosis. Emerging Infectious Diseases, 2016, 22, 1127-1129.	4.3	15
49	Proteome analysis of the Mycobacterium tuberculosis Beijing B0/W148 cluster. Scientific Reports, 2016, 6, 28985.	3.3	34
50	Emerging clones of Mycobacterium tuberculosis in Russia and former Soviet Union countries: Beijing genotype and beyond. International Journal of Mycobacteriology, 2016, 5, S69-S70.	0.6	3
51	Urgent Implementation in a Hospital Setting of a Strategy To Rule Out Secondary Cases Caused by Imported Extensively Drug-Resistant Mycobacterium tuberculosis Strains at Diagnosis. Journal of Clinical Microbiology, 2016, 54, 2969-2974.	3.9	15
52	Evolutionary History and Ongoing Transmission of Phylogenetic Sublineages of Mycobacterium tuberculosis Beijing Genotype in China. Scientific Reports, 2016, 6, 34353.	3.3	28
53	Emerging resistant clone of Mycobacterium tuberculosis in west Asia. Lancet Infectious Diseases, The, 2016, 16, 1326-1327.	9.1	12
54	Latin-American-Mediterranean lineage of Mycobacterium tuberculosis: Human traces across pathogenâ€™s phylogeography. Molecular Phylogenetics and Evolution, 2016, 99, 133-143.	2.7	42

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55	Compensatory Mutations of Rifampin Resistance Are Associated with Transmission of Multidrug-Resistant Mycobacterium tuberculosis Beijing Genotype Strains in China. Antimicrobial Agents and Chemotherapy, 2016, 60, 2807-2812.	3.2	62
56	Trends in molecular epidemiology of drug-resistant tuberculosis in Republic of Karelia, Russian Federation. BMC Microbiology, 2015, 15, 279.	3.3	27
57	Molecular snapshot of Mycobacterium tuberculosis population in Kazakhstan: A country-wide study. Tuberculosis, 2015, 95, 538-546.	1.9	37
58	Evolutionary history and global spread of the Mycobacterium tuberculosis Beijing lineage. Nature Genetics, 2015, 47, 242-249.	21.4	466
59	Tuberculous Spondylitis in Russia and Prominent Role of Multidrug-Resistant Clone Mycobacterium tuberculosis Beijing B0/W148. Antimicrobial Agents and Chemotherapy, 2015, 59, 2349-2357.	3.2	35
60	Prevalence of Latin-American-Mediterranean genetic family in population structure of Mycobacterium tuberculosis in Bulgaria. International Journal of Mycobacteriology, 2015, 4, 191-195.	0.6	2
61	Genetic diversity of the Mycobacterium tuberculosis Beijing family in Brazil and Mozambique and relation with infectivity and induction of necrosis in THP-1 cells. Tuberculosis, 2015, 95, S190-S196.	1.9	8
62	Mycobacterium tuberculosis phylogeography in the context of human migration and pathogen's pathobiology: Insights from Beijing and Ural families. Tuberculosis, 2015, 95, S167-S176.	1.9	39
63	Spacer-Based Macroarrays for CRISPR Genotyping. Methods in Molecular Biology, 2015, 1311, 111-131.	0.9	17
64	Tuberculosis Epidemiology and Selection in an Autochthonous Siberian Population from the 16th-19th Century. PLoS ONE, 2014, 9, e89877.	2.5	28
65	Resolution Threshold of Current Molecular Epidemiology of Diphtheria. Emerging Infectious Diseases, 2014, 20, 1937-1938.	4.3	2
66	Mycobacterium tuberculosis Strains of the Modern Sublineage of the Beijing Family Are More Likely To Display Increased Virulence than Strains of the Ancient Sublineage. Journal of Clinical Microbiology, 2014, 52, 2615-2624.	3.9	149
67	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
68	Stranger in a strange land: Ibero-American strain of Mycobacterium tuberculosis in Tibet, China. Infection, Genetics and Evolution, 2014, 26, 323-326.	2.3	10
69	Real-Time PCR Assay for Rapid Detection of Epidemiologically and Clinically Significant Mycobacterium tuberculosis Beijing Genotype Isolates. Journal of Clinical Microbiology, 2014, 52, 1691-1693.	3.9	28
70	Mycobacterium tuberculosis Latin American-Mediterranean Family and Its Sublineages in the Light of Robust Evolutionary Markers. Journal of Bacteriology, 2014, 196, 1833-1841.	2.2	31
71	Widely-used laboratory and clinical Mycobacterium tuberculosis strains: To what extent they are representative of their phylogenetic lineages?. Tuberculosis, 2014, 94, 355-356.	1.9	6
72	Molecular snapshot of Mycobacterium tuberculosis population structure and drug-resistance in Kyrgyzstan. Tuberculosis, 2013, 93, 501-507.	1.9	12

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73	Corynebacterium diphtheriae. , 2013, , 283-300.		2
74	Insights into the Origin, Emergence, and Current Spread of a Successful Russian Clone of Mycobacterium tuberculosis. Clinical Microbiology Reviews, 2013, 26, 342-360.	13.6	90
75	Russian â€œSuccessfulâ€•Clone B0/W148 of Mycobacterium tuberculosis Beijing Genotype: a Multiplex PCR Assay for Rapid Detection and Global Screening. Journal of Clinical Microbiology, 2012, 50, 3757-3759.	3.9	51
76	Mycobacterium tuberculosis Population in Northwestern Russia: An Update from Russian-EU/Latvian Border Region. PLoS ONE, 2012, 7, e41318.	2.5	36
77	Designation of subtypes of Mycobacterium tuberculosis Beijing family: an issue of priority. Apmis, 2012, 120, 167-168.	2.0	0
78	High-resolution MIRU-VNTRs typing reveals the unique nature of Mycobacterium tuberculosis Beijing genotype in Okinawa, Japan. Infection, Genetics and Evolution, 2012, 12, 637-641.	2.3	10
79	The quiet and controversial: Ural family of Mycobacterium tuberculosis. Infection, Genetics and Evolution, 2012, 12, 619-629.	2.3	50
80	â€˜Lethalâ€™ combination of Mycobacterium tuberculosis Beijing genotype and human CD209 â^'336G allele in Russian male population. Infection, Genetics and Evolution, 2012, 12, 732-736.	2.3	44
81	SITVITWEB â€“ A publicly available international multimarker database for studying Mycobacterium tuberculosis genetic diversity and molecular epidemiology. Infection, Genetics and Evolution, 2012, 12, 755-766.	2.3	380
82	Special Issue on Molecular evolution, epidemiology and pathogenesis of Mycobacterium tuberculosis and other mycobacteria. Infection, Genetics and Evolution, 2012, 12, 601.	2.3	0
83	Drug-Resistance inMycobacterium Tuberculosis:Molecular Basis and Genotypic Detection. Biotechnology and Biotechnological Equipment, 2011, 25, 18-23.	1.3	2
84	Polymorphism of 3â€²UTR region of TNFR2 coding gene and its role in clinical tuberculosis in Han Chinese pediatric population. Infection, Genetics and Evolution, 2011, 11, 1312-1318.	2.3	14
85	Innovations in the molecular epidemiology of tuberculosis. Enfermedades Infecciosas Y MicrobiologÃa ClÃnica, 2011, 29, 8-13.	0.5	48
86	Tag SNP Polymorphism of CCL2 and Its Role in Clinical Tuberculosis in Han Chinese Pediatric Population. PLoS ONE, 2011, 6, e14652.	2.5	29
87	Mycobacterium bovis BCG-Russia Clinical Isolate with Noncanonical Spoligotyping Profile. Journal of Clinical Microbiology, 2011, 49, 767-767.	3.9	0
88	Emerging multidrug resistant Mycobacterium tuberculosis strains of the Beijing genotype circulating in Russia express a pattern of biological properties associated with enhanced virulence. Microbes and Infection, 2010, 12, 467-475.	1.9	71
89	Bulgarian specificity and controversial phylogeography ofMycobacterium tuberculosisspoligotype ST125_BGR. FEMS Immunology and Medical Microbiology, 2010, 59, 90-99.	2.7	9
90	Mycobacterium bovis BCG-Russia Clinical Isolate with Noncanonical Spoligotyping Profile. Journal of Clinical Microbiology, 2010, 48, 4686-4687.	3.9	5

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91	Novel macroarray-based method of Corynebacterium diphtheriae genotyping: evaluation in a field study in Belarus. European Journal of Clinical Microbiology and Infectious Diseases, 2009, 28, 701-703.	2.9	46
92	At Baltic crossroads: a molecular snapshot ofMycobacterium tuberculosispopulation diversity in Kaliningrad, Russia. FEMS Immunology and Medical Microbiology, 2009, 55, 13-22.	2.7	30
93	Lack of association between polymorphisms in the P2X7gene and tuberculosis in a Chinese Han population. FEMS Immunology and Medical Microbiology, 2009, 55, 107-111.	2.7	31
94	Penitentiary population of Mycobacterium tuberculosis in Kyrgyzstan: Exceptionally high prevalence of the Beijing genotype and its Russia-specific subtype. Infection, Genetics and Evolution, 2009, 9, 1400-1405.	2.3	54
95	Corynebacterium diphtheriae: Genome diversity, population structure and genotyping perspectives. Infection, Genetics and Evolution, 2009, 9, 1-15.	2.3	58
96	Genetic geography of Mycobacterium tuberculosis Beijing genotype: A multifacet mirror of human history?. Infection, Genetics and Evolution, 2008, 8, 777-785.	2.3	59
97	Molecular snapshot of drug-resistant and drug-susceptible Mycobacterium tuberculosis strains circulating in Bulgaria. Infection, Genetics and Evolution, 2008, 8, 657-663.	2.3	19
98	Exhibition of persistent and drug-tolerant L-form habit of Mycobacterium tuberculosis during infection in rats. Open Life Sciences, 2008, 3, 407-416.	1.4	9
99	Mycobacterium tuberculosis Beijing Genotype in Russia: in Search of Informative Variable-Number Tandem-Repeat Loci. Journal of Clinical Microbiology, 2008, 46, 3576-3584.	3.9	69
100	Evaluation of New Variable-Number Tandem-Repeat Systems for TypingMycobacterium tuberculosiswith Beijing Genotype Isolates from Beijing, China. Journal of Clinical Microbiology, 2008, 46, 1045-1049.	3.9	44
101	Mycobacterium tuberculosis co-existence with humans: making an imprint on the macrophage P2X7 receptor gene?. Journal of Medical Microbiology, 2008, 57, 581-584.	1.8	43
102	Molecular Characterization of Ofloxacin-Resistant Mycobacterium tuberculosis Strains from Russia. Antimicrobial Agents and Chemotherapy, 2008, 52, 2937-2939.	3.2	89
103	Molecular Characterization ofMycobacterium tuberculosisIsolates from Different Regions of Bulgaria. Journal of Clinical Microbiology, 2008, 46, 1014-1018.	3.9	20
104	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
105	Designation of Major Mycobacterial Interspersed Repetitive-Unit Types within Mycobacterium tuberculosis Beijing Genotype, an Important Point. Journal of Clinical Microbiology, 2007, 45, 4092-4093.	3.9	0
106	Towards a quantitative perception of human-microbial co-evolution. Frontiers in Bioscience - Landmark, 2007, 12, 4818.	3.0	10
107	Molecular characteristics of rifampin and isoniazid resistant Mycobacterium tuberculosis strains from Beijing, China. Chinese Medical Journal, 2007, 120, 814-819.	2.3	40
108	Corynebacterium diphtheriae spoligotyping based on combined use of two CRISPR loci. Biotechnology Journal, 2007, 2, 901-906.	3.5	77

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109	Molecular characteristics of rifampin and isoniazid resistant Mycobacterium tuberculosis strains from Beijing, China. Chinese Medical Journal, 2007, 120, 814-9.	2.3	15
110	Evaluation of the rpoB macroarray assay to detect rifampin resistance in Mycobacterium tuberculosis in Beijing, China. European Journal of Clinical Microbiology and Infectious Diseases, 2006, 25, 703-710.	2.9	8
111	Mycobacterium tuberculosis complex genetic diversity: mining the fourth international spoligotyping database (SpolDB4) for classification, population genetics and epidemiology. BMC Microbiology, 2006, 6, 23.	3.3	900
112	Rapid Detection of the Mycobacterium tuberculosis Beijing Genotype and Its Ancient and Modern Sublineages by IS6110-Based Inverse PCR. Journal of Clinical Microbiology, 2006, 44, 2851-2856.	3.9	26
113	Evolution of Drug Resistance in Different Sublineages of Mycobacterium tuberculosis Beijing Genotype. Antimicrobial Agents and Chemotherapy, 2006, 50, 2820-2823.	3.2	64
114	Mycobacterium tuberculosis Beijing Genotype and Mycobacterial Interspersed Repetitive Unit Typing. Journal of Clinical Microbiology, 2006, 44, 1614-1615.	3.9	2
115	Efficient Discrimination within a Corynebacterium diphtheriae Epidemic Clonal Group by a Novel Macroarray-Based Method. Journal of Clinical Microbiology, 2005, 43, 1662-1668.	3.9	47
116	Origin and primary dispersal of the Mycobacterium tuberculosis Beijing genotype: Clues from human phylogeography. Genome Research, 2005, 15, 1357-1364.	5.5	188
117	Analysis of the Allelic Diversity of the Mycobacterial Interspersed Repetitive Units in Mycobacterium tuberculosis Strains of the Beijing Family: Practical Implications and Evolutionary Considerations. Journal of Clinical Microbiology, 2004, 42, 2438-2444.	3.9	100
118	Multicenter evaluation of reverse line blot assay for detection of drug resistance in Mycobacterium tuberculosis clinical isolates. Journal of Microbiological Methods, 2004, 57, 323-335.	1.6	52
119	Multiple rpoB mutants of Mycobacterium tuberculosis and second-order selection. Emerging Infectious Diseases, 2004, 10, 1337-8.	4.3	16
120	PCR-Based Methodology for Detecting Multidrug-Resistant Strains of Mycobacterium tuberculosis Beijing Family Circulating in Russia. European Journal of Clinical Microbiology and Infectious Diseases, 2003, 22, 342-348.	2.9	52
121	Allele-Specific rpoB PCR Assays for Detection of Rifampin-Resistant Mycobacterium tuberculosis in Sputum Smears. Antimicrobial Agents and Chemotherapy, 2003, 47, 2231-2235.	3.2	87
122	Snapshot of Moving and Expanding Clones of Mycobacterium tuberculosis and Their Global Distribution Assessed by Spoligotyping in an International Study. Journal of Clinical Microbiology, 2003, 41, 1963-1970.	3.9	233
123	Detection of embB306 Mutations in Ethambutol-Susceptible Clinical Isolates of Mycobacterium tuberculosis from Northwestern Russia: Implications for Genotypic Resistance Testing. Journal of Clinical Microbiology, 2002, 40, 3810-3813.	3.9	108
124	Detection of Isoniazid-Resistant Mycobacterium tuberculosis Strains by a Multiplex Allele-Specific PCR Assay Targeting katG Codon 315 Variation. Journal of Clinical Microbiology, 2002, 40, 2509-2512.	3.9	87
125	Novel IS6110 Insertion Sites in the Direct Repeat Locus of Mycobacterium tuberculosis Clinical Strains from the St. Petersburg Area of Russia and Evolutionary and Epidemiological Considerations. Journal of Clinical Microbiology, 2002, 40, 1504-1507.	3.9	17
126	High Prevalence of KatG Ser315Thr Substitution among Isoniazid-Resistant Mycobacterium tuberculosis Clinical Isolates from Northwestern Russia, 1996 to 2001. Antimicrobial Agents and Chemotherapy, 2002, 46, 1417-1424.	3.2	162

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127	Study of Corynebacterium diphtheriae strains isolated in Romania, northwestern Russia and the Republic of Moldova. Research in Microbiology, 2002, 153, 99-106.	2.1	13
128	Molecular characterization of multiple-drug-resistant Mycobacterium tuberculosis 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 rpoB gene. Research in Microbiology, 2002, 153, 213-219.	2.1	37
129	Phylogenetic reconstruction within Mycobacterium tuberculosis Beijing genotype in northwestern Russia. Research in Microbiology, 2002, 153, 629-637.	2.1	85
130	Global Distribution of Mycobacterium tuberculosis Spoligotypes. Emerging Infectious Diseases, 2002, 8, 1347-1349.	4.3	180
131	Detection of Ethambutol-Resistant Mycobacterium tuberculosis Strains by Multiplex Allele-Specific PCR Assay Targeting embB306 Mutations. Journal of Clinical Microbiology, 2002, 40, 1617-1620.	3.9	42
132	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
133	Spoligotype Database ofMycobacterium tuberculosis: Biogeographic Distribution of Shared Types and Epidemiologic and Phylogenetic Perspectives. Emerging Infectious Diseases, 2001, 7, 390-396.	4.3	100
134	Spoligotype Database of Mycobacterium tuberculosis: Biogeographic Distribution of Shared Types and Epidemiologic and Phylogenetic Perspectives. Emerging Infectious Diseases, 2001, 7, 390-396.	4.3	130
135	Human migratory history: through the looking-glass of genetic geography of Mycobacterium tuberculosis. , 0, , 317-341.		5