

Igor Mokrousov

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/442218/publications.pdf>

Version: 2024-02-01

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	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
2	Evolutionary history and global spread of the Mycobacterium tuberculosis Beijing lineage. Nature Genetics, 2015, 47, 242-249.	21.4	466
3	SITVITWEB – A publicly available international multimer database for studying Mycobacterium tuberculosis genetic diversity and molecular epidemiology. Infection, Genetics and Evolution, 2012, 12, 755-766.	2.3	380
4	Snapshot of Moving and Expanding Clones of <i>Mycobacterium tuberculosis</i> and Their Global Distribution Assessed by Spoligotyping in an International Study. Journal of Clinical Microbiology, 2003, 41, 1963-1970.	3.9	233
5	Origin and primary dispersal of the Mycobacterium tuberculosis Beijing genotype: Clues from human phylogeography. Genome Research, 2005, 15, 1357-1364.	5.5	188
6	Global Distribution of Mycobacterium tuberculosis Spoligotypes. Emerging Infectious Diseases, 2002, 8, 1347-1349.	4.3	180
7	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
8	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
9	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
10	Diphtheria. Nature Reviews Disease Primers, 2019, 5, 81.	30.5	117
11	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
12	Detection of <i>embB306</i> Mutations in Ethambutol-Susceptible Clinical Isolates of <i>Mycobacterium tuberculosis</i> from Northwestern Russia: Implications for Genotypic Resistance Testing. Journal of Clinical Microbiology, 2002, 40, 3810-3813.	3.9	108
13	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
14	Spoligotype Database of <i>Mycobacterium tuberculosis</i> : Biogeographic Distribution of Shared Types and Epidemiologic and Phylogenetic Perspectives. Emerging Infectious Diseases, 2001, 7, 390-396.	4.3	100
15	Evolutionary pathway analysis and unified classification of East Asian lineage of Mycobacterium tuberculosis. Scientific Reports, 2017, 7, 9227.	3.3	98
16	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
17	Molecular Characterization of Ofloxacin-Resistant <i>Mycobacterium tuberculosis</i> Strains from Russia. Antimicrobial Agents and Chemotherapy, 2008, 52, 2937-2939.	3.2	89
18	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

#	ARTICLE	IF	CITATIONS
19	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
20	Phylogenetic reconstruction within Mycobacterium tuberculosis Beijing genotype in northwestern Russia. Research in Microbiology, 2002, 153, 629-637.	2.1	85
21	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
22	Corynebacterium diphtheriae spoligotyping based on combined use of two CRISPR loci. Biotechnology Journal, 2007, 2, 901-906.	3.5	77
23	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
24	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
25	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
26	Evolution of Drug Resistance in Different Sublineages of Mycobacterium tuberculosis Beijing Genotype. Antimicrobial Agents and Chemotherapy, 2006, 50, 2820-2823.	3.2	64
27	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
28	Genetic geography of Mycobacterium tuberculosis Beijing genotype: A multifacet mirror of human history?. Infection, Genetics and Evolution, 2008, 8, 777-785.	2.3	59
29	Corynebacterium diphtheriae: Genome diversity, population structure and genotyping perspectives. Infection, Genetics and Evolution, 2009, 9, 1-15.	2.3	58
30	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
31	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
32	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
33	Russian Successful 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
34	The quiet and controversial: Ural family of Mycobacterium tuberculosis. Infection, Genetics and Evolution, 2012, 12, 619-629.	2.3	50
35	Innovations in the molecular epidemiology of tuberculosis. Enfermedades Infecciosas Y Microbiología Clínica, 2011, 29, 8-13.	0.5	48
36	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

#	ARTICLE	IF	CITATIONS
37	Novel microarray-based method of <i>Corynebacterium diphtheriae</i> genotyping: evaluation in a field study in Belarus. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2009, 28, 701-703.	2.9	46
38	Evaluation of New Variable-Number Tandem-Repeat Systems for Typing <i>Mycobacterium tuberculosis</i> with Beijing Genotype Isolates from Beijing, China. <i>Journal of Clinical Microbiology</i> , 2008, 46, 1045-1049.	3.9	44
39	“Lethal” combination of <i>Mycobacterium tuberculosis</i> Beijing genotype and human CD209 α 336G allele in Russian male population. <i>Infection, Genetics and Evolution</i> , 2012, 12, 732-736.	2.3	44
40	<i>Mycobacterium tuberculosis</i> co-existence with humans: making an imprint on the macrophage P2X7 receptor gene?. <i>Journal of Medical Microbiology</i> , 2008, 57, 581-584.	1.8	43
41	Detection of Ethambutol-Resistant <i>Mycobacterium tuberculosis</i> Strains by Multiplex Allele-Specific PCR Assay Targeting embB306 Mutations. <i>Journal of Clinical Microbiology</i> , 2002, 40, 1617-1620.	3.9	42
42	Latin-American-Mediterranean lineage of <i>Mycobacterium tuberculosis</i> : Human traces across pathogen’s phylogeography. <i>Molecular Phylogenetics and Evolution</i> , 2016, 99, 133-143.	2.7	42
43	Utility of New 24-Locus Variable-Number Tandem-Repeat Typing for Discriminating <i>Mycobacterium tuberculosis</i> Clinical Isolates Collected in Bulgaria. <i>Journal of Clinical Microbiology</i> , 2008, 46, 3005-3011.	3.9	41
44	Molecular characteristics of rifampin and isoniazid resistant <i>Mycobacterium tuberculosis</i> strains from Beijing, China. <i>Chinese Medical Journal</i> , 2007, 120, 814-819.	2.3	40
45	<i>Mycobacterium tuberculosis</i> phylogeography in the context of human migration and pathogen’s pathobiology: Insights from Beijing and Ural families. <i>Tuberculosis</i> , 2015, 95, S167-S176.	1.9	39
46	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 rpoB gene. <i>Research in Microbiology</i> , 2002, 153, 213-219.	2.1	37
47	Molecular snapshot of <i>Mycobacterium tuberculosis</i> population in Kazakhstan: A country-wide study. <i>Tuberculosis</i> , 2015, 95, 538-546.	1.9	37
48	<i>Mycobacterium tuberculosis</i> Population in Northwestern Russia: An Update from Russian-EU/Latvian Border Region. <i>PLoS ONE</i> , 2012, 7, e41318.	2.5	36
49	Tuberculous Spondylitis in Russia and Prominent Role of Multidrug-Resistant Clone <i>Mycobacterium tuberculosis</i> Beijing B0/W148. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 2349-2357.	3.2	35
50	Proteome analysis of the <i>Mycobacterium tuberculosis</i> Beijing B0/W148 cluster. <i>Scientific Reports</i> , 2016, 6, 28985.	3.3	34
51	Lack of association between polymorphisms in the P2X7 gene and tuberculosis in a Chinese Han population. <i>FEMS Immunology and Medical Microbiology</i> , 2009, 55, 107-111.	2.7	31
52	<i>Mycobacterium tuberculosis</i> Latin American-Mediterranean Family and Its Sublineages in the Light of Robust Evolutionary Markers. <i>Journal of Bacteriology</i> , 2014, 196, 1833-1841.	2.2	31
53	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
54	Tag SNP Polymorphism of CCL2 and Its Role in Clinical Tuberculosis in Han Chinese Pediatric Population. <i>PLoS ONE</i> , 2011, 6, e14652.	2.5	29

#	ARTICLE	IF	CITATIONS
55	Tuberculosis Epidemiology and Selection in an Autochthonous Siberian Population from the 16th-19th Century. PLoS ONE, 2014, 9, e89877.	2.5	28
56	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
57	Evolutionary History and Ongoing Transmission of Phylogenetic Sublineages of Mycobacterium tuberculosis Beijing Genotype in China. Scientific Reports, 2016, 6, 34353.	3.3	28
58	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
59	Trends in molecular epidemiology of drug-resistant tuberculosis in Republic of Karelia, Russian Federation. BMC Microbiology, 2015, 15, 279.	3.3	27
60	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
61	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
62	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
63	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
64	Molecular Characterization of Mycobacterium tuberculosis Isolates from Different Regions of Bulgaria. Journal of Clinical Microbiology, 2008, 46, 1014-1018.	3.9	20
65	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
66	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
67	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
68	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
69	Spacer-Based Macroarrays for CRISPR Genotyping. Methods in Molecular Biology, 2015, 1311, 111-131.	0.9	17
70	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
71	Multiple rpoB mutants of Mycobacterium tuberculosis and second-order selection. Emerging Infectious Diseases, 2004, 10, 1337-8.	4.3	16
72	Next-Generation Sequencing of Mycobacterium tuberculosis. Emerging Infectious Diseases, 2016, 22, 1127-1129.	4.3	15

#	ARTICLE	IF	CITATIONS
73	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. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2969-2974.	3.9	15
74	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. <i>Infection, Genetics and Evolution</i> , 2019, 74, 103923.	2.3	15
75	Increased transmissibility of Russian successful strain Beijing B0/W148 of Mycobacterium tuberculosis: Indirect clues from history and demographics. <i>Tuberculosis</i> , 2020, 122, 101937.	1.9	15
76	Molecular characteristics of rifampin and isoniazid resistant Mycobacterium tuberculosis strains from Beijing, China. <i>Chinese Medical Journal</i> , 2007, 120, 814-9.	2.3	15
77	Polymorphism of 3'UTR region of TNFR2 coding gene and its role in clinical tuberculosis in Han Chinese pediatric population. <i>Infection, Genetics and Evolution</i> , 2011, 11, 1312-1318.	2.3	14
78	Revisiting the Hunter Gaston discriminatory index: Note of caution and courses of change. <i>Tuberculosis</i> , 2017, 104, 20-23.	1.9	14
79	Acquisition of bedaquiline resistance by extensively drug-resistant Mycobacterium tuberculosis strain of Central Asian Outbreak clade. <i>Clinical Microbiology and Infection</i> , 2019, 25, 1295-1297.	6.0	14
80	Emergence of multidrug-resistant Mycobacterium tuberculosis of the Beijing lineage in Portugal and Guinea-Bissau: a snapshot of moving clones by whole-genome sequencing. <i>Emerging Microbes and Infections</i> , 2020, 9, 1342-1353.	6.5	14
81	Study of Corynebacterium diphtheriae strains isolated in Romania, northwestern Russia and the Republic of Moldova. <i>Research in Microbiology</i> , 2002, 153, 99-106.	2.1	13
82	Frequent acquisition of bedaquiline resistance by epidemic extensively drug-resistant Mycobacterium tuberculosis strains in Russia during long-term treatment. <i>Clinical Microbiology and Infection</i> , 2021, 27, 478-480.	6.0	13
83	Molecular snapshot of Mycobacterium tuberculosis population structure and drug-resistance in Kyrgyzstan. <i>Tuberculosis</i> , 2013, 93, 501-507.	1.9	12
84	Emerging resistant clone of Mycobacterium tuberculosis in west Asia. <i>Lancet Infectious Diseases</i> , The, 2016, 16, 1326-1327.	9.1	12
85	Early ancient sublineages of Mycobacterium tuberculosis Beijing genotype: unexpected clues from phylogenomics of the pathogen and human history. <i>Clinical Microbiology and Infection</i> , 2019, 25, 1039.e1-1039.e6.	6.0	12
86	Towards a quantitative perception of human-microbial co-evolution. <i>Frontiers in Bioscience - Landmark</i> , 2007, 12, 4818.	3.0	10
87	High-resolution MIRU-VNTRs typing reveals the unique nature of Mycobacterium tuberculosis Beijing genotype in Okinawa, Japan. <i>Infection, Genetics and Evolution</i> , 2012, 12, 637-641.	2.3	10
88	Stranger in a strange land: Ibero-American strain of Mycobacterium tuberculosis in Tibet, China. <i>Infection, Genetics and Evolution</i> , 2014, 26, 323-326.	2.3	10
89	Mutations of Mycobacterium tuberculosis induced by anti-tuberculosis treatment result in metabolism changes and elevation of ethambutol resistance. <i>Infection, Genetics and Evolution</i> , 2019, 72, 151-158.	2.3	10
90	Exhibition of persistent and drug-tolerant L-form habit of Mycobacterium tuberculosis during infection in rats. <i>Open Life Sciences</i> , 2008, 3, 407-416.	1.4	9

#	ARTICLE	IF	CITATIONS
91	Bulgarian specificity and controversial phylogeography of <i>Mycobacterium tuberculosis</i> spoligotype ST125_BGR. <i>FEMS Immunology and Medical Microbiology</i> , 2010, 59, 90-99.	2.7	9
92	Multidrug-resistant/extensively drug-resistant tuberculosis in Greece: predominance of <i>Mycobacterium tuberculosis</i> genotypes endemic in the Former Soviet Union countries. <i>Clinical Microbiology and Infection</i> , 2017, 23, 1002-1004.	6.0	9
93	Whole-Genome Analysis of <i>Mycobacterium tuberculosis</i> from Patients with Tuberculous Spondylitis, Russia. <i>Emerging Infectious Diseases</i> , 2018, 24, 579-583.	4.3	9
94	The role of IS6110 in micro- and macroevolution of <i>Mycobacterium tuberculosis</i> lineage 2. <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106559.	2.7	9
95	Molecular characteristics of <i>Mycobacterium tuberculosis</i> in the closed Russian town with limited population migration. <i>Infection, Genetics and Evolution</i> , 2020, 79, 104174.	2.3	9
96	Transborder molecular analysis of drug-resistant tuberculosis in Mongolia and Eastern Siberia, Russia. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	3.0	9
97	Evaluation of the <i>rpoB</i> macroarray assay to detect rifampin resistance in <i>Mycobacterium tuberculosis</i> in Beijing, China. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2006, 25, 703-710.	2.9	8
98	Genetic diversity of the <i>Mycobacterium tuberculosis</i> Beijing family in Brazil and Mozambique and relation with infectivity and induction of necrosis in THP-1 cells. <i>Tuberculosis</i> , 2015, 95, S190-S196.	1.9	8
99	On sunspots, click science and molecular iconography. <i>Tuberculosis</i> , 2018, 110, 91-95.	1.9	8
100	Genomic signatures of drug resistance in highly resistant <i>Mycobacterium tuberculosis</i> strains of the early ancient sublineage of Beijing genotype in Russia. <i>International Journal of Antimicrobial Agents</i> , 2020, 56, 106036.	2.5	8
101	System OMICs analysis of <i>Mycobacterium tuberculosis</i> Beijing B0/W148 cluster. <i>Scientific Reports</i> , 2019, 9, 19255.	3.3	7
102	First insight into the whole-genome sequence variations in <i>Mycobacterium bovis</i> BCG-1 (Russia) vaccine seed lots and their progeny clinical isolates from children with BCG-induced adverse events. <i>BMC Genomics</i> , 2020, 21, 567.	2.8	7
103	Widely-used laboratory and clinical <i>Mycobacterium tuberculosis</i> strains: To what extent they are representative of their phylogenetic lineages?. <i>Tuberculosis</i> , 2014, 94, 355-356.	1.9	6
104	Extremely lethal and hypervirulent <i>Mycobacterium tuberculosis</i> strain cluster emerging in Far East, Russia. <i>Emerging Microbes and Infections</i> , 2021, 10, 1691-1701.	6.5	6
105	<i>Mycobacterium bovis</i> BCG-Russia Clinical Isolate with Noncanonical Spoligotyping Profile. <i>Journal of Clinical Microbiology</i> , 2010, 48, 4686-4687.	3.9	5
106	Human migratory history: through the looking-glass of genetic geography of <i>Mycobacterium tuberculosis</i> . , 0, , 317-341.		5
107	FATE: the new partnership to Fight Against TB in Central and Eastern Europe. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 363.	9.1	5
108	Practical approach to detection and surveillance of emerging highly resistant <i>Mycobacterium tuberculosis</i> Beijing 1071-32-cluster. <i>Scientific Reports</i> , 2021, 11, 21392.	3.3	5

#	ARTICLE	IF	CITATIONS
109	Emerging resistant clones of <i>Mycobacterium tuberculosis</i> in a spatiotemporal context. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 325-331.	3.0	4
110	Clinical and Drug Resistance Characteristics of New Pediatric Tuberculosis Cases in Northern China. <i>Microbial Drug Resistance</i> , 2018, 24, 1397-1403.	2.0	4
111	Current topics of molecular mycobacteriology. <i>Infection, Genetics and Evolution</i> , 2019, 73, 132-138.	2.3	4
112	Peculiar features of the <i>Mycobacterium tuberculosis</i> population structure in Albania. <i>Infection, Genetics and Evolution</i> , 2020, 78, 104136.	2.3	4
113	Ubiquitous and multifaceted: SIT53 spoligotype does not correlate with any particular family of <i>Mycobacterium tuberculosis</i> . <i>Tuberculosis</i> , 2021, 126, 102024.	1.9	4
114	Impact of pathobiological diversity of <i>Mycobacterium tuberculosis</i> on clinical features and lethal outcome of tuberculosis. <i>BMC Microbiology</i> , 2022, 22, 50.	3.3	4
115	<i>Mycobacterium bovis</i> and <i>M. caprae</i> in Bulgaria: insight into transmission and phylogeography gained through whole-genome sequencing. <i>BMC Veterinary Research</i> , 2022, 18, 148.	1.9	4
116	Emerging clones of <i>Mycobacterium tuberculosis</i> in Russia and former Soviet Union countries: Beijing genotype and beyond. <i>International Journal of Mycobacteriology</i> , 2016, 5, S69-S70.	0.6	3
117	<i>Mycobacterium tuberculosis</i> RD-Rio Strain in Kazakhstan. <i>Emerging Infectious Diseases</i> , 2019, 25, 604-606.	4.3	3
118	Genetic Variation Putatively Associated with <i>Mycobacterium tuberculosis</i> Resistance to Perchlorone, a New Thiosemicarbazone: Clues from Whole Genome Sequencing and Implications for Treatment of Multidrug-Resistant Tuberculosis. <i>Antibiotics</i> , 2020, 9, 669.	3.7	3
119	Spatiotemporal dynamics of drug-resistant <i>Mycobacterium tuberculosis</i> : Contrasting trends and implications for tuberculosis control in EU high-priority country. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 896-906.	3.0	3
120	<i>Mycobacterium tuberculosis</i> Beijing Genotype and Mycobacterial Interspersed Repetitive Unit Typing. <i>Journal of Clinical Microbiology</i> , 2006, 44, 1614-1615.	3.9	2
121	Drug-Resistance in <i>Mycobacterium Tuberculosis</i> : Molecular Basis and Genotypic Detection. <i>Biotechnology and Biotechnological Equipment</i> , 2011, 25, 18-23.	1.3	2
122	<i>Corynebacterium diphtheriae</i> . , 2013, , 283-300.		2
123	Resolution Threshold of Current Molecular Epidemiology of Diphtheria. <i>Emerging Infectious Diseases</i> , 2014, 20, 1937-1938.	4.3	2
124	Prevalence of Latin-American-Mediterranean genetic family in population structure of <i>Mycobacterium tuberculosis</i> in Bulgaria. <i>International Journal of Mycobacteriology</i> , 2015, 4, 191-195.	0.6	2
125	Probable long-term prevalence for a predominant <i>Mycobacterium tuberculosis</i> clone of a Beijing genotype in Colon, Panama. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 2229-2238.	3.0	2
126	Molecular snapshot of drug-resistant <i>Mycobacterium tuberculosis</i> strains from the Plateau State, Nigeria. <i>PLoS ONE</i> , 2022, 17, e0266837.	2.5	2

#	ARTICLE	IF	CITATIONS
127	Tuberculosis in Estonia: a major impact of Russian MDR Mycobacterium tuberculosis Beijing B0/W148-cluster. , 2020, , .		1
128	Genomic analysis of new pre-XDR/XDR cluster of Mycobacterium tuberculosis Beijing genotype emerging in Russia. , 2020, , .		1
129	Designation of Major Mycobacterial Interspersed Repetitive-Unit Types within <i>Mycobacterium tuberculosis</i> Beijing Genotype, an Important Point. Journal of Clinical Microbiology, 2007, 45, 4092-4093.	3.9	0
130	Mycobacterium bovis BCG-Russia Clinical Isolate with Noncanonical Spoligotyping Profile. Journal of Clinical Microbiology, 2011, 49, 767-767.	3.9	0
131	Designation of subtypes of <i>Mycobacterium tuberculosis</i> Beijing family: an issue of priority. Apmis, 2012, 120, 167-168.	2.0	0
132	Special Issue on Molecular evolution, epidemiology and pathogenesis of Mycobacterium tuberculosis and other mycobacteria. Infection, Genetics and Evolution, 2012, 12, 601.	2.3	0
133	Special Issue on Molecular aspects of mycobacterial infections. Infection, Genetics and Evolution, 2019, 72, 1-3.	2.3	0
134	Molecular analysis of mutations in genes associated with multidrug-resistance in Mycobacterium tuberculosis isolates from patients with tuberculosis in Moscow region, Russia. , 2018, , .		0
135	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