

# Daro Garca de Viedma

## List of Publications by Citations

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113  
papers

3,308  
citations

30  
h-index

54  
g-index

117  
ext. papers

3,694  
ext. citations

6.6  
avg, IF

4.59  
L-index

#	Paper	IF	Citations
113	Mycobacterium tuberculosis complex genetic diversity: mining the fourth international spoligotyping database (SpolDB4) for classification, population genetics and epidemiology. <i>BMC Microbiology</i> , <b>2006</b> , 6, 23	4.5	796
112	In vitro activities of linezolid against clinical isolates of Mycobacterium tuberculosis that are susceptible or resistant to first-line antituberculous drugs. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2003</b> , 47, 416-7	5.9	142
111	Whole genome sequencing analysis of inpatient microevolution in Mycobacterium tuberculosis: potential impact on the inference of tuberculosis transmission. <i>Journal of Infectious Diseases</i> , <b>2014</b> , 209, 98-108	7	106
110	Treatment of AIDS-associated progressive multifocal leukoencephalopathy with highly active antiretroviral therapy. <i>Aids</i> , <b>1998</b> , 12, 2467-72	3.5	91
109	Inflammatory reactions in progressive multifocal leukoencephalopathy after highly active antiretroviral therapy. <i>Aids</i> , <b>2001</b> , 15, 1900-2	3.5	81
108	Application of sensitive and specific molecular methods to uncover global dissemination of the major RDRio Sublineage of the Latin American-Mediterranean Mycobacterium tuberculosis spoligotype family. <i>Journal of Clinical Microbiology</i> , <b>2008</b> , 46, 1259-67	9.7	76
107	Rapid detection of resistance in Mycobacterium tuberculosis: a review discussing molecular approaches. <i>Clinical Microbiology and Infection</i> , <b>2003</b> , 9, 349-59	9.5	76
106	New real-time PCR able to detect in a single tube multiple rifampin resistance mutations and high-level isoniazid resistance mutations in Mycobacterium tuberculosis. <i>Journal of Clinical Microbiology</i> , <b>2002</b> , 40, 988-95	9.7	71
105	Prolonged viral shedding in pandemic influenza A(H1N1): clinical significance and viral load analysis in hospitalized patients. <i>Clinical Microbiology and Infection</i> , <b>2011</b> , 17, 1160-5	9.5	63
104	Evaluation of the new advanced 15-loci MIRU-VNTR genotyping tool in Mycobacterium tuberculosis molecular epidemiology studies. <i>BMC Microbiology</i> , <b>2008</b> , 8, 34	4.5	57
103	Polyclonal and compartmentalized infection by Mycobacterium tuberculosis in patients with both respiratory and extrapulmonary involvement. <i>Journal of Infectious Diseases</i> , <b>2003</b> , 187, 695-9	7	56
102	A non-canonical mismatch repair pathway in prokaryotes. <i>Nature Communications</i> , <b>2017</b> , 8, 14246	17.4	53
101	Characterization of clonal complexity in tuberculosis by mycobacterial interspersed repetitive unit-variable-number tandem repeat typing. <i>Journal of Clinical Microbiology</i> , <b>2005</b> , 43, 5660-4	9.7	53
100	JC virus load in progressive multifocal leukoencephalopathy: analysis of the correlation between the viral burden in cerebrospinal fluid, patient survival, and the volume of neurological lesions. <i>Clinical Infectious Diseases</i> , <b>2002</b> , 34, 1568-75	11.6	52
99	Current knowledge and pending challenges in zoonosis caused by Mycobacterium bovis: a review. <i>Research in Veterinary Science</i> , <b>2014</b> , 97 Suppl, S94-S100	2.5	50
98	Association between the infectivity of Mycobacterium tuberculosis strains and their efficiency for extrapulmonary infection. <i>Journal of Infectious Diseases</i> , <b>2005</b> , 192, 2059-65	7	49
97	Analysis of changes in recent tuberculosis transmission patterns after a sharp increase in immigration. <i>Journal of Clinical Microbiology</i> , <b>2007</b> , 45, 63-9	9.7	45

96	Rapid direct detection of multiple rifampin and isoniazid resistance mutations in Mycobacterium tuberculosis in respiratory samples by real-time PCR. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2004</b> , 48, 4293-300	5.9	45
95	Innovations in the molecular epidemiology of tuberculosis. <i>Enfermedades Infecciosas Y Microbiología Clínica</i> , <b>2011</b> , 29 Suppl 1, 8-13	0.9	44
94	Host growth temperature and a conservative amino acid substitution in the replication protein of pPS10 influence plasmid host range. <i>Journal of Bacteriology</i> , <b>1995</b> , 177, 4377-84	3.5	43
93	Systematic survey of clonal complexity in tuberculosis at a populational level and detailed characterization of the isolates involved. <i>Journal of Clinical Microbiology</i> , <b>2011</b> , 49, 4131-7	9.7	41
92	Isolation of Mycobacterium tuberculosis strains with a silent mutation in rpoB leading to potential misassignment of resistance category. <i>Journal of Clinical Microbiology</i> , <b>2011</b> , 49, 2688-90	9.7	41
91	Molecular epidemiology of Aspergillus fumigatus: an in-depth genotypic analysis of isolates involved in an outbreak of invasive aspergillosis. <i>Journal of Clinical Microbiology</i> , <b>2011</b> , 49, 3498-503	9.7	41
90	First worldwide proficiency study on variable-number tandem-repeat typing of Mycobacterium tuberculosis complex strains. <i>Journal of Clinical Microbiology</i> , <b>2012</b> , 50, 662-9	9.7	41
89	The clonal composition of Mycobacterium tuberculosis in clinical specimens could be modified by culture. <i>Tuberculosis</i> , <b>2010</b> , 90, 201-7	2.6	41
88	Humans as source of Mycobacterium tuberculosis infection in cattle, Spain. <i>Emerging Infectious Diseases</i> , <b>2011</b> , 17, 2393-5	10.2	35
87	Epidemiology of infections due to nonpigmented rapidly growing mycobacteria diagnosed in an urban area. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , <b>2008</b> , 27, 951-7	5.3	35
86	Advanced survey of tuberculosis transmission in a complex socioepidemiologic scenario with a high proportion of cases in immigrants. <i>Clinical Infectious Diseases</i> , <b>2008</b> , 47, 8-14	11.6	32
85	Molecular analysis of relapse vs re-infection in HIV-positive patients suffering from recurrent Clostridium difficile associated diarrhoea. <i>Journal of Hospital Infection</i> , <b>2001</b> , 48, 86-92	6.9	31
84	Rapid detection of toxigenic Clostridium difficile from stool samples by a nested PCR of toxin B gene. <i>Journal of Hospital Infection</i> , <b>1999</b> , 41, 145-9	6.9	30
83	Prospective universal application of mycobacterial interspersed repetitive-unit-variable-number tandem-repeat genotyping to characterize Mycobacterium tuberculosis isolates for fast identification of clustered and orphan cases. <i>Journal of Clinical Microbiology</i> , <b>2009</b> , 47, 2026-32	9.7	28
82	Analysis of mutations in streptomycin-resistant strains reveals a simple and reliable genetic marker for identification of the Mycobacterium tuberculosis Beijing genotype. <i>Journal of Clinical Microbiology</i> , <b>2013</b> , 51, 2124-30	9.7	27
81	Transmission permeability of tuberculosis involving immigrants, revealed by a multicentre analysis of clusters. <i>Clinical Microbiology and Infection</i> , <b>2009</b> , 15, 435-42	9.5	27
80	Characterization of microevolution events in Mycobacterium tuberculosis strains involved in recent transmission clusters. <i>Journal of Clinical Microbiology</i> , <b>2011</b> , 49, 3771-6	9.7	27
79	Analysis of clonal composition of Mycobacterium tuberculosis isolates in primary infections in children. <i>Journal of Clinical Microbiology</i> , <b>2004</b> , 42, 3415-8	9.7	27

78	Transcription of repA, the gene of the initiation protein of the Pseudomonas plasmid pPS10, is autoregulated by interactions of the RepA protein at a symmetrical operator. <i>Journal of Molecular Biology</i> , <b>1995</b> , 247, 211-23	6.5	27
77	Comparison of real-time RT-PCR, shell vial culture, and conventional cell culture for the detection of the pandemic influenza A (H1N1) in hospitalized patients. <i>Diagnostic Microbiology and Infectious Disease</i> , <b>2011</b> , 69, 428-31	2.9	26
76	The use of microbead-based spoligotyping for Mycobacterium tuberculosis complex to evaluate the quality of the conventional method: providing guidelines for Quality Assurance when working on membranes. <i>BMC Infectious Diseases</i> , <b>2011</b> , 11, 110	4	26
75	Splitting of a prevalent Mycobacterium bovis spoligotype by variable-number tandem-repeat typing reveals high heterogeneity in an evolving clonal group. <i>Journal of Clinical Microbiology</i> , <b>2013</b> , 51, 3658-65	9.7	24
74	Should lower respiratory tract secretions from intensive care patients be systematically screened for influenza virus during the influenza season?. <i>Critical Care</i> , <b>2012</b> , 16, R104	10.8	23
73	New route of importation of Mycobacterium tuberculosis Beijing genotype. <i>Emerging Infectious Diseases</i> , <b>2006</b> , 12, 169-70	10.2	22
72	Rapid clonal analysis of recurrent tuberculosis by direct MIRU-VNTR typing on stored isolates. <i>BMC Microbiology</i> , <b>2007</b> , 7, 73	4.5	21
71	Complex clonal features in an mycobacterium tuberculosis infection in a two-year-old child. <i>Pediatric Infectious Disease Journal</i> , <b>2006</b> , 25, 457-9	3.4	21
70	Second worldwide proficiency study on variable number of tandem repeats typing of Mycobacterium tuberculosis complex. <i>International Journal of Tuberculosis and Lung Disease</i> , <b>2014</b> , 18, 594-600	2.1	20
69	Real-time molecular epidemiology of tuberculosis by direct genotyping of smear-positive clinical specimens. <i>Journal of Clinical Microbiology</i> , <b>2012</b> , 50, 1755-7	9.7	19
68	Comparison of phenotypic with genotypic procedures for confirmation of coagulase-negative Staphylococcus catheter-related bloodstream infections. <i>Journal of Clinical Microbiology</i> , <b>2006</b> , 44, 3529-32	9.7	19
67	Fast and low-cost decentralized surveillance of transmission of tuberculosis based on strain-specific PCRs tailored from whole genome sequencing data: a pilot study. <i>Clinical Microbiology and Infection</i> , <b>2015</b> , 21, 249.e1-9	9.5	18
66	Mammalian target of rapamycin signal inhibitors could play a role in the treatment of BK polyomavirus nephritis in renal allograft recipients. <i>Transplant Infectious Disease</i> , <b>2011</b> , 13, 584-91	2.7	18
65	Characterization of Mycobacterium tuberculosis Beijing isolates from the Mediterranean area. <i>BMC Microbiology</i> , <b>2010</b> , 10, 151	4.5	18
64	Inference of Active Viral Replication in Cases with Sustained Positive Reverse Transcription-PCR Results for SARS-CoV-2. <i>Journal of Clinical Microbiology</i> , <b>2021</b> , 59,	9.7	18
63	IS6110-based global phylogeny of Mycobacterium tuberculosis. <i>Infection, Genetics and Evolution</i> , <b>2011</b> , 11, 132-8	4.5	17
62	Impact of laboratory cross-contamination on molecular epidemiology studies of tuberculosis. <i>Journal of Clinical Microbiology</i> , <b>2006</b> , 44, 2967-9	9.7	17
61	Ultrafast Assessment of the Presence of a High-Risk Mycobacterium tuberculosis Strain in a Population. <i>Journal of Clinical Microbiology</i> , <b>2016</b> , 54, 779-81	9.7	16

60	Differences in gene expression between clonal variants of Mycobacterium tuberculosis emerging as a result of microevolution. <i>International Journal of Medical Microbiology</i> , <b>2013</b> , 303, 674-7	3.7	16
59	Evaluation of the upgraded amplified Mycobacterium tuberculosis direct test (gen-probe) for direct detection of Mycobacterium tuberculosis in respiratory and non-respiratory specimens. <i>Diagnostic Microbiology and Infectious Disease</i> , <b>2001</b> , 41, 51-6	2.9	16
58	A novel method for the rapid and prospective identification of Beijing Mycobacterium tuberculosis strains by high-resolution melting analysis. <i>Clinical Microbiology and Infection</i> , <b>2011</b> , 17, 349-57	9.5	15
57	Analysis of Mycobacterium tuberculosis genotypes in Madrid and identification of two new families specific to Spain-related settings. <i>Journal of Clinical Microbiology</i> , <b>2005</b> , 43, 1797-806	9.7	15
56	Co-infection with Drug-Susceptible and Reactivated Latent Multidrug-Resistant Mycobacterium tuberculosis. <i>Emerging Infectious Diseases</i> , <b>2015</b> , 21, 2098-100	10.2	14
55	Rapid detection and identification of Aspergillus from lower respiratory tract specimens by use of a combined probe-high-resolution melting analysis. <i>Journal of Clinical Microbiology</i> , <b>2012</b> , 50, 3238-43	9.7	14
54	Persistent Infection by a Mycobacterium tuberculosis Strain That Was Theorized To Have Advantageous Properties, as It Was Responsible for a Massive Outbreak. <i>Journal of Clinical Microbiology</i> , <b>2015</b> , 53, 3423-9	9.7	13
53	BK virus infection in human immunodeficiency virus-infected patients. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , <b>2012</b> , 31, 1531-5	5.3	12
52	Unmasking subtle differences in the infectivity of microevolved Mycobacterium tuberculosis variants coinfecting the same patient. <i>International Journal of Medical Microbiology</i> , <b>2013</b> , 303, 693-6	3.7	12
51	Evaluation of the inaccurate assignment of mixed infections by Mycobacterium tuberculosis as exogenous reinfection and analysis of the potential role of bacterial factors in reinfection. <i>Journal of Clinical Microbiology</i> , <b>2011</b> , 49, 1331-8	9.7	12
50	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> , <b>2016</b> , 54, 2969-2974	9.7	12
49	BK polyomavirus genotyping at inter- and intra-patient level in Spain. <i>Journal of Medical Virology</i> , <b>2013</b> , 85, 1402-8	19.7	11
48	Optimized molecular resolution of cross-contamination alerts in clinical mycobacteriology laboratories. <i>BMC Microbiology</i> , <b>2008</b> , 8, 30	4.5	11
47	Evaluation of bone marrow and blood cultures for the recovery of mycobacteria in the diagnosis of disseminated mycobacterial infections. <i>Clinical Microbiology and Infection</i> , <b>2004</b> , 10, 734-7	9.5	11
46	Differences between a probable and proven BCG infection following intravesical instillations: 16 years experience in a tertiary care hospital. <i>Diagnostic Microbiology and Infectious Disease</i> , <b>2016</b> , 85, 338-343	2.9	11
45	Multiple sampling and discriminatory fingerprinting reveals clonally complex and compartmentalized infections by M. bovis in cattle. <i>Veterinary Microbiology</i> , <b>2015</b> , 175, 99-104	3.3	10
44	Acquires Limited Genetic Diversity in Prolonged Infections, Reactivations and Transmissions Involving Multiple Hosts. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 2661	5.7	10
43	Rapid identification of linezolid resistance in Enterococcus spp. based on high-resolution melting analysis. <i>Journal of Microbiological Methods</i> , <b>2014</b> , 98, 41-3	2.8	10

42	Low dose aerosol fitness at the innate phase of murine infection better predicts virulence amongst clinical strains of <i>Mycobacterium tuberculosis</i> . <i>PLoS ONE</i> , <b>2012</b> , 7, e29010	3.7	10
41	Detailed chronological analysis of microevolution events in herds infected persistently by <i>Mycobacterium bovis</i> . <i>Veterinary Microbiology</i> , <b>2016</b> , 183, 97-102	3.3	9
40	A novel strategy based on genomics and specific PCR reveals how a multidrug-resistant <i>Mycobacterium tuberculosis</i> strain became prevalent in Equatorial Guinea 15 years after its emergence. <i>Clinical Microbiology and Infection</i> , <b>2017</b> , 23, 92-97	9.5	9
39	Genotyping of a nosocomial outbreak of pandemic influenza A/H1N1 2009. <i>Journal of Clinical Virology</i> , <b>2011</b> , 52, 129-32	14.5	9
38	Molecular and epidemiological population-based integrative analysis of human and animal <i>Mycobacterium bovis</i> infections in a low-prevalence setting. <i>Veterinary Microbiology</i> , <b>2016</b> , 195, 30-36	3.3	9
37	Susceptibility testing to second-line drugs and ethambutol by GenoType MTBDRsl and Bactec MGIT 960 comparing with agar proportion method. <i>Tuberculosis</i> , <b>2012</b> , 92, 417-21	2.6	8
36	Re-analysis of epidemiologically linked tuberculosis cases not supported by IS6110-RFLP-based genotyping. <i>Clinical Microbiology and Infection</i> , <b>2009</b> , 15, 763-9	9.5	8
35	Revealing hidden clonal complexity in <i>Mycobacterium tuberculosis</i> infection by qualitative and quantitative improvement of sampling. <i>Clinical Microbiology and Infection</i> , <b>2015</b> , 21, 147.e1-7	9.5	7
34	Optimizing and accelerating the assignment of lineages in <i>Mycobacterium tuberculosis</i> using novel alternative single-tube assays. <i>PLoS ONE</i> , <b>2017</b> , 12, e0186956	3.7	7
33	High-throughput multiplex MIRU-VNTR typing of <i>Mycobacterium bovis</i> . <i>Research in Veterinary Science</i> , <b>2014</b> , 96, 422-5	2.5	7
32	Molecular, epidemiological and infectivity characterisation of a <i>Mycobacterium tuberculosis</i> strain prevalent in Madrid. <i>Clinical Microbiology and Infection</i> , <b>2007</b> , 13, 1210-3	9.5	7
31	Differential findings regarding molecular epidemiology of tuberculosis between two consecutive periods in the context of steady increase of immigration. <i>Clinical Microbiology and Infection</i> , <b>2013</b> , 19, 292-7	9.5	6
30	Diagnostic performance of Anyplex II MTB/MDR/XDR for detection of resistance to first and second line drugs in <i>Mycobacterium tuberculosis</i> . <i>Journal of Microbiological Methods</i> , <b>2017</b> , 139, 74-78	2.8	5
29	Qualitative Analysis To Ascertain Genotypic Identity of or Differences between <i>Mycobacterium tuberculosis</i> Isolates in Laboratories with Limited Resources. <i>Journal of Clinical Microbiology</i> , <b>2013</b> , 51, 4230-3	9.7	5
28	Differences in the robustness of clusters involving the <i>Mycobacterium tuberculosis</i> strains most frequently isolated from immigrant cases in Madrid. <i>Clinical Microbiology and Infection</i> , <b>2010</b> , 16, 1544-54	9.5	5
27	A proposal for applying molecular markers as an aid to identifying potential cases of imported tuberculosis in immigrants. <i>Tuberculosis</i> , <b>2008</b> , 88, 641-7	2.6	5
26	Dynamic and complex <i>Mycobacterium tuberculosis</i> microevolution unrevealed by standard genotyping. <i>Tuberculosis</i> , <b>2012</b> , 92, 232-5	2.6	4
25	Subtle genotypic changes can be observed soon after diagnosis in <i>Mycobacterium tuberculosis</i> infection. <i>International Journal of Medical Microbiology</i> , <b>2016</b> , 306, 401-5	3.7	4



24	Recurrences of multidrug-resistant tuberculosis: Strains involved, within-host diversity, and fine-tuned allocation of reinfections. <i>Transboundary and Emerging Diseases</i> , <b>2021</b> ,	4.2	4
23	Clonal Complexity in Mycobacterium tuberculosis Can Hamper Diagnostic Procedures. <i>Journal of Clinical Microbiology</i> , <b>2017</b> , 55, 1388-1395	9.7	3
22	In-Depth Characterization and Functional Analysis of Clonal Variants in a Strain Prone to Microevolution. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 694	5.7	3
21	Decreased tuberculosis incidence and declining clustered case rates, Madrid. <i>Emerging Infectious Diseases</i> , <b>2008</b> , 14, 1641-3	10.2	3
20	Effect of potentially interfering substances on the measurement of HIV-1 viral load by the bDNA assay. <i>Journal of Virological Methods</i> , <b>1999</b> , 78, 149-52	2.6	3
19	Different dynamics of mean SARS-CoV-2 RT-PCR Ct values between the first and second COVID-19 waves in the Madrid population. <i>Transboundary and Emerging Diseases</i> , <b>2021</b> , 68, 3103-3106	4.2	3
18	Different Within-Host Viral Evolution Dynamics in Severely Immunosuppressed Cases with Persistent SARS-CoV-2. <i>Biomedicines</i> , <b>2021</b> , 9,	4.8	3
17	Usefulness of Genotype MTBDRplus assay in acid-fast bacilli positive smear specimens in Almeria, Spain. <i>Enfermedades Infecciosas Y Microbiología Clínica</i> , <b>2014</b> , 32, 511-4	0.9	2
16	Complete Analysis of the Epidemiological Scenario around a SARS-CoV-2 Reinfection: Previous Infection Events and Subsequent Transmission. <i>MSphere</i> , <b>2021</b> , 6, e0059621	5	2
15	Genetic features shared by Mycobacterium tuberculosis strains involved in microevolution events. <i>Infection, Genetics and Evolution</i> , <b>2013</b> , 16, 326-9	4.5	1
14	SARS-CoV-2 superinfection and reinfection with three different strains. <i>Transboundary and Emerging Diseases</i> , <b>2021</b> ,	4.2	1
13	Expanded tracking of a Beijing Mycobacterium tuberculosis strain involved in an outbreak in France. <i>Travel Medicine and Infectious Disease</i> , <b>2021</b> , 44, 102167	8.4	1
12	Evaluation of the potential role of a new mutation in mabA in modifying the response of Mycobacterium tuberculosis to isoniazid. <i>Tuberculosis</i> , <b>2013</b> , 93, 664-7	2.6	0
11	Nosocomial Transmission of SARS-CoV-2 Involving Vaccinated Health Care Workers.. <i>Microbiology Spectrum</i> , <b>2022</b> , e0153221	8.9	0
10	SARS-CoV-2 B.1.1.7 Decline Is Not Driven by the Introduction of a More Successful Variant. <i>Microbiology Spectrum</i> , <b>2021</b> , e0112821	8.9	0
9	Probable long-term prevalence for a predominant Mycobacterium tuberculosis clone of a Beijing genotype in Colon, Panama. <i>Transboundary and Emerging Diseases</i> , <b>2021</b> , 68, 2229-2238	4.2	0
8	A deletion hampering appropriate typing of Mycobacterium africanum. <i>Tuberculosis</i> , <b>2017</b> , 103, 24-27	2.6	
7	Equatorial Guinea, a multidrug-resistant tuberculosis hotspot in Central Africa. <i>European Respiratory Journal</i> , <b>2017</b> , 49,	13.6	

6	O450 Infections due to non-pigmented rapidly growing mycobacteria in Madrid, 2005. <i>International Journal of Antimicrobial Agents</i> , <b>2007</b> , 29, S94-S95	14.3
5	Insights into the Complexity of a Dormant Cluster Once Transmission Is Resumed.. <i>Microbiology Spectrum</i> , <b>2022</b> , e0138121	8.9
4	Shared Mutations in Emerging SARS-CoV-2 Circulating Variants May Lead to Reverse Transcription-PCR (RT-PCR)-Based Misidentification of B.1.351 and P.1 Variants of Concern. <i>Microbiology Spectrum</i> , <b>2021</b> , 9, e0081621	8.9
3	Paying attention to the details in Mycobacterium tuberculosis: Strain-specific single-nucleotide polymorphisms and clonal variants. <i>International Journal of Mycobacteriology</i> , <b>2016</b> , 5 Suppl 1, S76	0.9
2	Host Genetic Analysis Should Be Mandatory for Proper Classification of COVID-19 Reinfections. <i>Open Forum Infectious Diseases</i> , <b>2021</b> , 8, ofab402	1
1	Detection of Minority Variants and Mixed Infections in Mycobacterium tuberculosis by Direct Whole-Genome Sequencing on Noncultured Specimens Using a Specific-DNA Capture Strategy.. <i>MSphere</i> , <b>2021</b> , 6, e0074421	5