Jaime Robledo

List of Publications by Year in descending order

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LAIME ROBLEDO

#	Article	IF	CITATIONS
1	The 2021 WHO catalogue of Mycobacterium tuberculosis complex mutations associated with drug resistance: a genotypic analysis. Lancet Microbe, The, 2022, 3, e265-e273.	7.3	114
2	Characterization of Mycobacterium tuberculosis var. africanum isolated from a patient with pulmonary tuberculosis in Brazil. Infection, Genetics and Evolution, 2020, 85, 104550.	2.3	6
3	Risk of infection and disease progression in children exposed to tuberculosis at home, Colombia. Colombia Medica, 2019, 50, 261-274.	0.2	2
4	Toxin–antitoxin systems shows variability among <i>Mycobacterium tuberculosis</i> lineages. FEMS Microbiology Letters, 2019, 366, .	1.8	5
5	Identificación directa de microorganismos a partir de muestras de orina y hemocultivos utilizando MALDI-TOF. Infectio, 2019, 23, 364.	0.4	1
6	Genome-wide analysis of multi- and extensively drug-resistant Mycobacterium tuberculosis. Nature Genetics, 2018, 50, 307-316.	21.4	271
7	Comparative study of Candida spp. isolates: Identification and echinocandin susceptibility in isolates obtained from blood cultures in 15 hospitals in MedellĀn, Colombia. Journal of Global Antimicrobial Resistance, 2018, 13, 254-260.	2.2	12
8	Some Synonymous and Nonsynonymous <i>gyrA</i> Mutations in Mycobacterium tuberculosis Lead to Systematic False-Positive Fluoroquinolone Resistance Results with the Hain GenoType MTBDR <i>sl</i> Assays. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	29
9	Whole-Genome Sequencing of a Haarlem Extensively Drug-Resistant Mycobacterium tuberculosis Clinical Isolate from MedellAn, Colombia. Genome Announcements, 2016, 4, .	0.8	1
10	Tuberculous Lymphadenitis and Parotitis. Microbiology Spectrum, 2016, 4, .	3.0	19
11	Whole-Genome Sequencing of Two Latin American–Mediterranean Extensively Drug-ResistantÂ Mycobacterium tuberculosis ÂClinical Isolates from MedellÃn, Colombia. Genome Announcements, 2016, 4, .	0.8	1
12	Draft Genome Sequence of a Mycobacterium africanum Clinical Isolate from Antioquia, Colombia. Genome Announcements, 2016, 4, .	0.8	3
13	Whole-Genome Sequence of a Beijing Extensively Drug-Resistant Mycobacterium tuberculosis Clinical Isolate from Buenaventura, Colombia. Genome Announcements, 2016, 4, .	0.8	5
14	Genotypic Analysis of Genes Associated with Independent Resistance and Cross-Resistance to Isoniazid and Ethionamide in Mycobacterium tuberculosis Clinical Isolates. Antimicrobial Agents and Chemotherapy, 2015, 59, 7805-7810.	3.2	45
15	The Structural Modeling of the Interaction between Levofloxacin and the <i>Mycobacterium tuberculosis</i> Gyrase Catalytic Site Sheds Light on the Mechanisms of Fluoroquinolones Resistant Tuberculosis in Colombian Clinical Isolates. BioMed Research International, 2014, 2014, 1-9.	1.9	15
16	Population Structure among Mycobacterium tuberculosis Isolates from Pulmonary Tuberculosis Patients in Colombia. PLoS ONE, 2014, 9, e93848.	2.5	46
17	Association of clinical and demographic factors in invasive candidiasis caused by fluconazole-resistant Candida species: a study in 15 hospitals, MedellÃn, Colombia 2010–2011. Diagnostic Microbiology and Infectious Disease, 2014, 79, 280-286.	1.8	17
18	Whole genome shotgun sequencing of one Colombian clinical isolate of Mycobacterium tuberculosis reveals DosR regulon gene deletions. FEMS Microbiology Letters, 2012, 330, 113-120.	1.8	20

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19	IFNÎ ³ Response to Mycobacterium tuberculosis, Risk of Infection and Disease in Household Contacts of Tuberculosis Patients in Colombia. PLoS ONE, 2009, 4, e8257.	2.5	90
20	Mycobacterium tuberculosis strains of the Beijing genotype are rarely observed in tuberculosis patients in South America. Memorias Do Instituto Oswaldo Cruz, 2008, 103, 489-492.	1.6	51
21	La espectrometrÃa de masas MALDI-TOF en el laboratorio de microbiologÃa clÃnica. Infectio, 0, , .	0.4	6