

Jaime Robledo

List of Publications by Year in descending order

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papers

771
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840776

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24
times ranked

1188
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide analysis of multi- and extensively drug-resistant <i>Mycobacterium tuberculosis</i> . <i>Nature Genetics</i> , 2018, 50, 307-316.	21.4	271
2	The 2021 WHO catalogue of <i>Mycobacterium tuberculosis</i> complex mutations associated with drug resistance: a genotypic analysis. <i>Lancet Microbe</i> , The, 2022, 3, e265-e273.	7.3	114
3	IFN γ Response to <i>Mycobacterium tuberculosis</i> , Risk of Infection and Disease in Household Contacts of Tuberculosis Patients in Colombia. <i>PLoS ONE</i> , 2009, 4, e8257.	2.5	90
4	<i>Mycobacterium tuberculosis</i> strains of the Beijing genotype are rarely observed in tuberculosis patients in South America. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2008, 103, 489-492.	1.6	51
5	Population Structure among <i>Mycobacterium tuberculosis</i> Isolates from Pulmonary Tuberculosis Patients in Colombia. <i>PLoS ONE</i> , 2014, 9, e93848.	2.5	46
6	Genotypic Analysis of Genes Associated with Independent Resistance and Cross-Resistance to Isoniazid and Ethionamide in <i>Mycobacterium tuberculosis</i> Clinical Isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 7805-7810.	3.2	45
7	Some Synonymous and Nonsynonymous <i>gyrA</i> Mutations in <i>Mycobacterium tuberculosis</i> Lead to Systematic False-Positive Fluoroquinolone Resistance Results with the Hain GenoType MTBDR Assays. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	29
8	Whole genome shotgun sequencing of one Colombian clinical isolate of <i>Mycobacterium tuberculosis</i> reveals DosR regulon gene deletions. <i>FEMS Microbiology Letters</i> , 2012, 330, 113-120.	1.8	20
9	Tuberculous Lymphadenitis and Parotitis. <i>Microbiology Spectrum</i> , 2016, 4, .	3.0	19
10	Association of clinical and demographic factors in invasive candidiasis caused by fluconazole-resistant <i>Candida</i> species: a study in 15 hospitals, Medellín, Colombia 2010-2011. <i>Diagnostic Microbiology and Infectious Disease</i> , 2014, 79, 280-286.	1.8	17
11	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. <i>BioMed Research International</i> , 2014, 2014, 1-9.	1.9	15
12	Comparative study of <i>Candida</i> spp. isolates: Identification and echinocandin susceptibility in isolates obtained from blood cultures in 15 hospitals in Medellín, Colombia. <i>Journal of Global Antimicrobial Resistance</i> , 2018, 13, 254-260.	2.2	12
13	Characterization of <i>Mycobacterium tuberculosis</i> var. <i>africanum</i> isolated from a patient with pulmonary tuberculosis in Brazil. <i>Infection, Genetics and Evolution</i> , 2020, 85, 104550.	2.3	6
14	La espectrometría de masas MALDI-TOF en el laboratorio de microbiología clínica. <i>Infectio</i> , 0, .	0.4	6
15	Whole-Genome Sequence of a Beijing Extensively Drug-Resistant <i>Mycobacterium tuberculosis</i> Clinical Isolate from Buenaventura, Colombia. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
16	Toxin-antitoxin systems shows variability among <i>Mycobacterium tuberculosis</i> lineages. <i>FEMS Microbiology Letters</i> , 2019, 366, .	1.8	5
17	Draft Genome Sequence of a <i>Mycobacterium africanum</i> Clinical Isolate from Antioquia, Colombia. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
18	Risk of infection and disease progression in children exposed to tuberculosis at home, Colombia. <i>Colombia Medica</i> , 2019, 50, 261-274.	0.2	2

#	ARTICLE	IF	CITATIONS
19	Whole-Genome Sequencing of a Haarlem Extensively Drug-Resistant Mycobacterium tuberculosis Clinical Isolate from Medellín, Colombia. Genome Announcements, 2016, 4, .	0.8	1
20	Whole-Genome Sequencing of Two Latin American "Mediterranean Extensively Drug-Resistant" Mycobacterium tuberculosis Clinical Isolates from Medellín, Colombia. Genome Announcements, 2016, 4, .	0.8	1
21	Identificación directa de microorganismos a partir de muestras de orina y hemocultivos utilizando MALDI-TOF. Infectio, 2019, 23, 364.	0.4	1