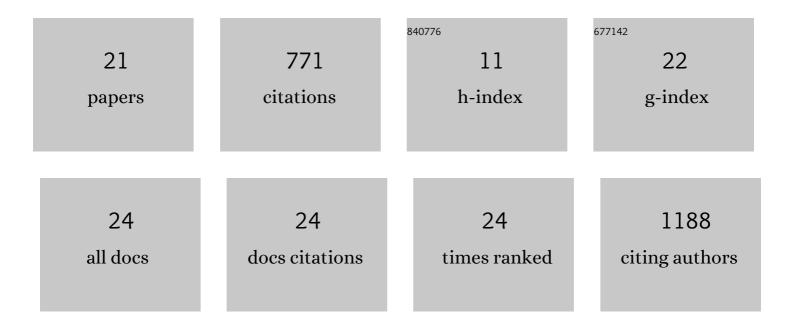
## Jaime Robledo

List of Publications by Year in descending order

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LAIME PORIEDO

#	Article	IF	CITATIONS
1	Genome-wide analysis of multi- and extensively drug-resistant Mycobacterium tuberculosis. Nature Genetics, 2018, 50, 307-316.	21.4	271
2	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
3	IFNÎ <sup>3</sup> 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
4	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
5	Population Structure among Mycobacterium tuberculosis Isolates from Pulmonary Tuberculosis Patients in Colombia. PLoS ONE, 2014, 9, e93848.	2.5	46
6	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
7	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
8	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
9	Tuberculous Lymphadenitis and Parotitis. Microbiology Spectrum, 2016, 4, .	3.0	19
10	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
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. BioMed Research International, 2014, 2014, 1-9.	1.9	15
12	Comparative study of Candida spp. isolates: Identification and echinocandin susceptibility in isolates obtained from blood cultures in 15 hospitals in MedellÃn, Colombia. Journal of Global Antimicrobial Resistance, 2018, 13, 254-260.	2.2	12
13	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
14	La espectrometrÃa de masas MALDI-TOF en el laboratorio de microbiologÃa clÃnica. Infectio, 0, , .	0.4	6
15	Whole-Genome Sequence of a Beijing Extensively Drug-Resistant Mycobacterium tuberculosis Clinical Isolate from Buenaventura, Colombia. Genome Announcements, 2016, 4, .	0.8	5
16	Toxin–antitoxin systems shows variability among <i>Mycobacterium tuberculosis</i> lineages. FEMS Microbiology Letters, 2019, 366, .	1.8	5
17	Draft Genome Sequence of a Mycobacterium africanum Clinical Isolate from Antioquia, Colombia. Genome Announcements, 2016, 4, .	0.8	3
18	Risk of infection and disease progression in children exposed to tuberculosis at home, Colombia. Colombia Medica, 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 MedellAn, Colombia. Genome Announcements, 2016, 4, .	0.8	1
20	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
21	Identificación directa de microorganismos a partir de muestras de orina y hemocultivos utilizando MALDI-TOF. Infectio, 2019, 23, 364.	0.4	1