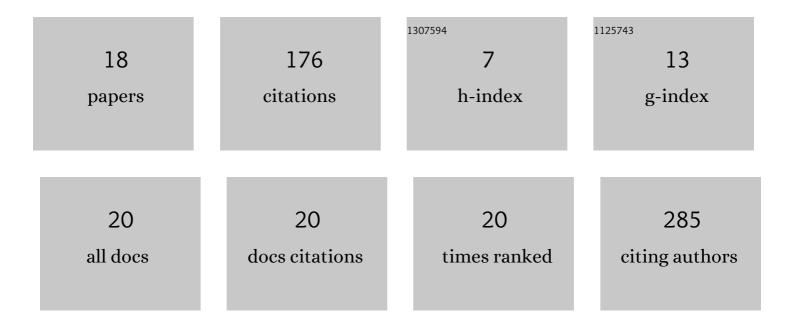
Julio Guerra

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4474446/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Heterogeneous fitness landscape cues, pknG high expression, and phthiocerol dimycocerosate low production of Mycobacterium tuberculosis ATCC25618 rpoB S450L in enriched broth. Tuberculosis, 2022, 132, 102156.	1.9	3
2	Close Related Drug-Resistance Beijing Isolates of Mycobacterium tuberculosis Reveal a Different Transcriptomic Signature in a Murine Disease Progression Model. International Journal of Molecular Sciences, 2022, 23, 5157.	4.1	3
3	First approach to the population structure of Mycobacterium tuberculosis complex in the indigenous population in Puerto Nariño-Amazonas, Colombia. PLoS ONE, 2021, 16, e0245084.	2.5	5
4	Profiling the immune response to <i>Mycobacterium tuberculosis</i> Beijing family infection: a perspective from the transcriptome. Virulence, 2021, 12, 1689-1704.	4.4	9
5	Title is missing!. , 2021, 16, e0245084.		0
6	Title is missing!. , 2021, 16, e0245084.		0
7	Title is missing!. , 2021, 16, e0245084.		0
8	Title is missing!. , 2021, 16, e0245084.		0
9	Genetic diversity of Mycobacterium tuberculosis clinical isolates from HIV-TB patients from two public hospitals at BogotÃ;, Colombia. Infection, Genetics and Evolution, 2020, 77, 104059.	2.3	0
10	Population structure of multidrug-resistant Mycobacterium tuberculosis clinical isolates in Colombia. Tuberculosis, 2020, 125, 102011.	1.9	4
11	Characterization of clinical isolates of Mycobacterium tuberculosis from indigenous peoples of Colombia. Biomedica, 2019, 39, 78-92.	0.7	3
12	Active and latent tuberculosis among inmates in La Esperanza prison in Guaduas, Colombia. PLoS ONE, 2019, 14, e0209895.	2.5	12
13	Circulation of <i>M. tuberculosis</i> Beijing genotype in Latin America and the Caribbean. Pathogens and Global Health, 2019, 113, 336-351.	2.3	13
14	Comparative genomic analysis of Mycobacterium tuberculosis Beijing-like strains revealed specific genetic variations associated with virulence and drug resistance. Infection, Genetics and Evolution, 2017, 54, 314-323.	2.3	30
15	Complete Genome Sequence of the Clinical Beijing-Like Strain Mycobacterium tuberculosis 323 Using the PacBio Real-Time Sequencing Platform. Genome Announcements, 2015, 3, .	0.8	10
16	Virulence and Immune Response Induced by Mycobacterium avium Complex Strains in a Model of Progressive Pulmonary Tuberculosis and Subcutaneous Infection in BALB/c Mice. Infection and Immunity, 2013, 81, 4001-4012.	2.2	18
17	A first insight on the population structure of Mycobacterium tuberculosis complex as studied by spoligotyping and MIRU-VNTRs in BogotÃį, Colombia. Infection, Genetics and Evolution, 2012, 12, 657-663.	2.3	42
18	First case of multidrug-resistant tuberculosis caused by a rare "Beijing-like―genotype of Mycobacterium tuberculosis in Bogotá, Colombia. Infection, Genetics and Evolution, 2010, 10, 678-681.	2.3	16