

Sofia Samper

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

3,366
citations

304368

22
h-index

197535

49
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52
all docs

52
docs citations

52
times ranked

3455
citing authors

#	ARTICLE	IF	CITATIONS
1	In-depth Analysis of IS6110 Genomic Variability in the Mycobacterium tuberculosis Complex. <i>Frontiers in Microbiology</i> , 2022, 13, 767912.	1.5	2
2	The MtZ Strain: Molecular Characteristics and Outbreak Investigation of the Most Successful Mycobacterium tuberculosis Strain in Aragon Using Whole-Genome Sequencing. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, .	1.8	3
3	A whole-genome sequencing study of an X-family tuberculosis outbreak focus on transmission chain along 25 years. <i>Tuberculosis</i> , 2021, 126, 102022.	0.8	7
4	Analysis of Mycobacterium africanum in the last 17 years in Aragon identifies a specific location of IS6110 in Lineage 6. <i>Scientific Reports</i> , 2021, 11, 10359.	1.6	2
5	The value of the continuous genotyping of multi-drug resistant tuberculosis over 20 years in Spain. <i>Scientific Reports</i> , 2020, 10, 20433.	1.6	9
6	Live attenuated TB vaccines representing the three modern Mycobacterium tuberculosis lineages reveal that the Euro-American genetic background confers optimal vaccine potential. <i>EBioMedicine</i> , 2020, 55, 102761.	2.7	22
7	Investigation of a rapidly spreading tuberculosis outbreak using whole-genome sequencing. <i>Infection, Genetics and Evolution</i> , 2020, 81, 104184.	1.0	13
8	A Mycobacterium tuberculosis Beijing strain persists at high rates and extends its geographic boundaries 20 years after importation. <i>Scientific Reports</i> , 2019, 9, 4687.	1.6	11
9	Microbiological diagnosis of infections caused by the genus Mycobacterium. <i>Enfermedades Infecciosas Y Microbiología Clínica (English Ed)</i> , 2018, 36, 104-111.	0.2	1
10	Diagnóstico microbiológico de las infecciones causadas por el género Mycobacterium. <i>Enfermedades Infecciosas Y Microbiología Clínica</i> , 2018, 36, 104-111.	0.3	2
11	Antimicrobial photodynamic activity of Rose Bengal, alone or in combination with Gentamicin, against planktonic and biofilm Staphylococcus aureus. <i>Photodiagnosis and Photodynamic Therapy</i> , 2018, 21, 211-216.	1.3	45
12	Data-driven model for the assessment of Mycobacterium tuberculosis transmission in evolving demographic structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3238-E3245.	3.3	36
13	New insights into the transposition mechanisms of IS6110 and its dynamic distribution between Mycobacterium tuberculosis Complex lineages. <i>PLoS Genetics</i> , 2018, 14, e1007282.	1.5	57
14	Diagnóstico rápido de la tuberculosis. Detección de mecanismos de resistencia. <i>Enfermedades Infecciosas Y Microbiología Clínica</i> , 2017, 35, 520-528.	0.3	12
15	Rapid diagnosis of tuberculosis. Detection of drug resistance mechanisms. <i>Enfermedades Infecciosas Y Microbiología Clínica (English Ed)</i> , 2017, 35, 518-526.	0.2	6
16	Mycobacterium tuberculosis genotypes and predominant clones among the multidrug-resistant isolates in Spain 1998-2005. <i>Infection, Genetics and Evolution</i> , 2017, 55, 117-126.	1.0	3
17	Molecular Characterization of Mycobacterium tuberculosis Strains with TB-SPRINT. <i>American Journal of Tropical Medicine and Hygiene</i> , 2017, 97, 806-809.	0.6	8
18	In-depth analysis of the genome sequence of a clinical, extensively drug-resistant Mycobacterium bovis strain. <i>Tuberculosis</i> , 2016, 100, 46-52.	0.8	9

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19	Peritoneal tuberculosis due to <i>Mycobacterium caprae</i> . <i>IDCases</i> , 2016, 4, 50-52.	0.4	2
20	Evolutionary history and global spread of the <i>Mycobacterium tuberculosis</i> Beijing lineage. <i>Nature Genetics</i> , 2015, 47, 242-249.	9.4	466
21	Pyrosequencing for rapid detection of <i>Mycobacterium tuberculosis</i> second-line drugs and ethambutol resistance. <i>Diagnostic Microbiology and Infectious Disease</i> , 2015, 83, 263-269.	0.8	14
22	<i>In Vivo</i> IS6110 Profile Changes in a <i>Mycobacterium tuberculosis</i> Strain as Determined by Tracking over 14 Years. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2359-2361.	1.8	5
23	A Specific Polymorphism in <i>Mycobacterium tuberculosis</i> H37Rv Causes Differential ESAT-6 Expression and Identifies <i>WhiB6</i> as a Novel ESX-1 Component. <i>Infection and Immunity</i> , 2014, 82, 3446-3456.	1.0	74
24	Role of Wild Bird and Rodents in the Epidemiology of Subclinical Salmonellosis in Finishing Pigs. <i>Foodborne Pathogens and Disease</i> , 2014, 11, 689-697.	0.8	41
25	Single nucleotide polymorphism (SNP) analysis used for the phylogeny of the <i>Mycobacterium tuberculosis</i> complex based on a pyrosequencing assay. <i>BMC Microbiology</i> , 2014, 14, 21.	1.3	11
26	Proposal of a Consensus Set of Hypervariable <i>Mycobacterial</i> Interspersed Repetitive-Unit Variable-Number Tandem-Repeat Loci for Subtyping of <i>Mycobacterium tuberculosis</i> Beijing Isolates. <i>Journal of Clinical Microbiology</i> , 2014, 52, 164-172.	1.8	81
27	Mapping IS6110 in high-copy number <i>Mycobacterium tuberculosis</i> strains shows specific insertion points in the Beijing genotype. <i>BMC Genomics</i> , 2013, 14, 422.	1.2	43
28	<i>Mycobacterium simiae</i> pulmonary infection unmasked during immune reconstitution in an HIV patient. <i>Diagnostic Microbiology and Infectious Disease</i> , 2013, 75, 101-103.	0.8	9
29	Global Study of IS6110 in a Successful <i>Mycobacterium tuberculosis</i> Strain: Clues for Deciphering Its Behavior and for Its Rapid Detection. <i>Journal of Clinical Microbiology</i> , 2013, 51, 3631-3637.	1.8	15
30	Analysis of Mutations in Streptomycin-Resistant Strains Reveals a Simple and Reliable Genetic Marker for Identification of the <i>Mycobacterium tuberculosis</i> Beijing Genotype. <i>Journal of Clinical Microbiology</i> , 2013, 51, 2124-2130.	1.8	33
31	Rapid Test for Identification of a Highly Transmissible <i>Mycobacterium tuberculosis</i> Beijing Strain of Sub-Saharan Origin. <i>Journal of Clinical Microbiology</i> , 2012, 50, 516-518.	1.8	16
32	IS-seq: a novel high throughput survey of <i>in vivo</i> IS6110 transposition in multiple <i>Mycobacterium tuberculosis</i> genomes. <i>BMC Genomics</i> , 2012, 13, 249.	1.2	29
33	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> , 2012, 7, e29010.	1.1	14
34	Long-term molecular surveillance of multidrug-resistant tuberculosis in Spain. <i>Infection, Genetics and Evolution</i> , 2012, 12, 701-710.	1.0	18
35	Conspicuous multidrug-resistant <i>Mycobacterium tuberculosis</i> cluster strains do not trespass country borders in Latin America and Spain. <i>Infection, Genetics and Evolution</i> , 2012, 12, 711-717.	1.0	30
36	Deciphering the role of IS6110 in a highly transmissible <i>Mycobacterium tuberculosis</i> Beijing strain, GC1237. <i>Tuberculosis</i> , 2011, 91, 117-126.	0.8	47

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37	First insights into the genetic diversity of <i>Mycobacterium tuberculosis</i> isolates from HIV-infected Mexican patients and mutations causing multidrug resistance. <i>BMC Microbiology</i> , 2010, 10, 82.	1.3	23
38	Multidrug-Resistant <i>Mycobacterium tuberculosis</i> Strain from Equatorial Guinea Detected in Spain. <i>Emerging Infectious Diseases</i> , 2009, 15, 1858b-1860.	2.0	11
39	Unsuspected and extensive transmission of a drug-susceptible <i>Mycobacterium tuberculosis</i> strain. <i>BMC Pulmonary Medicine</i> , 2009, 9, 3.	0.8	15
40	Multidrug-resistant <i>Mycobacterium tuberculosis</i> Beijing/W genotype in Venezuela. <i>Journal of Medical Microbiology</i> , 2007, 56, 1707-1708.	0.7	5
41	Spread of Extensively Drug-resistant Tuberculosis. <i>Emerging Infectious Diseases</i> , 2007, 13, 647-648.	2.0	21
42	<i>Mycobacterium tuberculosis</i> complex genetic diversity: mining the fourth international spoligotyping database (SpolDB4) for classification, population genetics and epidemiology. <i>BMC Microbiology</i> , 2006, 6, 23.	1.3	900
43	Molecular characterisation of <i>Mycobacterium tuberculosis</i> isolates in the First National Survey of Anti-tuberculosis Drug Resistance from Venezuela. <i>BMC Microbiology</i> , 2006, 6, 90.	1.3	39
44	Molecular characterization of <i>Mycobacterium tuberculosis</i> complex isolates from wild ungulates in south-central Spain. <i>Veterinary Research</i> , 2005, 36, 43-52.	1.1	109
45	IS 6110 Mediates Increased Transcription of the <i>phoP</i> Virulence Gene in a Multidrug-Resistant Clinical Isolate Responsible for Tuberculosis Outbreaks. <i>Journal of Clinical Microbiology</i> , 2004, 42, 212-219.	1.8	130
46	Mutations in Putative Mutator Genes of <i>Mycobacterium tuberculosis</i> Strains of the W-Beijing Family. <i>Emerging Infectious Diseases</i> , 2003, 9, 838-845.	2.0	240
47	An essential role for <i>phoP</i> in <i>Mycobacterium tuberculosis</i> virulence. <i>Molecular Microbiology</i> , 2001, 41, 179-187.	1.2	363
48	Epidemiological Evidence of the Spread of a <i>Mycobacterium tuberculosis</i> Strain of the Beijing Genotype on Gran Canaria Island. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2001, 164, 1165-1170.	2.5	163
49	Usefulness of Spoligotyping in Molecular Epidemiology of <i>Mycobacterium bovis</i> -Related Infections in South America. <i>Journal of Clinical Microbiology</i> , 1999, 37, 296-303.	1.8	75
50	Transmission between HIV-infected patients of multidrug-resistant tuberculosis caused by <i>Mycobacterium bovis</i> . <i>Aids</i> , 1997, 11, 1237-1242.	1.0	76