

# Sofia Samper

## List of Publications by Year in descending order

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50  
papers

3,366  
citations

304368

22  
h-index

197535

49  
g-index

52  
all docs

52  
docs citations

52  
times ranked

3455  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mycobacterium tuberculosis complex genetic diversity: mining the fourth international spoligotyping database (SpolDB4) for classification, population genetics and epidemiology. BMC Microbiology, 2006, 6, 23.	1.3	900
2	Evolutionary history and global spread of the Mycobacterium tuberculosis Beijing lineage. Nature Genetics, 2015, 47, 242-249.	9.4	466
3	An essential role for phoP in Mycobacterium tuberculosis virulence. Molecular Microbiology, 2001, 41, 179-187.	1.2	363
4	Mutations in Putative Mutator Genes of Mycobacterium tuberculosis Strains of the W-Beijing Family. Emerging Infectious Diseases, 2003, 9, 838-845.	2.0	240
5	Epidemiological Evidence of the Spread of a Mycobacterium tuberculosis Strain of the Beijing Genotype on Gran Canaria Island. American Journal of Respiratory and Critical Care Medicine, 2001, 164, 1165-1170.	2.5	163
6	IS 6110 Mediates Increased Transcription of the phoP Virulence Gene in a Multidrug-Resistant Clinical Isolate Responsible for Tuberculosis Outbreaks. Journal of Clinical Microbiology, 2004, 42, 212-219.	1.8	130
7	Molecular characterization of Mycobacterium tuberculosis complex isolates from wild ungulates in south-central Spain. Veterinary Research, 2005, 36, 43-52.	1.1	109
8	Proposal of a Consensus Set of Hypervariable Mycobacterial Interspersed Repetitive-Unit Variable-Number Tandem-Repeat Loci for Subtyping of Mycobacterium tuberculosis Beijing Isolates. Journal of Clinical Microbiology, 2014, 52, 164-172.	1.8	81
9	Transmission between HIV-infected patients of multidrug-resistant tuberculosis caused by Mycobacterium bovis. Aids, 1997, 11, 1237-1242.	1.0	76
10	Usefulness of Spoligotyping in Molecular Epidemiology of Mycobacterium bovis-Related Infections in South America. Journal of Clinical Microbiology, 1999, 37, 296-303.	1.8	75
11	A Specific Polymorphism in Mycobacterium tuberculosis H37Rv Causes Differential ESAT-6 Expression and Identifies WhiB6 as a Novel ESX-1 Component. Infection and Immunity, 2014, 82, 3446-3456.	1.0	74
12	New insights into the transposition mechanisms of IS6110 and its dynamic distribution between Mycobacterium tuberculosis Complex lineages. PLoS Genetics, 2018, 14, e1007282.	1.5	57
13	Deciphering the role of IS6110 in a highly transmissible Mycobacterium tuberculosis Beijing strain, GC1237. Tuberculosis, 2011, 91, 117-126.	0.8	47
14	Antimicrobial photodynamic activity of Rose Bengal, alone or in combination with Gentamicin, against planktonic and biofilm Staphylococcus aureus. Photodiagnosis and Photodynamic Therapy, 2018, 21, 211-216.	1.3	45
15	Mapping IS6110 in high-copy number Mycobacterium tuberculosis strains shows specific insertion points in the Beijing genotype. BMC Genomics, 2013, 14, 422.	1.2	43
16	Role of Wild Bird and Rodents in the Epidemiology of Subclinical Salmonellosis in Finishing Pigs. Foodborne Pathogens and Disease, 2014, 11, 689-697.	0.8	41
17	Molecular characterisation of Mycobacterium tuberculosis isolates in the First National Survey of Anti-tuberculosis Drug Resistance from Venezuela. BMC Microbiology, 2006, 6, 90.	1.3	39
18	Data-driven model for the assessment of Mycobacterium tuberculosis transmission in evolving demographic structures. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3238-E3245.	3.3	36

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19	Analysis of Mutations in Streptomycin-Resistant Strains Reveals a Simple and Reliable Genetic Marker for Identification of the Mycobacterium tuberculosis Beijing Genotype. <i>Journal of Clinical Microbiology</i> , 2013, 51, 2124-2130.	1.8	33
20	Conspicuous multidrug-resistant Mycobacterium tuberculosis 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
21	IS-seq: a novel high throughput survey of in vivo IS6110 transposition in multiple Mycobacterium tuberculosis genomes. <i>BMC Genomics</i> , 2012, 13, 249.	1.2	29
22	First insights into the genetic diversity of Mycobacterium tuberculosis isolates from HIV-infected Mexican patients and mutations causing multidrug resistance. <i>BMC Microbiology</i> , 2010, 10, 82.	1.3	23
23	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
24	Spread of Extensively Drug-resistant Tuberculosis. <i>Emerging Infectious Diseases</i> , 2007, 13, 647-648.	2.0	21
25	Long-term molecular surveillance of multidrug-resistant tuberculosis in Spain. <i>Infection, Genetics and Evolution</i> , 2012, 12, 701-710.	1.0	18
26	Rapid Test for Identification of a Highly Transmissible Mycobacterium tuberculosis Beijing Strain of Sub-Saharan Origin. <i>Journal of Clinical Microbiology</i> , 2012, 50, 516-518.	1.8	16
27	Unsuspected and extensive transmission of a drug-susceptible Mycobacterium tuberculosis strain. <i>BMC Pulmonary Medicine</i> , 2009, 9, 3.	0.8	15
28	Global Study of IS6110 in a Successful Mycobacterium tuberculosis Strain: Clues for Deciphering Its Behavior and for Its Rapid Detection. <i>Journal of Clinical Microbiology</i> , 2013, 51, 3631-3637.	1.8	15
29	Low Dose Aerosol Fitness at the Innate Phase of Murine Infection Better Predicts Virulence amongst Clinical Strains of Mycobacterium tuberculosis. <i>PLoS ONE</i> , 2012, 7, e29010.	1.1	14
30	Pyrosequencing for rapid detection of Mycobacterium tuberculosis second-line drugs and ethambutol resistance. <i>Diagnostic Microbiology and Infectious Disease</i> , 2015, 83, 263-269.	0.8	14
31	Investigation of a rapidly spreading tuberculosis outbreak using whole-genome sequencing. <i>Infection, Genetics and Evolution</i> , 2020, 81, 104184.	1.0	13
32	Diagnóstico rápido de la tuberculosis. Detección de mecanismos de resistencia. <i>Enfermedades Infecciosas Y Microbiología Clínica</i> , 2017, 35, 520-528.	0.3	12
33	Multidrug-Resistant Mycobacterium tuberculosis Strain from Equatorial Guinea Detected in Spain. <i>Emerging Infectious Diseases</i> , 2009, 15, 1858b-1860.	2.0	11
34	Single nucleotide polymorphism (SNP) analysis used for the phylogeny of the Mycobacterium tuberculosis complex based on a pyrosequencing assay. <i>BMC Microbiology</i> , 2014, 14, 21.	1.3	11
35	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
36	Mycobacterium simiae pulmonary infection unmasked during immune reconstitution in an HIV patient. <i>Diagnostic Microbiology and Infectious Disease</i> , 2013, 75, 101-103.	0.8	9

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37	In-depth analysis of the genome sequence of a clinical, extensively drug-resistant <i>Mycobacterium bovis</i> strain. <i>Tuberculosis</i> , 2016, 100, 46-52.	0.8	9
38	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
39	Molecular Characterization of <i>Mycobacterium tuberculosis</i> Strains with TB-SPRINT. <i>American Journal of Tropical Medicine and Hygiene</i> , 2017, 97, 806-809.	0.6	8
40	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
41	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
42	Multidrug-resistant <i>Mycobacterium tuberculosis</i> Beijing/W genotype in Venezuela. <i>Journal of Medical Microbiology</i> , 2007, 56, 1707-1708.	0.7	5
43	<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
44	<i>Mycobacterium tuberculosis</i> 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
45	The MtZ Strain: Molecular Characteristics and Outbreak Investigation of the Most Successful <i>Mycobacterium tuberculosis</i> Strain in Aragon Using Whole-Genome Sequencing. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, .	1.8	3
46	Peritoneal tuberculosis due to <i>Mycobacterium caprae</i> . <i>IDCases</i> , 2016, 4, 50-52.	0.4	2
47	Diagnóstico microbiológico de las infecciones causadas por el género <i>Mycobacterium</i> . <i>Enfermedades Infecciosas Y Microbiología Clínica</i> , 2018, 36, 104-111.	0.3	2
48	Analysis of <i>Mycobacterium africanum</i> 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
49	In-depth Analysis of IS6110 Genomic Variability in the <i>Mycobacterium tuberculosis</i> Complex. <i>Frontiers in Microbiology</i> , 2022, 13, 767912.	1.5	2
50	Microbiological diagnosis of infections caused by the genus <i>Mycobacterium</i> . <i>Enfermedades Infecciosas Y Microbiología Clínica (English Ed)</i> , 2018, 36, 104-111.	0.2	1