Yurena navarro

List of Publications by Year
in descending order

22 papers	655 citations	687363 13 h-index	677142 22 g-index
23 all docs	23 docs citations	23 times ranked	971 citing authors

#	ARTICLE	IF	CITATIONS
1	Effect of a Multistarter Yeast Inoculum on Ethanol Reduction and Population Dynamics in Wine Fermentation. Foods, 2021, 10, 623.	4.3	11
2	Viability-PCR Allows Monitoring Yeast Population Dynamics in Mixed Fermentations Including Viable but Non-Culturable Yeasts. Foods, 2020, 9, 1373.	4.3	9
3	Dual functionality of the amyloid protein TasA in Bacillus physiology and fitness on the phylloplane. Nature Communications, 2020, 11, 1859.	12.8	59
4	A Rapid Method for Selecting Non-Saccharomyces Strains with a Low Ethanol Yield. Microorganisms, 2020, 8, 658.	3.6	28
5	The extracellular matrix protects Bacillus subtilis colonies from Pseudomonas invasion and modulates plant co-colonization. Nature Communications, 2019, 10, 1919.	12.8	102
6	Clonal Complexity in Mycobacterium tuberculosis Can Hamper Diagnostic Procedures. Journal of Clinical Microbiology, 2017, 55, 1388-1395.	3.9	3
7	In-Depth Characterization and Functional Analysis of Clonal Variants in a Mycobacterium tuberculosis Strain Prone to Microevolution. Frontiers in Microbiology, 2017, 8, 694.	3.5	11
8	Molecular and epidemiological population-based integrative analysis of human and animal Mycobacterium bovis infections in a low-prevalence setting. Veterinary Microbiology, 2016, 195, 30-36.	1.9	10
9	Detailed chronological analysis of microevolution events in herds infected persistently by Mycobacterium bovis. Veterinary Microbiology, 2016, 183, 97-102.	1.9	11
10	Co-infection with Drug-Susceptible and Reactivated Latent Multidrug-ResistantMycobacterium tuberculosis. Emerging Infectious Diseases, 2015, 21, 2098-2100.	4.3	15
11	Persistent Infection by a Mycobacterium tuberculosis Strain That Was Theorized To Have Advantageous Properties, as It Was Responsible for a Massive Outbreak. Journal of Clinical Microbiology, 2015, 53, 3423-3429.	3.9	21
12	Multiple sampling and discriminatory fingerprinting reveals clonally complex and compartmentalized infections by M. bovis in cattle. Veterinary Microbiology, 2015, 175, 99-104.	1.9	13
13	Whole Genome Sequencing Analysis of Intrapatient Microevolution in Mycobacterium tuberculosis: Potential Impact on the Inference of Tuberculosis Transmission. Journal of Infectious Diseases, 2014, 209, 98-108.	4.0	120
14	Current knowledge and pending challenges in zoonosis caused by Mycobacterium bovis: A review. Research in Veterinary Science, 2014, 97, S94-S100.	1.9	69
15	High-throughput multiplex MIRU-VNTR typing of Mycobacterium bovis. Research in Veterinary Science, 2014, 96, 422-425.	1.9	8
16	Genetic features shared by Mycobacterium tuberculosis strains involved in microevolution events. Infection, Genetics and Evolution, 2013, 16, 326-329.	2.3	3
17	Differences in gene expression between clonal variants of Mycobacterium tuberculosis emerging as a result of microevolution. International Journal of Medical Microbiology, 2013, 303, 674-677.	3.6	26
18	Unmasking subtle differences in the infectivity of microevolved Mycobacterium tuberculosis variants coinfecting the same patient. International Journal of Medical Microbiology, 2013, 303, 693-696.	3.6	13

#	Article	IF	Citations
19	Splitting of a Prevalent Mycobacterium bovis Spoligotype by Variable-Number Tandem-Repeat Typing Reveals High Heterogeneity in an Evolving Clonal Group. Journal of Clinical Microbiology, 2013, 51, 3658-3665.	3.9	40
20	A novel method for the rapid and prospective identification of Beijing Mycobacterium tuberculosis strains by high-resolution melting analysis. Clinical Microbiology and Infection, 2011, 17, 349-357.	6.0	15
21	Systematic Survey of Clonal Complexity in Tuberculosis at a Populational Level and Detailed Characterization of the Isolates Involved. Journal of Clinical Microbiology, 2011, 49, 4131-4137.	3.9	52
22	Evaluation of the Inaccurate Assignment of Mixed Infections by Mycobacterium tuberculosis as Exogenous Reinfection and Analysis of the Potential Role of Bacterial Factors in Reinfection. Journal of Clinical Microbiology, 2011, 49, 1331-1338.	3.9	14