

Yurena navarro

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8132485/publications.pdf>

Version: 2024-02-01

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 | Whole Genome Sequencing Analysis of Inpatient Microevolution in <i>Mycobacterium tuberculosis</i> : Potential Impact on the Inference of Tuberculosis Transmission. <i>Journal of Infectious Diseases</i> , 2014, 209, 98-108. | 4.0 | 120 |
| 2 | The extracellular matrix protects <i>Bacillus subtilis</i> colonies from <i>Pseudomonas</i> invasion and modulates plant co-colonization. <i>Nature Communications</i> , 2019, 10, 1919. | 12.8 | 102 |
| 3 | Current knowledge and pending challenges in zoonosis caused by <i>Mycobacterium bovis</i> : A review. <i>Research in Veterinary Science</i> , 2014, 97, S94-S100. | 1.9 | 69 |
| 4 | Dual functionality of the amyloid protein TasA in <i>Bacillus</i> physiology and fitness on the phylloplane. <i>Nature Communications</i> , 2020, 11, 1859. | 12.8 | 59 |
| 5 | Systematic Survey of Clonal Complexity in Tuberculosis at a Populational Level and Detailed Characterization of the Isolates Involved. <i>Journal of Clinical Microbiology</i> , 2011, 49, 4131-4137. | 3.9 | 52 |
| 6 | Splitting of a Prevalent <i>Mycobacterium bovis</i> Spoligotype by Variable-Number Tandem-Repeat Typing Reveals High Heterogeneity in an Evolving Clonal Group. <i>Journal of Clinical Microbiology</i> , 2013, 51, 3658-3665. | 3.9 | 40 |
| 7 | A Rapid Method for Selecting Non- <i>Saccharomyces</i> Strains with a Low Ethanol Yield. <i>Microorganisms</i> , 2020, 8, 658. | 3.6 | 28 |
| 8 | Differences in gene expression between clonal variants of <i>Mycobacterium tuberculosis</i> emerging as a result of microevolution. <i>International Journal of Medical Microbiology</i> , 2013, 303, 674-677. | 3.6 | 26 |
| 9 | Persistent Infection by a <i>Mycobacterium tuberculosis</i> Strain That Was Theorized To Have Advantageous Properties, as It Was Responsible for a Massive Outbreak. <i>Journal of Clinical Microbiology</i> , 2015, 53, 3423-3429. | 3.9 | 21 |
| 10 | A novel method for the rapid and prospective identification of Beijing <i>Mycobacterium tuberculosis</i> strains by high-resolution melting analysis. <i>Clinical Microbiology and Infection</i> , 2011, 17, 349-357. | 6.0 | 15 |
| 11 | Co-infection with Drug-Susceptible and Reactivated Latent Multidrug-Resistant <i>Mycobacterium tuberculosis</i> . <i>Emerging Infectious Diseases</i> , 2015, 21, 2098-2100. | 4.3 | 15 |
| 12 | Evaluation of the Inaccurate Assignment of Mixed Infections by <i>Mycobacterium tuberculosis</i> as Exogenous Reinfection and Analysis of the Potential Role of Bacterial Factors in Reinfection. <i>Journal of Clinical Microbiology</i> , 2011, 49, 1331-1338. | 3.9 | 14 |
| 13 | Unmasking subtle differences in the infectivity of microevolved <i>Mycobacterium tuberculosis</i> variants coinfecting the same patient. <i>International Journal of Medical Microbiology</i> , 2013, 303, 693-696. | 3.6 | 13 |
| 14 | Multiple sampling and discriminatory fingerprinting reveals clonally complex and compartmentalized infections by <i>M. bovis</i> in cattle. <i>Veterinary Microbiology</i> , 2015, 175, 99-104. | 1.9 | 13 |
| 15 | Detailed chronological analysis of microevolution events in herds infected persistently by <i>Mycobacterium bovis</i> . <i>Veterinary Microbiology</i> , 2016, 183, 97-102. | 1.9 | 11 |
| 16 | In-Depth Characterization and Functional Analysis of Clonal Variants in a <i>Mycobacterium tuberculosis</i> Strain Prone to Microevolution. <i>Frontiers in Microbiology</i> , 2017, 8, 694. | 3.5 | 11 |
| 17 | Effect of a Multistarter Yeast Inoculum on Ethanol Reduction and Population Dynamics in Wine Fermentation. <i>Foods</i> , 2021, 10, 623. | 4.3 | 11 |
| 18 | Molecular and epidemiological population-based integrative analysis of human and animal <i>Mycobacterium bovis</i> infections in a low-prevalence setting. <i>Veterinary Microbiology</i> , 2016, 195, 30-36. | 1.9 | 10 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 19 | Viability-PCR Allows Monitoring Yeast Population Dynamics in Mixed Fermentations Including Viable but Non-Culturable Yeasts. <i>Foods</i> , 2020, 9, 1373. | 4.3 | 9 |
| 20 | High-throughput multiplex MIRU-VNTR typing of <i>Mycobacterium bovis</i> . <i>Research in Veterinary Science</i> , 2014, 96, 422-425. | 1.9 | 8 |
| 21 | Genetic features shared by <i>Mycobacterium tuberculosis</i> strains involved in microevolution events. <i>Infection, Genetics and Evolution</i> , 2013, 16, 326-329. | 2.3 | 3 |
| 22 | Clonal Complexity in <i>Mycobacterium tuberculosis</i> Can Hamper Diagnostic Procedures. <i>Journal of Clinical Microbiology</i> , 2017, 55, 1388-1395. | 3.9 | 3 |