

# Lalitha Gade

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11373760/publications.pdf>

Version: 2024-02-01

29  
papers

2,236  
citations

361413

20  
h-index

477307

29  
g-index

32  
all docs

32  
docs citations

32  
times ranked

1840  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | MycoSNP: A Portable Workflow for Performing Whole-Genome Sequencing Analysis of <i>Candida auris</i> . <i>Methods in Molecular Biology</i> , 2022, , 215-228.  | 0.9  | 13        |
| 2  | Clade-specific chromosomal rearrangements and loss of subtelomeric adhesins in <i>Candida auris</i> . <i>Genetics</i> , 2021, 218, .   | 2.9  | 54        |
| 3  | Genomic Diversity of Azole-Resistant <i>Aspergillus fumigatus</i> in the United States. <i>MBio</i> , 2021, 12, e0180321.  | 4.1  | 17        |
| 4  | Rapid Assessment and Containment of <i>Candida auris</i> Transmission in Postacute Care Settings—Orange County, California, 2019. <i>Annals of Internal Medicine</i> , 2021, 174, 1554-1562.                                       | 3.9  | 17        |
| 5  | Factors Influencing Distribution of <i>Coccidioides immitis</i> in Soil, Washington State, 2016. <i>MSphere</i> , 2021, 6, e0059821.   | 2.9  | 17        |
| 6  | The detection of <i>Coccidioides</i> from ambient air in Phoenix, Arizona: Evidence of uneven distribution and seasonality. <i>Medical Mycology</i> , 2020, 58, 552-559.   | 0.7  | 23        |
| 7  | Mutations in <i>TAC1B</i> : a Novel Genetic Determinant of Clinical Fluconazole Resistance in <i>Candida auris</i> . <i>MBio</i> , 2020, 11, .   | 4.1  | 101       |
| 8  | <i>Candida auris</i> outbreak involving liver transplant recipients in a surgical intensive care unit. <i>American Journal of Transplantation</i> , 2020, 20, 3673-3679.   | 4.7  | 23        |
| 9  | Understanding the Emergence of Multidrug-Resistant <i>Candida</i> : Using Whole-Genome Sequencing to Describe the Population Structure of <i>Candida haemulonii</i> Species Complex. <i>Frontiers in Genetics</i> , 2020, 11, 554. | 2.3  | 24        |
| 10 | Tracing the Evolutionary History and Global Expansion of <i>Candida auris</i> Using Population Genomic Analyses. <i>MBio</i> , 2020, 11, .   | 4.1  | 224       |
| 11 | <i>Rhizopus microsporus</i> Infections Associated with Surgical Procedures, Argentina, 2006–2014. <i>Emerging Infectious Diseases</i> , 2020, 26, 937-944.   | 4.3  | 11        |
| 12 | Molecular Epidemiology of <i>Candida auris</i> in Colombia Reveals a Highly Related, Countrywide Colonization With Regional Patterns in Amphotericin B Resistance. <i>Clinical Infectious Diseases</i> , 2019, 68, 15-21.          | 5.8  | 132       |
| 13 | Utility of Whole-Genome Sequencing to Ascertain Locally Acquired Cases of <i>Coccidioidomycosis</i> , Washington, USA. <i>Emerging Infectious Diseases</i> , 2019, 25, 501-506.  | 4.3  | 24        |
| 14 | Genome Sequence of a Multidrug-Resistant <i>Candida haemulonii</i> Isolate from a Patient with Chronic Leg Ulcers in Israel. <i>Genome Announcements</i> , 2018, 6, .  | 0.8  | 11        |
| 15 | Genome Sequence of the Amphotericin B-Resistant <i>Candida duobushaemulonii</i> Strain B09383. <i>Genome Announcements</i> , 2018, 6, .  | 0.8  | 9         |
| 16 | Genomic insights into multidrug-resistance, mating and virulence in <i>Candida auris</i> and related emerging species. <i>Nature Communications</i> , 2018, 9, 5346.   | 12.8 | 298       |
| 17 | Multiple introductions and subsequent transmission of multidrug-resistant <i>Candida auris</i> in the USA: a molecular epidemiological survey. <i>Lancet Infectious Diseases</i> , The, 2018, 18, 1377-1384.                       | 9.1  | 204       |
| 18 | Notes from the Field: Ongoing Transmission of <i>Candida auris</i> in Health Care Facilities — United States, June 2016–May 2017. <i>Morbidity and Mortality Weekly Report</i> , 2017, 66, 514-515.                                | 15.1 | 124       |

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 19 | Local Population Structure and Patterns of Western Hemisphere Dispersal for <i>Coccidioides</i> spp., the Fungal Cause of Valley Fever. <i>MBio</i> , 2016, 7, e00550-16.   | 4.1  | 71        |
| 20 | Detection of mucormycetes and other pathogenic fungi in formalin fixed paraffin embedded and fresh tissues using the extended region of 28S rDNA. <i>Medical Mycology</i> , 2016, 55, myw083.   | 0.7  | 23        |
| 21 | Utility of Real-Time PCR for Detection of <i>Exserohilum rostratum</i> in Body and Tissue Fluids during the Multistate Outbreak of Fungal Meningitis and Other Infections. <i>Journal of Clinical Microbiology</i> , 2015, 53, 618-625.                         | 3.9  | 20        |
| 22 | Valley Fever: Finding New Places for an Old Disease: <i>Coccidioides immitis</i> Found in Washington State Soil Associated With Recent Human Infection. <i>Clinical Infectious Diseases</i> , 2015, 60, e1-e3.  | 5.8  | 153       |
| 23 | Utility of (1 $\alpha$ )- <sup>3</sup> - <sup>H</sup> -d-Glucan Testing for Diagnostics and Monitoring Response to Treatment During the Multistate Outbreak of Fungal Meningitis and Other Infections. <i>Clinical Infectious Diseases</i> , 2014, 58, 622-630. | 5.8  | 85        |
| 24 | Whole-Genome Analysis of <i>Exserohilum rostratum</i> from an Outbreak of Fungal Meningitis and Other Infections. <i>Journal of Clinical Microbiology</i> , 2014, 52, 3216-3222.  | 3.9  | 52        |
| 25 | <i>Coccidioides immitis</i> identified in soil outside of its known range - Washington, 2013. <i>Morbidity and Mortality Weekly Report</i> , 2014, 63, 450.   | 15.1 | 30        |
| 26 | Preliminary Laboratory Report of Fungal Infections Associated with Contaminated Methylprednisolone Injections. <i>Journal of Clinical Microbiology</i> , 2013, 51, 2654-2661.   | 3.9  | 41        |
| 27 | Detection of Fungal DNA in Human Body Fluids and Tissues during a Multistate Outbreak of Fungal Meningitis and Other Infections. <i>Eukaryotic Cell</i> , 2013, 12, 677-683.  | 3.4  | 62        |
| 28 | Necrotizing Cutaneous Mucormycosis after a Tornado in Joplin, Missouri, in 2011. <i>New England Journal of Medicine</i> , 2012, 367, 2214-2225.   | 27.0 | 297       |
| 29 | Whole Genome Sequence Typing to Investigate the <i>Apophysomyces</i> Outbreak following a Tornado in Joplin, Missouri, 2011. <i>PLoS ONE</i> , 2012, 7, e49989.   | 2.5  | 66        |