

Jin-Xing Lu

List of Publications by Year in descending order

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Version: 2024-02-01

12
papers

160
citations

1307366

7
h-index

1199470

12
g-index

12
all docs

12
docs citations

12
times ranked

209
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Molecular Characterization of <i>Clostridium difficile</i> Isolates in China From 2010 to 2015. <i>Frontiers in Microbiology</i> , 2018, 9, 845. | 1.5 | 40 |
| 2 | Extreme diversity and multiple SCCmec elements in coagulase-negative <i>Staphylococcus</i> found in the Clinic and Community in Beijing, China. <i>Annals of Clinical Microbiology and Antimicrobials</i> , 2017, 16, 57. | 1.7 | 23 |
| 3 | Independent Microevolution Mediated by Mobile Genetic Elements of Individual <i>Clostridium difficile</i> Isolates from Clade 4 Revealed by Whole-Genome Sequencing. <i>MSystems</i> , 2019, 4, . | 1.7 | 16 |
| 4 | Antibiotic resistance of clinical isolates of <i>Clostridioides difficile</i> in China and its association with geographical regions and patient age. <i>Anaerobe</i> , 2019, 60, 102094. | 1.0 | 15 |
| 5 | <i>Saccharicrinis marinus</i> sp. nov., isolated from marine sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 3427-3432. | 0.8 | 13 |
| 6 | The molecular characters and antibiotic resistance of <i>Clostridioides difficile</i> from economic animals in China. <i>BMC Microbiology</i> , 2020, 20, 70. | 1.3 | 12 |
| 7 | A Genome-Wide Transcriptional Analysis of Yeast-Hyphal Transition in <i>Candida tropicalis</i> by RNA-Seq. <i>PLoS ONE</i> , 2016, 11, e0166645. | 1.1 | 12 |
| 8 | A narrative review of <i>Clostridioides difficile</i> infection in China. <i>Anaerobe</i> , 2022, , 102540. | 1.0 | 8 |
| 9 | Direct Blood Culturing of <i>Candida</i> spp. on Solid Medium by a Rapid Enrichment Method with Magnetic Beads Coated with Recombinant Human Mannan-Binding Lectin. <i>Journal of Clinical Microbiology</i> , 2020, 58, . | 1.8 | 7 |
| 10 | Microevolution within ST11 group <i>Clostridioides difficile</i> isolates through mobile genetic elements based on complete genome sequencing. <i>BMC Genomics</i> , 2019, 20, 796. | 1.2 | 5 |
| 11 | Polymorphism analysis of virulence-related genes among <i>Candida tropicalis</i> isolates. <i>Chinese Medical Journal</i> , 2019, 132, 446-453. | 0.9 | 5 |
| 12 | Bacteria-induced susceptibility to <i>Candida albicans</i> super-infection in mice via monocyte methyltransferase Setdb2. <i>Cellular Microbiology</i> , 2018, 20, e12860. | 1.1 | 4 |