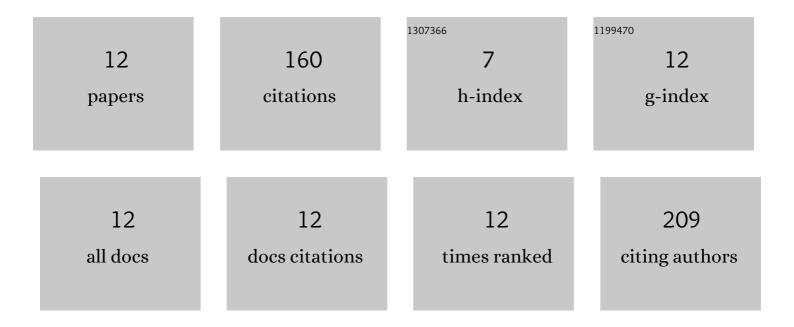
Jin-Xing Lu

List of Publications by Year in descending order

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IN XINC LU

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