

# Min Li

## List of Publications by Year in descending order

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12  
papers

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citations

1307594

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1199594

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490  
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparison of adverse drug reactions between tamoxifen and toremifene in breast cancer patients with different <sc>CYP2D6</sc> genotypes: A propensity score matched cohort study. International Journal of Cancer, 2022, 150, 1664-1676.	5.1	4
2	Virulence adaption to environment promotes the age-dependent nasal colonization of <i>Staphylococcus aureus</i>. Emerging Microbes and Infections, 2022, 11, 1402-1415.	6.5	3
3	The pro-inflammatory effect of Staphylokinase contributes to community-associated Staphylococcus aureus pneumonia. Communications Biology, 2022, 5, .	4.4	7
4	Mechanisms of high-level fosfomycin resistance in <i>Staphylococcus aureus</i> epidemic lineage ST5. Journal of Antimicrobial Chemotherapy, 2022, 77, 2816-2826.	3.0	5
5	Increasing prevalence of hypervirulent ST5 methicillin susceptible <i>Staphylococcus aureus</i> subtype poses a serious clinical threat. Emerging Microbes and Infections, 2021, 10, 109-122.	6.5	29
6	Extracellular DNA released by glycine-auxotrophic Staphylococcus epidermidis small colony variant facilitates catheter-related infections. Communications Biology, 2021, 4, 904.	4.4	4
7	Skin microbiota analysis-inspired development of novel anti-infectives. Microbiome, 2020, 8, 85.	11.1	42
8	Dynamic Changes of Staphylococcus aureus Susceptibility to Vancomycin, Teicoplanin, and Linezolid in a Central Teaching Hospital in Shanghai, China, 2008–2018. Frontiers in Microbiology, 2020, 11, 908.	3.5	25
9	Decreasing methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) infections is attributable to the disappearance of predominant MRSA ST239 clones, Shanghai, 2008–2017. Emerging Microbes and Infections, 2019, 8, 471-478.	6.5	63
10	Phylogenetic analysis and virulence determinant of the host-adapted <i>Staphylococcus aureus</i> lineage ST188 in China. Emerging Microbes and Infections, 2018, 7, 1-11.	6.5	37
11	Detection and analysis of methicillin-resistant human-adapted sequence type 398 allows insight into community-associated methicillin-resistant Staphylococcus aureus evolution. Genome Medicine, 2018, 10, 5.	8.2	43
12	Molecular Analysis of Staphylococcus epidermidis Strains Isolated from Community and Hospital Environments in China. PLoS ONE, 2013, 8, e62742.	2.5	95