

Zhaoqin Zhu

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

35
papers

797
citations

14
h-index

28
g-index

41
ext. papers

1,220
ext. citations

12
avg, IF

4.06
L-index

#	Paper	IF	Citations
35	Intra-host SARS-CoV-2 Single-Nucleotide Variants Emerged During the Early Stage of COVID-19 Pandemic Forecast Population Fixing Mutations.. <i>Journal of Infection</i> , 2022 ,	18.9	1
34	Rapid and ultrasensitive electromechanical detection of ions, biomolecules and SARS-CoV-2 RNA in unamplified samples.. <i>Nature Biomedical Engineering</i> , 2022 ,	19	22
33	Rapid SARS-CoV-2 Nucleic Acid Testing and Pooled Assay by Tetrahedral DNA Nanostructure Transistor. <i>Nano Letters</i> , 2021 , 21, 9450-9457	11.5	4
32	Ultraprecise Antigen 10-in-1 Pool Testing by Multiantibodies Transistor Assay. <i>Journal of the American Chemical Society</i> , 2021 , 143, 19794-19801	16.4	8
31	Distinct immune signatures discriminate between asymptomatic and presymptomatic SARS-CoV-2 subjects. <i>Cell Research</i> , 2021 , 31, 1148-1162	24.7	4
30	Quality Management for Point-Of-Care Testing of Pathogen Nucleic Acids: Chinese Expert Consensus. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021 , 11, 755508	5.9	1
29	Direct SARS-CoV-2 Nucleic Acid Detection by Y-Shaped DNA Dual-Probe Transistor Assay. <i>Journal of the American Chemical Society</i> , 2021 , 143, 17004-17014	16.4	14
28	Vitamin C supplementation is necessary for patients with coronavirus disease: An ultra-high-performance liquid chromatography-tandem mass spectrometry finding. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2021 , 196, 113927	3.5	9
27	Antimicrobial susceptibility profiles of Mycobacterium abscessus complex isolates from respiratory specimens in Shanghai, China. <i>Journal of Global Antimicrobial Resistance</i> , 2021 , 25, 72-76	3.4	0
26	Integrating longitudinal clinical laboratory tests with targeted proteomic and transcriptomic analyses reveal the landscape of host responses in COVID-19. <i>Cell Discovery</i> , 2021 , 7, 42	22.3	10
25	Virus-Host Interactome and Proteomic Survey Reveal Potential Virulence Factors Influencing SARS-CoV-2 Pathogenesis. <i>Med</i> , 2021 , 2, 99-112.e7	31.7	154
24	An inter-correlated cytokine network identified at the center of cytokine storm predicted COVID-19 prognosis. <i>Cytokine</i> , 2021 , 138, 155365	4	14
23	Regulatory CD4 and CD8 T cells are negatively correlated with CD4 /CD8 T cell ratios in patients acutely infected with SARS-CoV-2. <i>Journal of Leukocyte Biology</i> , 2021 , 109, 91-97	6.5	14
22	Label-Free Mass Spectrometry-Based Plasma Proteomics Identified LY6D, DSC3, CDSN, SERPINB12, and SLURP1 as Novel Protein Biomarkers For Pulmonary Tuberculosis. <i>Current Proteomics</i> , 2021 , 18, 50-61	9.7	0
21	Epigenetic Landscapes of Single-Cell Chromatin Accessibility and Transcriptomic Immune Profiles of T Cells in COVID-19 Patients. <i>Frontiers in Immunology</i> , 2021 , 12, 625881	8.4	5
20	Ultrasensitive Detection of SARS-CoV-2 Antibody by Graphene Field-Effect Transistors. <i>Nano Letters</i> , 2021 , 21, 7897-7904	11.5	13
19	Identifying Risk Factors for Secondary Infection Post-SARS-CoV-2 Infection in Patients With Severe and Critical COVID-19. <i>Frontiers in Immunology</i> , 2021 , 12, 715023	8.4	0

18	Pre-optimized phage therapy on secondary infection in four critical COVID-19 patients. <i>Emerging Microbes and Infections</i> , 2021 , 10, 612-618	18.9	34
17	clinical isolates carry mutational signatures of host immune environments. <i>Science Advances</i> , 2020 , 6, eaba4901	14.3	14
16	Epidemiology and clinical course of COVID-19 in Shanghai, China. <i>Emerging Microbes and Infections</i> , 2020 , 9, 1537-1545	18.9	16
15	Validation of the BD FACSPresto system for the measurement of CD4 T-lymphocytes and hemoglobin concentration in HIV-negative and HIV-positive subjects. <i>Scientific Reports</i> , 2020 , 10, 19605	4.9	1
14	Severe Coronavirus disease 2019 pneumonia patients showed signs of aggravated renal impairment. <i>Journal of Clinical Laboratory Analysis</i> , 2020 , 34, e23535	3	6
13	Risks and features of secondary infections in severe and critical ill COVID-19 patients. <i>Emerging Microbes and Infections</i> , 2020 , 9, 1958-1964	18.9	69
12	Heterogeneous Co-infections Complicate Personalized Bacteriophage Therapy. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020 , 10, 608402	5.9	17
11	IFITM3, TLR3, and CD55 Gene SNPs and Cumulative Genetic Risks for Severe Outcomes in Chinese Patients With H7N9/H1N1pdm09 Influenza. <i>Journal of Infectious Diseases</i> , 2017 , 216, 97-104	7	37
10	Nuclear translocation of HIF-1 α induced by influenza A (H1N1) infection is critical to the production of proinflammatory cytokines. <i>Emerging Microbes and Infections</i> , 2017 , 6, e39	18.9	27
9	Multiple gene mutations identified in patients infected with influenza A (H7N9) virus. <i>Scientific Reports</i> , 2016 , 6, 25614	4.9	6
8	Extra-pulmonary viral shedding in H7N9 Avian Influenza patients. <i>Journal of Clinical Virology</i> , 2015 , 69, 30-2	14.5	18
7	Genotype distribution of norovirus around the emergence of Sydney_2012 and the antigenic drift of contemporary GII.4 epidemic strains. <i>Journal of Clinical Virology</i> , 2015 , 72, 95-101	14.5	11
6	Distribution, virulence-associated genes and antimicrobial resistance of <i>Aeromonas</i> isolates from diarrheal patients and water, China. <i>Journal of Infection</i> , 2015 , 70, 600-8	18.9	23
5	Evaluation of Anti-TBGL Antibody in the Diagnosis of Tuberculosis Patients in China. <i>Journal of Immunology Research</i> , 2015 , 2015, 834749	4.5	7
4	Recovery from severe H7N9 disease is associated with diverse response mechanisms dominated by CD8+ T cells. <i>Nature Communications</i> , 2015 , 6, 6833	17.4	168
3	A novel norovirus GII.17 lineage contributed to adult gastroenteritis in Shanghai, China, during the winter of 2014-2015. <i>Emerging Microbes and Infections</i> , 2015 , 4, e67	18.9	34
2	Drug susceptibility profile and pathogenicity of H7N9 influenza virus (Anhui1 lineage) with R292K substitution. <i>Emerging Microbes and Infections</i> , 2014 , 3, e78	18.9	22
1	Infection of inbred BALB/c and C57BL/6 and outbred Institute of Cancer Research mice with the emerging H7N9 avian influenza virus. <i>Emerging Microbes and Infections</i> , 2013 , 2, e50	18.9	13

