

# Qiwei Zhang

## List of Publications by Year in descending order

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Version: 2024-02-01

62  
papers

4,136  
citations

279487

23  
h-index

128067

60  
g-index

79  
all docs

79  
docs citations

79  
times ranked

7137  
citing authors

#	ARTICLE	IF	CITATIONS
1	Optimization of loop-mediated isothermal amplification (LAMP) assay for robust visualization in SARS-CoV-2 and emerging variants diagnosis. <i>Chemical Engineering Science</i> , 2022, 251, 117430.	1.9	17
2	Editorial: Adenoviral Infection and Immunity, and Adenoviral Vectors for Gene Therapy Applications. <i>Frontiers in Microbiology</i> , 2022, 13, 869059.	1.5	1
3	Tracking SARS-CoV-2 Omicron diverse spike gene mutations identifies multiple inter-variant recombination events. <i>Signal Transduction and Targeted Therapy</i> , 2022, 7, 138.	7.1	140
4	Molecular Typing and Rapid Identification of Human Adenoviruses Associated With Respiratory Diseases Using Universal PCR and Sequencing Primers for the Three Major Capsid Genes: Penton Base, Hexon, and Fiber. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	13
5	Hypoxia signaling in human health and diseases: implications and prospects for therapeutics. <i>Signal Transduction and Targeted Therapy</i> , 2022, 7, .	7.1	81
6	Construction and Characterization of a Novel Recombinant Attenuated and Replication-Deficient Candidate Human Adenovirus Type 3 Vaccine: Adenovirus Vaccine Within an Adenovirus Vector. <i>Virologica Sinica</i> , 2021, 36, 354-364.	1.2	12
7	Sox4 represses host innate immunity to facilitate pathogen infection by hijacking the TLR signaling networks. <i>Virulence</i> , 2021, 12, 704-722.	1.8	9
8	Temperature dependence of the SARS-CoV-2 affinity to human ACE2 determines COVID-19 progression and clinical outcome. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 161-167.	1.9	33
9	Development and Application of a Fast Method to Acquire the Accurate Whole-Genome Sequences of Human Adenoviruses. <i>Frontiers in Microbiology</i> , 2021, 12, 661382.	1.5	1
10	DENV NS1 and MMP-9 cooperate to induce vascular leakage by altering endothelial cell adhesion and tight junction. <i>PLoS Pathogens</i> , 2021, 17, e1008603.	2.1	30
11	Desmoglein 2 (DSG2) Is A Receptor of Human Adenovirus Type 55 Causing Adult Severe Community-Acquired Pneumonia. <i>Virologica Sinica</i> , 2021, 36, 1400-1410.	1.2	10
12	V367F Mutation in SARS-CoV-2 Spike RBD Emerging during the Early Transmission Phase Enhances Viral Infectivity through Increased Human ACE2 Receptor Binding Affinity. <i>Journal of Virology</i> , 2021, 95, e0061721.	1.5	90
13	Genomic Elucidation of a COVID-19 Resurgence and Local Transmission of SARS-CoV-2 in Guangzhou, China. <i>Journal of Clinical Microbiology</i> , 2021, 59, e0007921.	1.8	5
14	SARS-CoV-2 N protein promotes NLRP3 inflammasome activation to induce hyperinflammation. <i>Nature Communications</i> , 2021, 12, 4664.	5.8	281
15	HIF-1 $\alpha$ promotes SARS-CoV-2 infection and aggravates inflammatory responses to COVID-19. <i>Signal Transduction and Targeted Therapy</i> , 2021, 6, 308.	7.1	124
16	Mechanism of Cross-Resistance to Fusion Inhibitors Conferred by the K394R Mutation in Respiratory Syncytial Virus Fusion Protein. <i>Journal of Virology</i> , 2021, 95, e0120521.	1.5	6
17	Sericin and sericin-derived peptide alleviate viral pathogenesis in mice though inhibiting lactate production and facilitating antiviral response. <i>Applied Materials Today</i> , 2021, 25, 101256.	2.3	6
18	High-Throughput Screening and Identification of Human Adenovirus Type 5 Inhibitors. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 767578.	1.8	1

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19	COVID-19: Coronavirus Vaccine Development Updates. <i>Frontiers in Immunology</i> , 2020, 11, 602256.	2.2	143
20	Characterization of Influenza A and B Viruses Circulating in Southern China During the 2017â€“2018 Season. <i>Frontiers in Microbiology</i> , 2020, 11, 1079.	1.5	10
21	MicroRNA expression profiling of peripheral blood mononuclear cells associated with syphilis. <i>BMC Infectious Diseases</i> , 2020, 20, 165.	1.3	13
22	Composition and divergence of coronavirus spike proteins and host ACE2 receptors predict potential intermediate hosts of SARSâ€“CoVâ€“2. <i>Journal of Medical Virology</i> , 2020, 92, 595-601.	2.5	546
23	MicroRNA-101-3p Downregulates TLR2 Expression, Leading to Reduction in Cytokine Production by <i>Treponema pallidum</i> â€“Stimulated Macrophages. <i>Journal of Investigative Dermatology</i> , 2020, 140, 1566-1575.e1.	0.3	21
24	Coronavirus infections and immune responses. <i>Journal of Medical Virology</i> , 2020, 92, 424-432.	2.5	1,371
25	COVID-19: Antiviral Agents, Antibody Development and Traditional Chinese Medicine. <i>Virologica Sinica</i> , 2020, 35, 685-698.	1.2	18
26	<i>Bacteroides fragilis</i> Strain ZY-312 Defense against <i>Cronobacter sakazakii</i> -Induced Necrotizing Enterocolitis <i>In Vitro</i> and in a Neonatal Rat Model. <i>MSystems</i> , 2019, 4, .	1.7	53
27	Household Transmission of Human Adenovirus Type 55 in Case of Fatal Acute Respiratory Disease. <i>Emerging Infectious Diseases</i> , 2019, 25, 1756-1758.	2.0	18
28	A Survey of Recent Adenoviral Respiratory Pathogens in Hong Kong Reveals Emergent and Recombinant Human Adenovirus Type 4 (HAdV-E4) Circulating in Civilian Populations. <i>Viruses</i> , 2019, 11, 129.	1.5	40
29	Research advancements in the neurological presentation of flaviviruses. <i>Reviews in Medical Virology</i> , 2019, 29, e2021.	3.9	9
30	Genomic analysis of a large set of currentlyâ€“and historicallyâ€“important human adenovirus pathogens. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-22.	3.0	39
31	Screening for host proteins interacting with <i>Escherichia coli</i> O157:H7 EspF using bimolecular fluorescence complementation. <i>Future Microbiology</i> , 2018, 13, 37-58.	1.0	16
32	Rapid Construction of a Replication-Competent Infectious Clone of Human Adenovirus Type 14 by Gibson Assembly. <i>Viruses</i> , 2018, 10, 568.	1.5	14
33	Comparative Genomic Analysis of Re-emergent Human Adenovirus Type 55 Pathogens Associated With Adult Severe Community-Acquired Pneumonia Reveals Conserved Genomes and Capsid Proteins. <i>Frontiers in Microbiology</i> , 2018, 9, 1180.	1.5	24
34	Evaluation and Comparison of Newly Built Linear B-Cell Epitope Prediction Software from a Users' Perspective. <i>Current Bioinformatics</i> , 2018, 13, 149-156.	0.7	5
35	Preliminary investigation of the role of BTB domain-containing 3 gene in the proliferation and metastasis of hepatocellular carcinoma. <i>Oncology Letters</i> , 2017, 14, 2505-2510.	0.8	3
36	Immunohistochemical Characterization and Sensitivity to Human Adenovirus Serotypes 3, 5, and 11p of New Cell Lines Derived from Human Diffuse Grade II to IV Gliomas. <i>Translational Oncology</i> , 2017, 10, 772-779.	1.7	5

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37	Comparative genomic analysis of two emergent human adenovirus type 14 respiratory pathogen isolates in China reveals similar yet divergent genomes. <i>Emerging Microbes and Infections</i> , 2017, 6, 1-12.	3.0	21
38	Effective Suckling C57BL/6, Kunming, and BALB/c Mouse Models with Remarkable Neurological Manifestation for Zika Virus Infection. <i>Viruses</i> , 2017, 9, 165.	1.5	31
39	The EspF N-Terminal of Enterohemorrhagic <i>Escherichia coli</i> O157:H7 EDL933w Imparts Stronger Toxicity Effects on HT-29 Cells than the C-Terminal. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 410.	1.8	15
40	Genome Sequence of a <i>Cynomolgus</i> Macaque Adenovirus (CynAdV-1) Isolate from a Primate Colony in the United Kingdom. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
41	Novel Mutations L228I and Y232H Cause Nonnucleoside Reverse Transcriptase Inhibitor Resistance in Combinational Pattern. <i>AIDS Research and Human Retroviruses</i> , 2016, 32, 909-917.	0.5	4
42	Computational approach for predicting the conserved B-cell epitopes of hemagglutinin H7 subtype influenza virus. <i>Experimental and Therapeutic Medicine</i> , 2016, 12, 2439-2446.	0.8	18
43	Pitfalls of restriction enzyme analysis in identifying, characterizing, typing, and naming viral pathogens in the era of whole genome data, as illustrated by HAdV type 55. <i>Virologica Sinica</i> , 2016, 31, 448-453.	1.2	10
44	Fatal Community-acquired Pneumonia in Children Caused by Re-emergent Human Adenovirus 7d Associated with Higher Severity of Illness and Fatality Rate. <i>Scientific Reports</i> , 2016, 6, 37216.	1.6	51
45	Molecular Identification and Epidemiological Features of Human Adenoviruses Associated with Acute Respiratory Infections in Hospitalized Children in Southern China, 2012-2013. <i>PLoS ONE</i> , 2016, 11, e0155412.	1.1	50
46	A novel mutation, D404N, in the connection subdomain of reverse transcriptase of HIV-1 CRF08_BC subtype confers cross-resistance to NNRTIs. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 1381-1390.	1.3	5
47	In Vitro Selection of HIV-1 CRF08_BC Variants Resistant to Reverse Transcriptase Inhibitors. <i>AIDS Research and Human Retroviruses</i> , 2015, 31, 260-270.	0.5	5
48	Re-emergent Human Adenovirus Genome Type 7d Caused an Acute Respiratory Disease Outbreak in Southern China After a Twenty-one Year Absence. <i>Scientific Reports</i> , 2014, 4, 7365.	1.6	73
49	Identification and typing of respiratory adenoviruses in Guangzhou, Southern China using a rapid and simple method. <i>Virologica Sinica</i> , 2013, 28, 103-108.	1.2	33
50	The N-Terminal Domain of EspF Induces Host Cell Apoptosis after Infection with Enterohaemorrhagic <i>Escherichia coli</i> O157:H7. <i>PLoS ONE</i> , 2013, 8, e55164.	1.1	14
51	Genome Sequence of Human Adenovirus Type 55, a Re-Emergent Acute Respiratory Disease Pathogen in China. <i>Journal of Virology</i> , 2012, 86, 12441-12442.	1.5	47
52	Genome Sequence of the First Human Adenovirus Type 14 Isolated in China. <i>Journal of Virology</i> , 2012, 86, 7019-7020.	1.5	27
53	Parental LTRs Are Important in a Construct of a Stable and Efficient Replication-Competent Infectious Molecular Clone of HIV-1 CRF08_BC. <i>PLoS ONE</i> , 2012, 7, e31233.	1.1	9
54	Complete genome analysis of a novel E3-partial-deleted human adenovirus type 7 strain isolated in Southern China. <i>Virology Journal</i> , 2011, 8, 91.	1.4	5

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55	Using the Whole-Genome Sequence To Characterize and Name Human Adenoviruses. <i>Journal of Virology</i> , 2011, 85, 5701-5702.	1.5	163
56	Applying Genomic and Bioinformatic Resources to Human Adenovirus Genomes for Use in Vaccine Development and for Applications in Vector Development for Gene Delivery. <i>Viruses</i> , 2010, 2, 1-26.	1.5	24
57	Wild Type and Mutant 2009 Pandemic Influenza A (H1N1) Viruses Cause More Severe Disease and Higher Mortality in Pregnant BALB/c Mice. <i>PLoS ONE</i> , 2010, 5, e13757.	1.1	86
58	A recombinant replication-defective human adenovirus type 3: A vaccine candidate. <i>Vaccine</i> , 2009, 27, 116-122.	1.7	7
59	Construction and characterization of a replication-competent human adenovirus type 3-based vector as a live-vaccine candidate and a viral delivery vector. <i>Vaccine</i> , 2009, 27, 1145-1153.	1.7	44
60	Inhibition of G1P3 expression found in the differential display study on respiratory syncytial virus infection. <i>Virology Journal</i> , 2008, 5, 114.	1.4	23
61	Comparative genomic analysis of two strains of human adenovirus type 3 isolated from children with acute respiratory infection in southern China. <i>Journal of General Virology</i> , 2006, 87, 1531-1541.	1.3	42
62	Prokaryotic expression and polyclonal antibody preparation of novel ZLG10 protein involved in infection of RSV on SPC-A1 cells. <i>Protein Expression and Purification</i> , 2005, 41, 170-176.	0.6	5