

# Qiangming Sun

## List of Publications by Year in descending order

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36  
papers

1,642  
citations

759055

12  
h-index

360920

35  
g-index

39  
all docs

39  
docs citations

39  
times ranked

4524  
citing authors

#	ARTICLE	IF	CITATIONS
1	The pathogenicity of SARS-CoV-2 in hACE2 transgenic mice. <i>Nature</i> , 2020, 583, 830-833.	13.7	992
2	Comparison of nonhuman primates identified the suitable model for COVID-19. <i>Signal Transduction and Targeted Therapy</i> , 2020, 5, 157.	7.1	190
3	Zika Virus Non-structural Protein 4A Blocks the RLR-MAVS Signaling. <i>Frontiers in Microbiology</i> , 2018, 9, 1350.	1.5	88
4	Antibody-dependent enhancement of dengue virus infection inhibits RLR-mediated Type-I IFN-independent signalling through upregulation of cellular autophagy. <i>Scientific Reports</i> , 2016, 6, 22303.	1.6	50
5	Semaphorin 4D is a potential biomarker in pediatric leukemia and promotes leukemogenesis by activating PI3K/AKT and ERK signaling pathways. <i>Oncology Reports</i> , 2021, 45, .	1.2	29
6	The epidemiological characteristics of enterovirus infection before and after the use of enterovirus 71 inactivated vaccine in Kunming, China. <i>Emerging Microbes and Infections</i> , 2021, 10, 619-628.	3.0	29
7	Prevalence and antibiotic resistance profiles of cerebrospinal fluid pathogens in children with acute bacterial meningitis in Yunnan province, China, 2012-2015. <i>PLoS ONE</i> , 2017, 12, e0180161.	1.1	26
8	The role of semaphorin 4D in tumor development and angiogenesis in human breast cancer. <i>OncoTargets and Therapy</i> , 2016, Volume 9, 5737-5750.	1.0	25
9	Genetic variability and functional implication of the long control region in HPV-16 variants in Southwest China. <i>PLoS ONE</i> , 2017, 12, e0182388.	1.1	23
10	Molecular Characterization and Viral Origin of the 2015 Dengue Outbreak in Xishuangbanna, Yunnan, China. <i>Scientific Reports</i> , 2016, 6, 34444.	1.6	20
11	Complete genome analysis of dengue virus type 3 isolated from the 2013 dengue outbreak in Yunnan, China. <i>Virus Research</i> , 2017, 238, 164-170.	1.1	17
12	Complete Genome Characterization of the 2017 Dengue Outbreak in Xishuangbanna, a Border City of China, Burma and Laos. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 148.	1.8	17
13	Molecular Characterization of Dengue Virus Serotype 2 Cosmopolitan Genotype From 2015 Dengue Outbreak in Yunnan, China. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 219.	1.8	14
14	The expression profile of human peripheral blood mononuclear cell miRNA is altered by antibody-dependent enhancement of infection with dengue virus serotype 3. <i>Virology Journal</i> , 2018, 15, 50.	1.4	13
15	Molecular characterization of the viral structural gene of the first dengue virus type 1 outbreak in Xishuangbanna: A border area of China, Burma and Laos. <i>International Journal of Infectious Diseases</i> , 2019, 79, 152-161.	1.5	12
16	Co-circulation of three dengue virus serotypes led to a severe dengue outbreak in Xishuangbanna, a border area of China, Myanmar, and Laos, in 2019. <i>International Journal of Infectious Diseases</i> , 2021, 107, 15-17.	1.5	12
17	The role of semaphorin 4D as a potential biomarker for antiangiogenic therapy in colorectal cancer. <i>OncoTargets and Therapy</i> , 2016, 9, 1189.	1.0	11
18	Isolation, characterization, and application of <i>Salmonella paratyphi</i> phage KM16 against <i>Salmonella paratyphi</i> biofilm. <i>Biofouling</i> , 2021, 37, 276-288.	0.8	11

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19	Molecular characterization of genomic DNA in mycoplasma pneumoniae strains isolated from serious mycoplasma pneumonia cases in 2016, Yunnan, China. <i>Infection, Genetics and Evolution</i> , 2018, 58, 125-134.	1.0	9
20	The polymorphisms of LCR, E6, and E7 of HPV-58 isolates in Yunnan, Southwest China. <i>Virology Journal</i> , 2018, 15, 76.	1.4	9
21	Genetic variability of HPV-58 E6 and E7 genes in Southwest China. <i>Infection, Genetics and Evolution</i> , 2014, 21, 395-400.	1.0	8
22	Tree Shrew as a New Animal Model for the Study of Dengue Virus. <i>Frontiers in Immunology</i> , 2021, 12, 621164.	2.2	8
23	Molecular characterization of the viral structural protein genes in the first outbreak of dengue virus type 2 in Hunan Province, inland China in 2018. <i>BMC Infectious Diseases</i> , 2021, 21, 166.	1.3	5
24	The Role of Autophagy-Mediated Dengue Virus Antibody-Dependent Enhancement Infection of THP-1 Cells. <i>Intervirology</i> , 2020, 63, 57-65.	1.2	3
25	Clinical Characteristics and Risk Factors for Severe Dengue Fever in Xishuangbanna, During the Dengue Outbreak in 2019. <i>Frontiers in Microbiology</i> , 2022, 13, 739970.	1.5	3
26	Regulatory sequence analysis of semaphorin 4D 5' non-coding region. <i>Journal of Cancer</i> , 2019, 10, 903-910.	1.2	2
27	The excretion rate and stability of HAAG in human fecal samples after live attenuated hepatitis A vaccination. <i>Journal of Medical Virology</i> , 2020, 92, 3312-3318.	2.5	2
28	Molecular characterization of structural protein genes of dengue virus serotype 1 epidemic in Yunnan, Southwest China, in 2018. <i>Archives of Virology</i> , 2021, 166, 863-870.	0.9	2
29	Complete genome characterization of the 2018 dengue outbreak in Hunan, an inland province in central South China. <i>Virus Research</i> , 2021, 297, 198358.	1.1	2
30	Two cases of hand, foot and mouth disease caused by enterovirus A71 after vaccination. <i>International Journal of Infectious Diseases</i> , 2021, 108, 190-197.	1.5	2
31	Sweeping analysis of transcript profile in dengue virus serotype 3 infection and antibody-dependent enhancement of infection. <i>Virulence</i> , 2021, 12, 2764-2776.	1.8	2
32	Molecular Characterization of the Viral Structural Genes of Human Rhinovirus A11 from Children Hospitalized with Lower Respiratory Tract Infection in Kunming. <i>International Journal of Infectious Diseases</i> , 2022, , .	1.5	2
33	Secondary cross infection with dengue virus serotype 2/3 aggravates vascular leakage in BALB/c mice. <i>Journal of Medical Virology</i> , 2022, 94, 4338-4347.	2.5	2
34	Comparison analysis of microRNAs in response to dengue virus type 2 infection between the Vero cell-adapted strain and its source, the clinical C6/36 isolated strain. <i>Virus Research</i> , 2018, 250, 65-74.	1.1	1
35	Soluble Sema4D Level Is Positively Correlated with Sema4D Expression in PBMCs and Peripheral Blast Number in Acute Leukemia. <i>Disease Markers</i> , 2022, 2022, 1-8.	0.6	1
36	The Safety, Immunogenicity, and Immunopersistence of Hepatitis A Vaccine in HBs-Ag-Positive Participants: A Retrospective Study. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 672221.	1.8	0