Yong-Zhen Zhang

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	10,112 citations	24 h-index	42 g-index
42 ext. papers	13,638 ext. citations	11.9 avg, IF	6.81 L-index

#	Paper	IF	Citations
35	Total infectome characterization of respiratory infections in pre-COVID-19 Wuhan, China.. *PLoS Pathogens*, **2022**, 18, e1010259	7.6	2
34	2021 Taxonomic update of phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. *Archives of Virology*, **2021**, 166, 3513-3566	2.6	10
33	Meta-Transcriptomic Identification of Divergent in Fish. *Viruses*, **2020**, 12,	6.2	2
32	Blood molecular markers associated with COVID-19 immunopathology and multi-organ damage. *EMBO Journal*, **2020**, 39, e105896	13	45
31	Newly identified viral genomes in pangolins with fatal disease. *Virus Evolution*, **2020**, 6, veaa020	3.7	16
30	Identification and characterization of Jingmen tick virus in rodents from Xinjiang, China. *Infection, Genetics and Evolution*, **2020**, 84, 104411	4.5	5
29	A Genomic Perspective on the Origin and Emergence of SARS-CoV-2. *Cell*, **2020**, 181, 223-227	56.2	459
28	A new coronavirus associated with human respiratory disease in China. *Nature*, **2020**, 579, 265-269	50.4	6055
27	Metatranscriptomics reveals that the death of a Mongolian wild ass was caused by in Inner Mongolia, China. *Journal of Veterinary Diagnostic Investigation*, **2020**, 32, 287-290	1.5	0
26	Extensive genetic diversity and host range of rodent-borne coronaviruses. *Virus Evolution*, **2020**, 6, veaa078	3.7	11
25	Diversity and circulation of Jingmen tick virus in ticks and mammals. *Virus Evolution*, **2020**, 6, veaa051	3.7	8
24	Identifying the Risk of SARS-CoV-2 Infection and Environmental Monitoring in Airborne Infectious Isolation Rooms (AIIRs). *Virologica Sinica*, **2020**, 35, 785-792	6.4	6
23	Diverse and abundant resistome in terrestrial and aquatic vertebrates revealed by transcriptional analysis. *Scientific Reports*, **2020**, 10, 18870	4.9	6
22	Taxonomy of the order Bunyavirales: update 2019. *Archives of Virology*, **2019**, 164, 1949-1965	2.6	148
21	Expanding the RNA Virosphere by Unbiased Metagenomics. *Annual Review of Virology*, **2019**, 6, 119-139	14.6	59
20	Taxonomy of the order Mononegavirales: update 2019. *Archives of Virology*, **2019**, 164, 1967-1980	2.6	133
19	Discovery of a highly divergent hepadnavirus in shrews from China. *Virology*, **2019**, 531, 162-170	3.6	5

(-2018)

18	Using Metagenomics to Characterize an Expanding Virosphere. *Cell*, **2018**, 172, 1168-1172	56.2	134
17	The evolutionary history of vertebrate RNA viruses. *Nature*, **2018**, 556, 197-202	50.4	354
16	Meta-transcriptomics and the evolutionary biology of RNA viruses. *Virus Research*, **2018**, 243, 83-90	6.4	72
15	The diversity, evolution and origins of vertebrate RNA viruses. *Current Opinion in Virology*, **2018**, 31, 9-16	7.5	33
14	Discovery of a Highly Divergent Coronavirus in the Asian House Shrew from China Illuminates the Origin of the Alphacoronaviruses. *Journal of Virology*, **2017**, 91,	6.6	25
13	Extensive diversity of coronaviruses in bats from China. *Virology*, **2017**, 507, 1-10	3.6	66
12	Redefining the invertebrate RNA virosphere. *Nature*, **2016**, 540, 539-543	50.4	821
11	Divergent Viruses Discovered in Arthropods and Vertebrates Revise the Evolutionary History of the Flaviviridae and Related Viruses. *Journal of Virology*, **2016**, 90, 659-69	6.6	162
10	The evolution and emergence of hantaviruses. *Current Opinion in Virology*, **2015**, 10, 27-33	7.5	62
9	Discovery, diversity and evolution of novel coronaviruses sampled from rodents in China. *Virology*, **2015**, 474, 19-27	3.6	84
8	Unprecedented genomic diversity of RNA viruses in arthropods reveals the ancestry of negative-sense RNA viruses. *ELife*, **2015**, 4,	8.9	435
7	What is the time-scale of hantavirus evolution?. *Infection, Genetics and Evolution*, **2014**, 25, 144-5	4.5	14
6	A tick-borne segmented RNA virus contains genome segments derived from unsegmented viral ancestors. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 6744-9	11.5	104
5	Phylogeny and origins of hantaviruses harbored by bats, insectivores, and rodents. *PLoS Pathogens*, **2013**, 9, e1003159	7.6	180
4	Migration of Norway rats resulted in the worldwide distribution of Seoul hantavirus today. *Journal of Virology*, **2012**, 86, 972-81	6.6	83
3	Cross-species transmission in the speciation of the currently known murinae-associated hantaviruses. *Journal of Virology*, **2012**, 86, 11171-82	6.6	24
2	Hantavirus infections in humans and animals, China. *Emerging Infectious Diseases*, **2010**, 16, 1195-203	10.2	192
1	Complete genome characterisation of a novel coronavirus associated with severe human respiratory disease in Wuhan, China		63