Yong-Zhen Zhang

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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 10,112 24 42 g-index

42 13,638 11.9 6.81 ext. papers ext. citations avg, IF L-index

#	Paper	IF	Citations
35	A new coronavirus associated with human respiratory disease in China. <i>Nature</i> , 2020 , 579, 265-269	50.4	6055
34	Redefining the invertebrate RNA virosphere. <i>Nature</i> , 2016 , 540, 539-543	50.4	821
33	A Genomic Perspective on the Origin and Emergence of SARS-CoV-2. <i>Cell</i> , 2020 , 181, 223-227	56.2	459
32	Unprecedented genomic diversity of RNA viruses in arthropods reveals the ancestry of negative-sense RNA viruses. <i>ELife</i> , 2015 , 4,	8.9	435
31	The evolutionary history of vertebrate RNA viruses. <i>Nature</i> , 2018 , 556, 197-202	50.4	354
30	Hantavirus infections in humans and animals, China. <i>Emerging Infectious Diseases</i> , 2010 , 16, 1195-203	10.2	192
29	Phylogeny and origins of hantaviruses harbored by bats, insectivores, and rodents. <i>PLoS Pathogens</i> , 2013 , 9, e1003159	7.6	180
28	Divergent Viruses Discovered in Arthropods and Vertebrates Revise the Evolutionary History of the Flaviviridae and Related Viruses. <i>Journal of Virology</i> , 2016 , 90, 659-69	6.6	162
27	Taxonomy of the order Bunyavirales: update 2019. Archives of Virology, 2019, 164, 1949-1965	2.6	148
26	Using Metagenomics to Characterize an Expanding Virosphere. Cell, 2018, 172, 1168-1172	56.2	134
25	Taxonomy of the order Mononegavirales: update 2019. Archives of Virology, 2019, 164, 1967-1980	2.6	133
24	A tick-borne segmented RNA virus contains genome segments derived from unsegmented viral ancestors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 6744-9	11.5	104
23	Discovery, diversity and evolution of novel coronaviruses sampled from rodents in China. <i>Virology</i> , 2015 , 474, 19-27	3.6	84
22	Migration of Norway rats resulted in the worldwide distribution of Seoul hantavirus today. <i>Journal of Virology</i> , 2012 , 86, 972-81	6.6	83
21	Meta-transcriptomics and the evolutionary biology of RNA viruses. <i>Virus Research</i> , 2018 , 243, 83-90	6.4	72
20	Extensive diversity of coronaviruses in bats from China. <i>Virology</i> , 2017 , 507, 1-10	3.6	66
19	Complete genome characterisation of a novel coronavirus associated with severe human respiratory disease in Wuhan, China		63

18	The evolution and emergence of hantaviruses. Current Opinion in Virology, 2015, 10, 27-33	7.5	62
17	Expanding the RNA Virosphere by Unbiased Metagenomics. <i>Annual Review of Virology</i> , 2019 , 6, 119-139	9 14.6	59
16	Blood molecular markers associated with COVID-19 immunopathology and multi-organ damage. <i>EMBO Journal</i> , 2020 , 39, e105896	13	45
15	The diversity, evolution and origins of vertebrate RNA viruses. Current Opinion in Virology, 2018, 31, 9-1	6 7.5	33
14	Discovery of a Highly Divergent Coronavirus in the Asian House Shrew from China Illuminates the Origin of the Alphacoronaviruses. <i>Journal of Virology</i> , 2017 , 91,	6.6	25
13	Cross-species transmission in the speciation of the currently known murinae-associated hantaviruses. <i>Journal of Virology</i> , 2012 , 86, 11171-82	6.6	24
12	Newly identified viral genomes in pangolins with fatal disease. Virus Evolution, 2020, 6, veaa020	3.7	16
11	What is the time-scale of hantavirus evolution?. <i>Infection, Genetics and Evolution</i> , 2014 , 25, 144-5	4.5	14
10	Extensive genetic diversity and host range of rodent-borne coronaviruses. Virus Evolution, 2020, 6, vea	1037 / 8	11
9	2021 Taxonomic update of phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. <i>Archives of Virology</i> , 2021 , 166, 3513-3566	2.6	10
8	Diversity and circulation of Jingmen tick virus in ticks and mammals. Virus Evolution, 2020, 6, veaa051	3.7	8
7	Identifying the Risk of SARS-CoV-2 Infection and Environmental Monitoring in Airborne Infectious Isolation Rooms (AIIRs). <i>Virologica Sinica</i> , 2020 , 35, 785-792	6.4	6
6	Diverse and abundant resistome in terrestrial and aquatic vertebrates revealed by transcriptional analysis. <i>Scientific Reports</i> , 2020 , 10, 18870	4.9	6
5	Discovery of a highly divergent hepadnavirus in shrews from China. <i>Virology</i> , 2019 , 531, 162-170	3.6	5
4	Identification and characterization of Jingmen tick virus in rodents from Xinjiang, China. <i>Infection, Genetics and Evolution</i> , 2020 , 84, 104411	4.5	5
3	Meta-Transcriptomic Identification of Divergent in Fish. <i>Viruses</i> , 2020 , 12,	6.2	2
2	Total infectome characterization of respiratory infections in pre-COVID-19 Wuhan, China <i>PLoS Pathogens</i> , 2022 , 18, e1010259	7.6	2
1	Metatranscriptomics reveals that the death of a Mongolian wild ass was caused by in Inner Mongolia, China. <i>Journal of Veterinary Diagnostic Investigation</i> , 2020 , 32, 287-290	1.5	О