Mang Shi

List of Publications by Citations

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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.

125 papers	8,473 citations	40 h-index	91 g-index
145 ext. papers	11,044 ext. citations	8.4 avg, IF	6.02 L-index

#	Paper	IF	Citations
125	New world bats harbor diverse influenza A viruses. *PLoS Pathogens*, **2013**, 9, e1003657	7.6	825
124	Redefining the invertebrate RNA virosphere. *Nature*, **2016**, 540, 539-543	50.4	821
123	A distinct lineage of influenza A virus from bats. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 4269-74	11.5	741
122	Transcriptomic characteristics of bronchoalveolar lavage fluid and peripheral blood mononuclear cells in COVID-19 patients. *Emerging Microbes and Infections*, **2020**, 9, 761-770	18.9	671
121	Unprecedented genomic diversity of RNA viruses in arthropods reveals the ancestry of negative-sense RNA viruses. *ELife*, **2015**, 4,	8.9	435
120	The evolutionary history of vertebrate RNA viruses. *Nature*, **2018**, 556, 197-202	50.4	354
119	RNA based mNGS approach identifies a novel human coronavirus from two individual pneumonia cases in 2019 Wuhan outbreak. *Emerging Microbes and Infections*, **2020**, 9, 313-319	18.9	337
118	Taxonomy of the order Mononegavirales: update 2016. *Archives of Virology*, **2016**, 161, 2351-60	2.6	324
117	Phylogeny-based evolutionary, demographical, and geographical dissection of North American type 2 porcine reproductive and respiratory syndrome viruses. *Journal of Virology*, **2010**, 84, 8700-11	6.6	238
116	Molecular epidemiology of PRRSV: a phylogenetic perspective. *Virus Research*, **2010**, 154, 7-17	6.4	227
115	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
114	Surveillance of Bat Coronaviruses in Kenya Identifies Relatives of Human Coronaviruses NL63 and 229E and Their Recombination History. *Journal of Virology*, **2017**, 91,	6.6	134
113	Using Metagenomics to Characterize an Expanding Virosphere. *Cell*, **2018**, 172, 1168-1172	56.2	134
112	Taxonomy of the order Mononegavirales: update 2019. *Archives of Virology*, **2019**, 164, 1967-1980	2.6	133
111	Importation and Recombination Are Responsible for the Latest Emergence of Highly Pathogenic Porcine Reproductive and Respiratory Syndrome Virus in China. *Journal of Virology*, **2015**, 89, 10712-6	6.6	129
110	Molecular inferences suggest multiple host shifts of rabies viruses from bats to mesocarnivores in Arizona during 2001-2009. *PLoS Pathogens*, **2012**, 8, e1002786	7.6	117
109	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

108	Second-pandemic strain of Vibrio cholerae from the Philadelphia cholera outbreak of 1849. *New England Journal of Medicine*, **2014**, 370, 334-40	59.2	104
107	High-Resolution Metatranscriptomics Reveals the Ecological Dynamics of Mosquito-Associated RNA Viruses in Western Australia. *Journal of Virology*, **2017**, 91,	6.6	104
106	Enteric involvement in hospitalised patients with COVID-19 outside Wuhan. *The Lancet Gastroenterology and Hepatology*, **2020**, 5, 534-535	18.8	97
105	A Diverse Range of Novel RNA Viruses in Geographically Distinct Honey Bee Populations. *Journal of Virology*, **2017**, 91,	6.6	88
104	Discovery, diversity and evolution of novel coronaviruses sampled from rodents in China. *Virology*, **2015**, 474, 19-27	3.6	84
103	Evolutionary conservation of the PA-X open reading frame in segment 3 of influenza A virus. *Journal of Virology*, **2012**, 86, 12411-3	6.6	80
102	Meta-transcriptomics and the evolutionary biology of RNA viruses. *Virus Research*, **2018**, 243, 83-90	6.4	72
101	Extensive diversity of Rickettsiales bacteria in two species of ticks from China and the evolution of the Rickettsiales. *BMC Evolutionary Biology*, **2014**, 14, 167	3	71
100	Genomic characterization of emergent pseudorabies virus in China reveals marked sequence divergence: Evidence for the existence of two major genotypes. *Virology*, **2015**, 483, 32-43	3.6	70
99	Extensive Diversity of RNA Viruses in Australian Ticks. *Journal of Virology*, **2019**, 93,	6.6	63
98	Dinucleotide Composition in Animal RNA Viruses Is Shaped More by Virus Family than by Host Species. *Journal of Virology*, **2017**, 91,	6.6	57
97	Clinical and epidemiological features of COVID-19 family clusters in Beijing, China. *Journal of Infection*, **2020**, 81, e26-e30	18.9	57
96	Characterizing the virome of Ixodes ricinus ticks from northern Europe. *Scientific Reports*, **2017**, 7, 10870	4.9	57
95	Recombination is associated with an outbreak of novel highly pathogenic porcine reproductive and respiratory syndrome viruses in China. *Journal of Virology*, **2013**, 87, 10904-7	6.6	57
94	Successful strategies implemented towards the elimination of canine rabies in the Western Hemisphere. *Antiviral Research*, **2017**, 143, 1-12	10.8	54
93	Evolution of Termite Symbiosis Informed by Transcriptome-Based Phylogenies. *Current Biology*, **2019**, 29, 3728-3734.e4	6.3	50
92	The history of rabies in the Western Hemisphere. *Antiviral Research*, **2017**, 146, 221-232	10.8	49
91	Evolutionary diversification of type 2 porcine reproductive and respiratory syndrome virus. *Journal of General Virology*, **2015**, 96, 1570-80	4.9	49

90	Virus-virus interactions and host ecology are associated with RNA virome structure in wild birds. *Molecular Ecology*, **2018**, 27, 5263-5278	5.7	49
89	Discovery of diverse polyomaviruses in bats and the evolutionary history of the Polyomaviridae. *Journal of General Virology*, **2013**, 94, 738-748	4.9	47
88	Identification of novel and diverse rotaviruses in rodents and insectivores, and evidence of cross-species transmission into humans. *Virology*, **2016**, 494, 168-77	3.6	46
87	Isolation and characterization of a novel arenavirus harbored by Rodents and Shrews in Zhejiang province, China. *Virology*, **2015**, 476, 37-42	3.6	44
86	A Divergent Hepatitis D-Like Agent in Birds. *Viruses*, **2018**, 10,	6.2	41
85	Meta-transcriptomics reveals a diverse antibiotic resistance gene pool in avian microbiomes. *BMC Biology*, **2019**, 17, 31	7.3	40
84	Phylogenetic evidence for homologous recombination within the family Birnaviridae. *Journal of General Virology*, **2008**, 89, 3156-3164	4.9	39
83	No detectable effect of Mel on the prevalence and abundance of the RNA virome of. *Proceedings of the Royal Society B: Biological Sciences*, **2018**, 285,	4.4	37
82	Virome heterogeneity and connectivity in waterfowl and shorebird communities. *ISME Journal*, **2019**, 13, 2603-2616	11.9	36
81	The spread of type 2 Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) in North America: a phylogeographic approach. *Virology*, **2013**, 447, 146-54	3.6	36
80	Genomic evolution of porcine reproductive and respiratory syndrome virus (PRRSV) isolates revealed by deep sequencing. *PLoS ONE*, **2014**, 9, e88807	3.7	36
79	Fourteen types of co-circulating recombinant enterovirus were associated with hand, foot, and mouth disease in children from Wenzhou, China. *Journal of Clinical Virology*, **2015**, 70, 29-38	14.5	34
78	Novel hepatitis D-like agents in vertebrates and invertebrates. *Virus Evolution*, **2019**, 5, vez021	3.7	34
77	Diversity and evolution of avian influenza viruses in live poultry markets, free-range poultry and wild wetland birds in China. *Journal of General Virology*, **2016**, 97, 844-854	4.9	34
76	The diversity, evolution and origins of vertebrate RNA viruses. *Current Opinion in Virology*, **2018**, 31, 9-16	7.5	33
75	Meta-Transcriptomic Comparison of the RNA Viromes of the Mosquito Vectors and in Northern Europe. *Viruses*, **2019**, 11,	6.2	33
74	Phylogenetic perspectives on the epidemiology and origins of SARS and SARS-like coronaviruses. *Infection, Genetics and Evolution*, **2009**, 9, 1185-96	4.5	31
73	Hidden diversity and evolution of viruses in market fish. *Virus Evolution*, **2018**, 4, vey031	3.7	30

72	Fecal Viral Diversity of Captive and Wild Tasmanian Devils Characterized Using Virion-Enriched Metagenomics and Metatranscriptomics. *Journal of Virology*, **2019**, 93,	6.6	29
71	Francisella tularensis ssp. holarctica in Ringtail Possums, Australia. *Emerging Infectious Diseases*, **2017**, 23, 1198-1201	10.2	28
70	Phylodynamics of H5N1 avian influenza virus in Indonesia. *Molecular Ecology*, **2012**, 21, 3062-77	5.7	28
69	Sustained RNA virome diversity in Antarctic penguins and their ticks. *ISME Journal*, **2020**, 14, 1768-1782	11.9	28
68	Phylogenetics, Genomic Recombination, and NSP2 Polymorphic Patterns of Porcine Reproductive and Respiratory Syndrome Virus in China and the United States in 2014-2018. *Journal of Virology*, **2020**, 94,	6.6	27
67	Diversity of Middle East respiratory syndrome coronaviruses in 109 dromedary camels based on full-genome sequencing, Abu Dhabi, United Arab Emirates. *Emerging Microbes and Infections*, **2017**, 6, e101	18.9	26
66	Genetic characterization and evolutionary analysis of 4 Newcastle disease virus isolate full genomes from waterbirds in South China during 2003-2007. *Veterinary Microbiology*, **2011**, 152, 46-54	3.3	26
65	Genomic characterization of seven distinct bat coronaviruses in Kenya. *Virus Research*, **2012**, 167, 67-73	6.4	24
64	Abundant and Diverse RNA Viruses in Insects Revealed by RNA-Seq Analysis: Ecological and Evolutionary Implications. *MSystems*, **2020**, 5,	7.6	21
63	Diversity, evolution and population dynamics of avian influenza viruses circulating in the live poultry markets in China. *Virology*, **2017**, 505, 33-41	3.6	19
62	A Novel Hepadnavirus Identified in an Immunocompromised Domestic Cat in Australia. *Viruses*, **2018**, 10,	6.2	19
61	Systematic phylogenetic analysis of influenza A virus reveals many novel mosaic genome segments. *Infection, Genetics and Evolution*, **2013**, 18, 367-78	4.5	18
60	New rabies virus variant found during an epizootic in white-nosed coatis from the Yucatan Peninsula. *Epidemiology and Infection*, **2010**, 138, 1586-9	4.3	18
59	A new lineage of segmented RNA viruses infecting animals. *Virus Evolution*, **2020**, 6, vez061	3.7	17
58	Evolutionary history and phylogeography of rabies viruses associated with outbreaks in Trinidad. *PLoS Neglected Tropical Diseases*, **2013**, 7, e2365	4.8	16
57	Porcine reproductive and respiratory syndrome virus in Ontario, Canada 1999 to 2010: genetic diversity and restriction fragment length polymorphisms. *Journal of General Virology*, **2011**, 92, 1391-1397	4.9	16
56	Comparative Analysis of RNA Virome Composition in Rabbits and Associated Ectoparasites. *Journal of Virology*, **2020**, 94,	6.6	15
55	Complete genome characterization of a East European Type 1 subtype 3 porcine reproductive and respiratory syndrome virus. *Virus Genes*, **2012**, 44, 51-4	2.3	14

54	Genetic diversity and multiple introductions of porcine reproductive and respiratory syndrome viruses in Thailand. *Virology Journal*, **2011**, 8, 164	6.1	12
53	Metatranscriptomic Analysis of Virus Diversity in Urban Wild Birds with Paretic Disease. *Journal of Virology*, **2020**, 94,	6.6	11
52	Virome characterization of game animals in China reveals a spectrum of emerging pathogens.. *Cell*, **2022**,	56.2	11
51	The discovery of three new hare lagoviruses reveals unexplored viral diversity in this genus. *Virus Evolution*, **2019**, 5, vez005	3.7	10
50	Rapid isolation and immune profiling of SARS-CoV-2 specific memory B cell in convalescent COVID-19 patients via LIBRA-seq. *Signal Transduction and Targeted Therapy*, **2021**, 6, 195	21	10
49	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
48	Insights into the evolutionary history and epidemiological characteristics of the emerging lineage 1 porcine reproductive and respiratory syndrome viruses in China. *Transboundary and Emerging Diseases*, **2020**, 67, 2630-2641	4.2	9
47	Tamdy Virus in Ixodid Ticks Infesting Bactrian Camels, Xinjiang, China, 2018. *Emerging Infectious Diseases*, **2019**, 25, 2136-2138	10.2	9
46	Complete genome of Aedes aegypti anphevirus in the Aag2 mosquito cell line. *Journal of General Virology*, **2018**, 99, 832-836	4.9	9
45	A Convenient and Biosafe Replicon with Accessory Genes of SARS-CoV-2 and Its Potential Application in Antiviral Drug Discovery. *Virologica Sinica*, **2021**, 36, 913-923	6.4	9
44	Metagenomic discovery and co-infection of diverse wobbly possum disease viruses and a novel hepacivirus in Australian brushtail possums. *One Health Outlook*, **2019**, 1, 5	5	9
43	Association between the nasopharyngeal microbiome and metabolome in patients with COVID-19. *Synthetic and Systems Biotechnology*, **2021**, 6, 135-143	4.2	9
42	ICTV Virus Taxonomy Profile: Rhabdoviridae 2022. *Journal of General Virology*, **2022**, 103,	4.9	8
41	High resolution metagenomic characterization of complex infectomes in paediatric acute respiratory infection. *Scientific Reports*, **2020**, 10, 3963	4.9	7
40	Viral Discovery in the Invasive Australian Cane Toad (Rhinella marina) Using Metatranscriptomic and Genomic Approaches. *Journal of Virology*, **2018**, 92,	6.6	7
39	Identification of A Novel Papillomavirus Associated with Squamous Cell Carcinoma in A Domestic Cat. *Viruses*, **2020**, 12,	6.2	6
38	Novel hepaci- and pegi-like viruses in native Australian wildlife and non-human primates. *Virus Evolution*, **2020**, 6, veaa064	3.7	6
37	Risk factors for the critical illness in SARS-CoV-2 infection: a multicenter retrospective cohort study. *Respiratory Research*, **2020**, 21, 277	7.3	6

36	Emerging Sand Fly-Borne Phlebovirus in China. *Emerging Infectious Diseases*, **2020**, 26, 2435-2438	10.2	6
35	Virome of bat-infesting arthropods: highly divergent viruses in different vectors. *Journal of Virology* , **2021**, JVI0146421	6.6	6
34	Feline Calicivirus Virulent Systemic Disease: Clinical Epidemiology, Analysis of Viral Isolates and In Vitro Efficacy of Novel Antivirals in Australian Outbreaks. *Viruses*, **2021**, 13,	6.2	5
33	Meta-Transcriptomic Analysis Reveals the Virome and Viral Genomic Evolution of Medically Important Mites. *Journal of Virology*, **2020**,	6.6	5
32	Unmapped RNA Virus Diversity in Termites and their Symbionts. *Viruses*, **2020**, 12,	6.2	4
31	Author response: Unprecedented genomic diversity of RNA viruses in arthropods reveals the ancestry of negative-sense RNA viruses **2015**,		4
30	Diversity and Evolution of Novel Invertebrate DNA Viruses Revealed by Meta-Transcriptomics. *Viruses*, **2019**, 11,	6.2	4
29	RNA virome abundance and diversity is associated with host age in a bird species. *Virology*, **2021**, 561, 98-106	3.6	4
28	Other Bat-Borne Viruses **2015**, 217-247		3
27	Sustained virome diversity in Antarctic penguins and their ticks: geographical connectedness and no evidence for low pathogen pressure		3
26	Characterisation of the faecal virome of captive and wild Tasmanian devils using virus-like particles metagenomics and meta-transcriptomics		3
25	A Novel Virus of Associated with Sexual Precocity in. *MSystems*, **2021**, 6, e0000321	7.6	3
24	The adenosine analog prodrug ATV006 is orally bioavailable and has preclinical efficacy against parental SARS-CoV-2 and variants.. *Science Translational Medicine*, **2022**, eabm7621	17.5	3
23	Meta-Transcriptomic Identification of Divergent in Fish. *Viruses*, **2020**, 12,	6.2	2
22	Discovery and Prevalence of Divergent RNA Viruses in European Field Voles and Rabbits. *Viruses*, **2019**, 12,	6.2	2
21	A Novel Bunyavirus Discovered in Oriental Shrimp ().. *Frontiers in Microbiology*, **2021**, 12, 751112	5.7	2
20	RNA virome diversity and infection in individual flies. *Journal of General Virology*, **2021**, 102,	4.9	2
19	Extensive Diversity of RNA Viruses in Australian Ticks		2

18	Use of partial N-gene sequences as a tool to monitor progress on rabies control and elimination efforts in Ethiopia. *Acta Tropica*, **2021**, 221, 106022	3.2	2
17	Total infectome characterization of respiratory infections in pre-COVID-19 Wuhan, China.. *PLoS Pathogens*, **2022**, 18, e1010259	7.6	2
16	A comprehensive evolutionary and epidemiological characterization of insertion and deletion mutations in SARS-CoV-2 genomes.. *Virus Evolution*, **2021**, 7, veab104	3.7	2
15	: a new taxonomical framework for a rapidly expanding order of unusual monjiviricete viruses broadly distributed among arthropod subphyla.. *Applied and Environmental Microbiology*, **2022**, AEM0195421	4.8	1
14	A time-series meta-transcriptomic analysis reveals the seasonal, host, and gender structure of mosquito viromes.. *Virus Evolution*, **2022**, 8, veac006	3.7	1
13	Meta-transcriptomic analysis of virus diversity in urban wild birds with paretic disease		1
12	The discovery of three new hare lagoviruses reveals unexplored viral diversity in this genus		1
11	A new lineage of segmented RNA viruses infecting animals		1
10	Metagenomic identification of diverse animal hepaciviruses and pegiviruses		1
9	A divergent hepatitis D-like agent in birds		1
8	Isolation and Identification of a Novel Phlebovirus, Hedi Virus, from Sandflies Collected in China. *Viruses*, **2021**, 13,	6.2	1
7	Transcriptome Analysis and In Situ Hybridization for FcaGHV1 in Feline Lymphoma. *Viruses*, **2018**, 10,	6.2	1
6	Wildlife-borne microorganisms and strategies to prevent and control emerging infectious diseases. *Journal of Biosafety and Biosecurity*, **2021**, 3, 67-71	1.4	1
5	A total infectome approach to understand the etiology of infectious disease in pigs.. *Microbiome*, **2022**, 10, 73	16.6	1
4	Two Rhabdoviruses, One Novel, Isolated from Armigeres subalbatus in China. *Pathogens*, **2022**, 11, 624	4.5	1
3	Characterization of the Gut Microbiome and Resistomes of Wild and Zoo-Captive Macaques.. *Frontiers in Veterinary Science*, **2021**, 8, 778556	3.1	0
2	Co-infecting pathogens can contribute to inflammatory responses and severe symptoms in COVID-19.. *Journal of Thoracic Disease*, **2022**, 14, 355-370	2.6	0
1	Molecular Epidemiology and Vaccine Compatibility Analysis of Seasonal Influenza Viruses in Wuhan, 2016-2019. *Virologica Sinica*, **2020**, 35, 556-565	6.4	