## Ben Hu

## List of Publications by Year in descending order

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27 24,798 19
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32 all docs

32 docs citations 32 times ranked

#	Article	IF	CITATIONS
1	Inactivated SARS-CoV-2 Vaccine Shows Cross-Protection against Bat SARS-Related Coronaviruses in Human ACE2 Transgenic Mice. Journal of Virology, 2022, 96, e0016922.	1.5	3
2	Characteristics of SARS-CoV-2 and COVID-19. Nature Reviews Microbiology, 2021, 19, 141-154.	13.6	3,334
3	Identification of a novel lineage bat SARS-related coronaviruses that use bat ACE2 receptor. Emerging Microbes and Infections, 2021, 10, 1507-1514.	3.0	47
4	Genetic Mutation of SARS-CoV-2 during Consecutive Passages in Permissive Cells. Virologica Sinica, 2021, 36, 1073-1076.	1.2	5
5	A Novel Potentially Recombinant Rodent Coronavirus with a Polybasic Cleavage Site in the Spike Protein. Journal of Virology, 2021, 95, e0117321.	1.5	16
6	Viromes and surveys of RNA viruses in camel-derived ticks revealing transmission patterns of novel tick-borne viral pathogens in Kenya. Emerging Microbes and Infections, 2021, 10, 1975-1987.	3.0	17
7	Characterization of Novel Rhabdoviruses in Chinese Bats. Viruses, 2021, 13, 64.	1.5	14
8	Genomic Characterization of Diverse Bat Coronavirus HKU10 in Hipposideros Bats. Viruses, 2021, 13, 1962.	1.5	3
9	A Cellâ€Free Platform Based on Nisin Biosynthesis for Discovering Novel Lanthipeptides and Guiding their Overproduction In Vivo. Advanced Science, 2020, 7, 2001616.	5 <b>.</b> 6	33
10	Origin and cross-species transmission of bat coronaviruses in China. Nature Communications, 2020, 11, 4235.	5.8	264
11	Nanopore Targeted Sequencing for the Accurate and Comprehensive Detection of SARS oVâ€2 and Other Respiratory Viruses. Small, 2020, 16, e2002169.	<b>5.</b> 2	169
12	A pneumonia outbreak associated with a new coronavirus of probable bat origin. Nature, 2020, 579, 270-273.	13.7	17,004
13	Molecular and serological investigation of 2019-nCoV infected patients: implication of multiple shedding routes. Emerging Microbes and Infections, 2020, 9, 386-389.	3.0	1,471
14	Serological evidence of MERS-CoV and HKU8-related CoV co-infection in Kenyan camels. Emerging Microbes and Infections, 2019, 8, 1528-1534.	3.0	18
15	Characterization of a New Member of Alphacoronavirus with Unique Genomic Features in Rhinolophus Bats. Viruses, 2019, 11, 379.	1.5	28
16	Geographical structure of bat SARS-related coronaviruses. Infection, Genetics and Evolution, 2019, 69, 224-229.	1.0	37
17	Molecular Detection and Genetic Characterization of Novel RNA Viruses in Wild and Synanthropic Rodents and Shrews in Kenya. Frontiers in Microbiology, 2019, 10, 2696.	1.5	16
18	Longitudinal Surveillance of Betacoronaviruses in Fruit Bats in Yunnan Province, China During 2009–2016. Virologica Sinica, 2018, 33, 87-95.	1.2	25

#	Article	IF	CITATION
19	Discovery of Novel Bat Coronaviruses in South China That Use the Same Receptor as Middle East Respiratory Syndrome Coronavirus. Journal of Virology, 2018, 92, .	1.5	106
20	Genetic Evidence of Middle East Respiratory Syndrome Coronavirus (MERS-Cov) and Widespread Seroprevalence among Camels in Kenya. Virologica Sinica, 2018, 33, 484-492.	1.2	42
21	Molecular detection of viruses in Kenyan bats and discovery of novel astroviruses, caliciviruses and rotaviruses. Virologica Sinica, 2017, 32, 101-114.	1.2	54
22	Discovery of a rich gene pool of bat SARS-related coronaviruses provides new insights into the origin of SARS coronavirus. PLoS Pathogens, 2017, 13, e1006698.	2.1	797
23	Coexistence of multiple coronaviruses in several bat colonies in an abandoned mineshaft. Virologica Sinica, 2016, 31, 31-40.	1.2	117
24	Longitudinal surveillance of SARS-like coronaviruses in bats by quantitative real-time PCR. Virologica Sinica, 2016, 31, 78-80.	1.2	20
25	Isolation and Characterization of a Novel Bat Coronavirus Closely Related to the Direct Progenitor of Severe Acute Respiratory Syndrome Coronavirus. Journal of Virology, 2016, 90, 3253-3256.	1.5	221
26	Bat origin of human coronaviruses. Virology Journal, 2015, 12, 221.	1.4	330
27	Detection of diverse novel astroviruses from small mammals in China. Journal of General Virology, 2014, 95, 2442-2449.	1.3	33