

Louise H Moncla

List of Publications by Year in descending order

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Version: 2024-02-01

11
papers

836
citations

933447

10
h-index

1281871

11
g-index

16
all docs

16
docs citations

16
times ranked

1907
citing authors

#	ARTICLE	IF	CITATIONS
1	Repeated introductions and intensive community transmission fueled a mumps virus outbreak in Washington State. <i>ELife</i> , 2021, 10, .	6.0	13
2	Viral genomes reveal patterns of the SARS-CoV-2 outbreak in Washington State. <i>Science Translational Medicine</i> , 2021, 13, .	12.4	58
3	Acute SARS-CoV-2 infections harbor limited within-host diversity and transmit via tight transmission bottlenecks. <i>PLoS Pathogens</i> , 2021, 17, e1009849.	4.7	80
4	Cryptic transmission of SARS-CoV-2 in Washington state. <i>Science</i> , 2020, 370, 571-575.	12.6	217
5	Quantifying within-host diversity of H5N1 influenza viruses in humans and poultry in Cambodia. <i>PLoS Pathogens</i> , 2020, 16, e1008191.	4.7	22
6	Genomic epidemiology supports multiple introductions and cryptic transmission of Zika virus in Colombia. <i>BMC Infectious Diseases</i> , 2019, 19, 963.	2.9	12
7	Comprehensive mapping of adaptation of the avian influenza polymerase protein PB2 to humans. <i>ELife</i> , 2019, 8, .	6.0	45
8	Within-Host Evolution of Human Influenza Virus. <i>Trends in Microbiology</i> , 2018, 26, 781-793.	7.7	96
9	Diversity of Influenza A(H5N1) Viruses in Infected Humans, Northern Vietnam, 2004â€“2010. <i>Emerging Infectious Diseases</i> , 2018, 24, 1128-1238.	4.3	25
10	Deep Sequencing Reveals Potential Antigenic Variants at Low Frequencies in Influenza A Virus-Infected Humans. <i>Journal of Virology</i> , 2016, 90, 3355-3365.	3.4	101
11	SNPGenie: estimating evolutionary parameters to detect natural selection using pooled next-generation sequencing data. <i>Bioinformatics</i> , 2015, 31, 3709-3711.	4.1	148