

Mariateresa de Cesare

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7107766/publications.pdf>

Version: 2024-02-01

25
papers

2,278
citations

623734

14
h-index

552781

26
g-index

30
all docs

30
docs citations

30
times ranked

4503
citing authors

#	ARTICLE	IF	CITATIONS
1	A highly virulent variant of HIV-1 circulating in the Netherlands. <i>Science</i> , 2022, 375, 540-545.	12.6	39
2	SARS-CoV-2 within-host diversity and transmission. <i>Science</i> , 2021, 372, .	12.6	278
3	Targeted capture and sequencing of <i>Orientia tsutsugamushi</i> genomes from chiggers and humans. <i>Infection, Genetics and Evolution</i> , 2021, 91, 104818.	2.3	6
4	Endemic HBV among hospital in-patients in Bangladesh, including evidence of occult infection. <i>Journal of General Virology</i> , 2021, 102, .	2.9	2
5	Distinct patterns of within-host virus populations between two subgroups of human respiratory syncytial virus. <i>Nature Communications</i> , 2021, 12, 5125.	12.8	16
6	Transfusion-transmitted hepatitis C: A cluster of cases in transfusion-dependent thalassaemia patients in Sri Lanka. <i>Transfusion Medicine</i> , 2020, 30, 377-383.	1.1	2
7	A Comprehensive Genomics Solution for HIV Surveillance and Clinical Monitoring in Low-Income Settings. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	3.9	39
8	Evidence of tenofovir resistance in chronic hepatitis B virus (HBV) infection: An observational case series of South African adults. <i>Journal of Clinical Virology</i> , 2020, 129, 104548.	3.1	16
9	Simultaneous Viral Whole-Genome Sequencing and Differential Expression Profiling in Respiratory Syncytial Virus Infection of Infants. <i>Journal of Infectious Diseases</i> , 2020, 222, S666-S671.	4.0	11
10	Performance of a high-throughput next-generation sequencing method for analysis of HIV drug resistance and viral load. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 3510-3516.	3.0	13
11	Epstein-Barr virus reactivation in sepsis due to community-acquired pneumonia is associated with increased morbidity and an immunosuppressed host transcriptomic endotype. <i>Scientific Reports</i> , 2020, 10, 9838.	3.3	13
12	Case Report: Application of hepatitis B virus (HBV) deep sequencing to distinguish between acute and chronic infection. <i>Wellcome Open Research</i> , 2020, 5, 240.	1.8	2
13	Oxford Nanopore MinION Sequencing Enables Rapid Whole Genome Assembly of <i>Rickettsia typhi</i> in a Resource-Limited Setting. <i>American Journal of Tropical Medicine and Hygiene</i> , 2020, 102, 408-414.	1.4	22
14	Case Report: Application of hepatitis B virus (HBV) deep sequencing to distinguish between acute and chronic infection. <i>Wellcome Open Research</i> , 2020, 5, 240.	1.8	3
15	Prolonged Zika Virus RNA Detection in Semen of Immunosuppressed Patient. <i>Emerging Infectious Diseases</i> , 2019, 25, 1598-1600.	4.3	8
16	Illumina and Nanopore methods for whole genome sequencing of hepatitis B virus (HBV). <i>Scientific Reports</i> , 2019, 9, 7081.	3.3	75
17	Sequencing of human genomes with nanopore technology. <i>Nature Communications</i> , 2019, 10, 1869.	12.8	140
18	Genomic Epidemiology Reconstructs the Introduction and Spread of Zika Virus in Central America and Mexico. <i>Cell Host and Microbe</i> , 2018, 23, 855-864.e7.	11.0	82

#	ARTICLE	IF	CITATIONS
19	PHYLOSCANNER: Inferring Transmission from Within- and Between-Host Pathogen Genetic Diversity. <i>Molecular Biology and Evolution</i> , 2018, 35, 719-733.	8.9	122
20	Comprehensive comparison of Pacific Biosciences and Oxford Nanopore Technologies and their applications to transcriptome analysis. <i>F1000Research</i> , 2017, 6, 100.	1.6	366
21	Comprehensive comparison of Pacific Biosciences and Oxford Nanopore Technologies and their applications to transcriptome analysis. <i>F1000Research</i> , 2017, 6, 100.	1.6	203
22	MinION Analysis and Reference Consortium: Phase 1 data release and analysis. <i>F1000Research</i> , 2015, 4, 1075.	1.6	270
23	Rapid antibiotic-resistance predictions from genome sequence data for <i>Staphylococcus aureus</i> and <i>Mycobacterium tuberculosis</i> . <i>Nature Communications</i> , 2015, 6, 10063.	12.8	479
24	Nuclear SSR Markers for <i>Miscanthus</i> , <i>Saccharum</i> , and Related Grasses (Saccharinae, Poaceae). <i>Applications in Plant Sciences</i> , 2013, 1, 1300042.	2.1	7
25	Chloroplast DNA markers (cpSSRs, SNPs) for <i>Miscanthus</i> , <i>Saccharum</i> and related grasses (Panicoideae.) <i>Tj ETQq1</i> 1,0,784314 rgBT /Ove	2.1	40