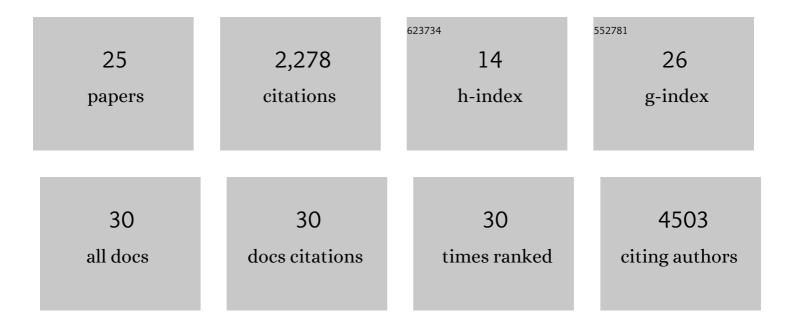
Mariateresa de Cesare

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7107766/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Rapid antibiotic-resistance predictions from genome sequence data for Staphylococcus aureus and Mycobacterium tuberculosis. Nature Communications, 2015, 6, 10063.	12.8	479
2	Comprehensive comparison of Pacific Biosciences and Oxford Nanopore Technologies and their applications to transcriptome analysis. F1000Research, 2017, 6, 100.	1.6	366
3	SARS-CoV-2 within-host diversity and transmission. Science, 2021, 372, .	12.6	278
4	MinION Analysis and Reference Consortium: Phase 1 data release and analysis. F1000Research, 2015, 4, 1075.	1.6	270
5	Comprehensive comparison of Pacific Biosciences and Oxford Nanopore Technologies and their applications to transcriptome analysis. F1000Research, 2017, 6, 100.	1.6	203
6	Sequencing of human genomes with nanopore technology. Nature Communications, 2019, 10, 1869.	12.8	140
7	PHYLOSCANNER: Inferring Transmission from Within- and Between-Host Pathogen Genetic Diversity. Molecular Biology and Evolution, 2018, 35, 719-733.	8.9	122
8	Genomic Epidemiology Reconstructs the Introduction and Spread of Zika Virus in Central America and Mexico. Cell Host and Microbe, 2018, 23, 855-864.e7.	11.0	82
9	Illumina and Nanopore methods for whole genome sequencing of hepatitis B virus (HBV). Scientific Reports, 2019, 9, 7081.	3.3	75
10	Chloroplast DNA markers (cpSSRs, SNPs) for Miscanthus, Saccharum and related grasses (Panicoideae,) Tj ETQq() 0 0 rgBT 2.1	/Overlock 10
11	A Comprehensive Genomics Solution for HIV Surveillance and Clinical Monitoring in Low-Income Settings. Journal of Clinical Microbiology, 2020, 58, .	3.9	39
12	A highly virulent variant of HIV-1 circulating in the Netherlands. Science, 2022, 375, 540-545.	12.6	39
13	Oxford Nanopore MinION Sequencing Enables Rapid Whole Genome Assembly of Rickettsia typhi in a Resource-Limited Setting. American Journal of Tropical Medicine and Hygiene, 2020, 102, 408-414.	1.4	22
14	Evidence of tenofovir resistance in chronic hepatitis B virus (HBV) infection: An observational case series of South African adults. Journal of Clinical Virology, 2020, 129, 104548.	3.1	16
15	Distinct patterns of within-host virus populations between two subgroups of human respiratory syncytial virus. Nature Communications, 2021, 12, 5125.	12.8	16
16	Performance of a high-throughput next-generation sequencing method for analysis of HIV drug resistance and viral load. Journal of Antimicrobial Chemotherapy, 2020, 75, 3510-3516.	3.0	13
17	Epstein-Barr virus reactivation in sepsis due to community-acquired pneumonia is associated with increased morbidity and an immunosuppressed host transcriptomic endotype. Scientific Reports, 2020, 10, 9838.	3.3	13

18Simultaneous Viral Whole-Genome Sequencing and Differential Expression Profiling in Respiratory
Syncytial Virus Infection of Infants. Journal of Infectious Diseases, 2020, 222, S666-S671.4.011

#	ARTICLE	IF	CITATIONS
19	Prolonged Zika Virus RNA Detection in Semen of Immunosuppressed Patient. Emerging Infectious Diseases, 2019, 25, 1598-1600.	4.3	8
20	Nuclear SSR Markers for Miscanthus, Saccharum, and Related Grasses (Saccharinae, Poaceae). Applications in Plant Sciences, 2013, 1, 1300042.	2.1	7
21	Targeted capture and sequencing of Orientia tsutsugamushi genomes from chiggers and humans. Infection, Genetics and Evolution, 2021, 91, 104818.	2.3	6
22	Case Report: Application of hepatitis B virus (HBV) deep sequencing to distinguish between acute and chronic infection. Wellcome Open Research, 2020, 5, 240.	1.8	3
23	Transfusionâ€transmitted hepatitis C: A cluster of cases in transfusionâ€dependent thalassaemia patients in Sri Lanka. Transfusion Medicine, 2020, 30, 377-383.	1.1	2
24	Endemic HBV among hospital in-patients in Bangladesh, including evidence of occult infection. Journal of General Virology, 2021, 102, .	2.9	2
25	Case Report: Application of hepatitis B virus (HBV) deep sequencing to distinguish between acute and chronic infection. Wellcome Open Research, 2020, 5, 240.	1.8	2