Jerome Bouquet

List of Publications by Year in descending order

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394421 642732 2,117 22 19 23 citations g-index h-index papers 26 26 26 4665 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Rapid metagenomic identification of viral pathogens in clinical samples by real-time nanopore sequencing analysis. Genome Medicine, 2015, 7, 99.	8.2	456
2	A cloud-compatible bioinformatics pipeline for ultrarapid pathogen identification from next-generation sequencing of clinical samples. Genome Research, 2014, 24, 1180-1192.	5. 5	421
3	The SARS-CoV-2 monoclonal antibody combination, AZD7442, is protective in nonhuman primates and has an extended half-life in humans. Science Translational Medicine, 2022, 14, eabl8124.	12.4	143
4	The eukaryotic gut virome in hematopoietic stem cell transplantation: new clues in enteric graft-versus-host disease. Nature Medicine, 2017, 23, 1080-1085.	30.7	109
5	Clinical metagenomic identification of Balamuthia mandrillaris encephalitis and assembly of the draft genome: the continuing case for reference genome sequencing. Genome Medicine, 2015, 7, 113.	8.2	102
6	Close Similarity between Sequences of Hepatitis E Virus Recovered from Humans and Swine, France, 2008â^2009. Emerging Infectious Diseases, 2011, 17, 2018-25.	4.3	92
7	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
8	Longitudinal Transcriptome Analysis Reveals a Sustained Differential Gene Expression Signature in Patients Treated for Acute Lyme Disease. MBio, 2016, 7, e00100-16.	4.1	76
9	Biological activities of nitidine, a potential anti-malarial lead compound. Malaria Journal, 2012, 11, 67.	2.3	59
10	Experimental Zika Virus Inoculation in a New World Monkey Model Reproduces Key Features of the Human Infection. Scientific Reports, 2017, 7, 17126.	3.3	58
11	Microbial burden and viral exacerbations in a longitudinal multicenter COPD cohort. Respiratory Research, 2020, 21, 77.	3.6	44
12	Metagenomic-based Surveillance of Pacific Coast tick Dermacentor occidentalis Identifies Two Novel Bunyaviruses and an Emerging Human Ricksettsial Pathogen. Scientific Reports, 2017, 7, 12234.	3.3	42
13	New models of hepatitis E virus replication in human and porcine hepatocyte cell lines. Journal of General Virology, 2013, 94, 549-558.	2.9	41
14	Genetic characterization and codon usage bias of full-length Hepatitis E virus sequences shed new lights on genotypic distribution, host restriction and genome evolution. Infection, Genetics and Evolution, 2012, 12, 1842-1853.	2.3	38
15	Identical Consensus Sequence and Conserved Genomic Polymorphism of Hepatitis E Virus during Controlled Interspecies Transmission. Journal of Virology, 2012, 86, 6238-6245.	3.4	27
16	Differentiation enhances Zika virus infection of neuronal brain cells. Scientific Reports, 2018, 8, 14543.	3.3	26
17	Quantitative Proteomics Identifies Host Factors Modulated during Acute Hepatitis E Virus Infection in the Swine Model. Journal of Virology, 2015, 89, 129-143.	3.4	22
18	Whole blood human transcriptome and virome analysis of ME/CFS patients experiencing post-exertional malaise following cardiopulmonary exercise testing. PLoS ONE, 2019, 14, e0212193.	2.5	22

#	Article	IF	CITATION
19	RNA-Seq Analysis of Gene Expression, Viral Pathogen, and B-Cell/T-Cell Receptor Signatures in Complex Chronic Disease. Clinical Infectious Diseases, 2017, 64, 476-481.	5.8	21
20	Metagenomic Next-Generation Sequencing of the 2014 Ebola Virus Disease Outbreak in the Democratic Republic of the Congo. Journal of Clinical Microbiology, 2019, 57, .	3.9	17
21	Early changes in the circulating T cells are associated with clinical outcomes after PD-L1 blockade by durvalumab in advanced NSCLC patients. Cancer Immunology, Immunotherapy, 2021, 70, 2095-2102.	4.2	17
22	Metagenomic sequencing of stool samples in Bangladeshi infants: virome association with poliovirus shedding after oral poliovirus vaccination. Scientific Reports, 2020, 10, 15392.	3.3	6