

Jerome Bouquet

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1474510/publications.pdf>

Version: 2024-02-01

22
papers

2,117
citations

394421

19
h-index

642732

23
g-index

26
all docs

26
docs citations

26
times ranked

4665
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | The SARS-CoV-2 monoclonal antibody combination, AZD7442, is protective in nonhuman primates and has an extended half-life in humans. <i>Science Translational Medicine</i> , 2022, 14, eabl8124. | 12.4 | 143 |
| 2 | Early changes in the circulating T cells are associated with clinical outcomes after PD-L1 blockade by durvalumab in advanced NSCLC patients. <i>Cancer Immunology, Immunotherapy</i> , 2021, 70, 2095-2102. | 4.2 | 17 |
| 3 | Metagenomic sequencing of stool samples in Bangladeshi infants: virome association with poliovirus shedding after oral poliovirus vaccination. <i>Scientific Reports</i> , 2020, 10, 15392. | 3.3 | 6 |
| 4 | Microbial burden and viral exacerbations in a longitudinal multicenter COPD cohort. <i>Respiratory Research</i> , 2020, 21, 77. | 3.6 | 44 |
| 5 | Metagenomic Next-Generation Sequencing of the 2014 Ebola Virus Disease Outbreak in the Democratic Republic of the Congo. <i>Journal of Clinical Microbiology</i> , 2019, 57, . | 3.9 | 17 |
| 6 | Whole blood human transcriptome and virome analysis of ME/CFS patients experiencing post-exertional malaise following cardiopulmonary exercise testing. <i>PLoS ONE</i> , 2019, 14, e0212193. | 2.5 | 22 |
| 7 | Differentiation enhances Zika virus infection of neuronal brain cells. <i>Scientific Reports</i> , 2018, 8, 14543. | 3.3 | 26 |
| 8 | 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 |
| 9 | Metagenomic-based Surveillance of Pacific Coast tick <i>Dermacentor occidentalis</i> Identifies Two Novel Bunyaviruses and an Emerging Human Rickettsial Pathogen. <i>Scientific Reports</i> , 2017, 7, 12234. | 3.3 | 42 |
| 10 | The eukaryotic gut virome in hematopoietic stem cell transplantation: new clues in enteric graft-versus-host disease. <i>Nature Medicine</i> , 2017, 23, 1080-1085. | 30.7 | 109 |
| 11 | RNA-Seq Analysis of Gene Expression, Viral Pathogen, and B-Cell/T-Cell Receptor Signatures in Complex Chronic Disease. <i>Clinical Infectious Diseases</i> , 2017, 64, 476-481. | 5.8 | 21 |
| 12 | Experimental Zika Virus Inoculation in a New World Monkey Model Reproduces Key Features of the Human Infection. <i>Scientific Reports</i> , 2017, 7, 17126. | 3.3 | 58 |
| 13 | Longitudinal Transcriptome Analysis Reveals a Sustained Differential Gene Expression Signature in Patients Treated for Acute Lyme Disease. <i>MBio</i> , 2016, 7, e00100-16. | 4.1 | 76 |
| 14 | Rapid metagenomic identification of viral pathogens in clinical samples by real-time nanopore sequencing analysis. <i>Genome Medicine</i> , 2015, 7, 99. | 8.2 | 456 |
| 15 | Clinical metagenomic identification of <i>Balamuthia mandrillaris</i> encephalitis and assembly of the draft genome: the continuing case for reference genome sequencing. <i>Genome Medicine</i> , 2015, 7, 113. | 8.2 | 102 |
| 16 | Quantitative Proteomics Identifies Host Factors Modulated during Acute Hepatitis E Virus Infection in the Swine Model. <i>Journal of Virology</i> , 2015, 89, 129-143. | 3.4 | 22 |
| 17 | A cloud-compatible bioinformatics pipeline for ultrarapid pathogen identification from next-generation sequencing of clinical samples. <i>Genome Research</i> , 2014, 24, 1180-1192. | 5.5 | 421 |
| 18 | New models of hepatitis E virus replication in human and porcine hepatocyte cell lines. <i>Journal of General Virology</i> , 2013, 94, 549-558. | 2.9 | 41 |

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|----|--|-----|-----------|
| 19 | Identical Consensus Sequence and Conserved Genomic Polymorphism of Hepatitis E Virus during Controlled Interspecies Transmission. <i>Journal of Virology</i> , 2012, 86, 6238-6245. | 3.4 | 27 |
| 20 | Genetic characterization and codon usage bias of full-length Hepatitis E virus sequences shed new lights on genotypic distribution, host restriction and genome evolution. <i>Infection, Genetics and Evolution</i> , 2012, 12, 1842-1853. | 2.3 | 38 |
| 21 | Biological activities of nitidine, a potential anti-malarial lead compound. <i>Malaria Journal</i> , 2012, 11, 67. | 2.3 | 59 |
| 22 | Close Similarity between Sequences of Hepatitis E Virus Recovered from Humans and Swine, France, 2008~2009. <i>Emerging Infectious Diseases</i> , 2011, 17, 2018-25. | 4.3 | 92 |