

Ana Da Silva Filipe

List of Publications by Year in descending order

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Version: 2024-02-01

63
papers

5,373
citations

236925

25
h-index

144013

57
g-index

72
all docs

72
docs citations

72
times ranked

11290
citing authors

#	ARTICLE	IF	CITATIONS
1	Real-World Outcomes of Direct-Acting Antiviral Treatment and Retreatment in United Kingdom-Based Patients Infected With Hepatitis C Virus Genotypes/Subtypes Endemic in Africa. <i>Journal of Infectious Diseases</i> , 2022, 226, 995-1004.	4.0	8
2	A clinical and molecular epidemiological survey of hepatitis C in Blantyre, Malawi, suggests a historic mechanism of transmission. <i>Journal of Viral Hepatitis</i> , 2022, , .	2.0	2
3	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission. <i>Nature Communications</i> , 2022, 13, 1012.	12.8	10
4	Genome Sequences of Five Arenaviruses from Pygmy Mice (<i>Mus minutoides</i>) in Sierra Leone. <i>Microbiology Resource Announcements</i> , 2022, 11, e0009522.	0.6	3
5	Implementation of corticosteroids in treatment of COVID-19 in the ISARIC WHO Clinical Characterisation Protocol UK: prospective, cohort study. <i>The Lancet Digital Health</i> , 2022, 4, e220-e234.	12.3	20
6	Longitudinal deep sequencing informs vector selection and future deployment strategies for transmissible vaccines. <i>PLoS Biology</i> , 2022, 20, e3001580.	5.6	10
7	SARS-CoV-2 Omicron is an immune escape variant with an altered cell entry pathway. <i>Nature Microbiology</i> , 2022, 7, 1161-1179.	13.3	352
8	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. <i>Cell</i> , 2021, 184, 64-75.e11.	28.9	843
9	Genomic epidemiology reveals multiple introductions of SARS-CoV-2 from mainland Europe into Scotland. <i>Nature Microbiology</i> , 2021, 6, 112-122.	13.3	88
10	A plasmid DNA-launched SARS-CoV-2 reverse genetics system and coronavirus toolkit for COVID-19 research. <i>PLoS Biology</i> , 2021, 19, e3001091.	5.6	163
11	Circulating SARS-CoV-2 spike N439K variants maintain fitness while evading antibody-mediated immunity. <i>Cell</i> , 2021, 184, 1171-1187.e20.	28.9	541
12	Subgenomic RNA identification in SARS-CoV-2 genomic sequencing data. <i>Genome Research</i> , 2021, 31, 645-658.	5.5	48
13	SARS-CoV-2 within-host diversity and transmission. <i>Science</i> , 2021, 372, .	12.6	278
14	Development and validation of the ISARIC 4C Deterioration model for adults hospitalised with COVID-19: a prospective cohort study. <i>Lancet Respiratory Medicine</i> , 2021, 9, 349-359.	10.7	161
15	Modified recombinant human IgG1 α FC is superior to natural intravenous immunoglobulin at inhibiting immune-mediated demyelination. <i>Immunology</i> , 2021, 164, 90-105.	4.4	2
16	Changes in symptomatology, reinfection, and transmissibility associated with the SARS-CoV-2 variant B.1.1.7: an ecological study. <i>Lancet Public Health</i> , 2021, 6, e335-e345.	10.0	269
17	Hepatitis E virus: Whole genome sequencing as a new tool for understanding HEV epidemiology and phenotypes. <i>Journal of Clinical Virology</i> , 2021, 139, 104738.	3.1	3
18	Recurrent emergence of SARS-CoV-2 spike deletion H69/V70 and its role in the Alpha variant B.1.1.7. <i>Cell Reports</i> , 2021, 35, 109292.	6.4	375

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19	Real world SOF/VEL/VOX retreatment outcomes and viral resistance analysis for HCV patients with prior failure to DAA therapy. <i>Journal of Viral Hepatitis</i> , 2021, 28, 1256-1264.	2.0	16
20	Changes in in-hospital mortality in the first wave of COVID-19: a multicentre prospective observational cohort study using the WHO Clinical Characterisation Protocol UK. <i>Lancet Respiratory Medicine</i> , 2021, 9, 773-785.	10.7	78
21	Characterisation of in-hospital complications associated with COVID-19 using the ISARIC WHO Clinical Characterisation Protocol UK: a prospective, multicentre cohort study. <i>Lancet, The</i> , 2021, 398, 223-237.	13.7	110
22	Genetic epidemiology of SARS-CoV-2 transmission in renal dialysis units – A high risk community-hospital interface. <i>Journal of Infection</i> , 2021, 83, 96-103.	3.3	12
23	Non-steroidal anti-inflammatory drug use and outcomes of COVID-19 in the ISARIC Clinical Characterisation Protocol UK cohort: a matched, prospective cohort study. <i>Lancet Rheumatology, The</i> , 2021, 3, e498-e506.	3.9	58
24	Co-infections, secondary infections, and antimicrobial use in patients hospitalised with COVID-19 during the first pandemic wave from the ISARIC WHO CCP-UK study: a multicentre, prospective cohort study. <i>Lancet Microbe, The</i> , 2021, 2, e354-e365.	7.3	216
25	In vitro selection of Remdesivir resistance suggests evolutionary predictability of SARS-CoV-2. <i>PLoS Pathogens</i> , 2021, 17, e1009929.	4.7	108
26	The antiviral state has shaped the CpG composition of the vertebrate interferome to avoid self-targeting. <i>PLoS Biology</i> , 2021, 19, e3001352.	5.6	18
27	A prenylated dsRNA sensor protects against severe COVID-19. <i>Science</i> , 2021, 374, eabj3624.	12.6	124
28	Zika Virus Infection Leads to Demyelination and Axonal Injury in Mature CNS Cultures. <i>Viruses</i> , 2021, 13, 91.	3.3	17
29	Seoul Virus Associated with Pet Rats, Scotland, UK, 2019. <i>Emerging Infectious Diseases</i> , 2021, 27, 2677-2680.	4.3	5
30	The impact of viral mutations on recognition by SARS-CoV-2 specific T cells. <i>iScience</i> , 2021, 24, 103353.	4.1	57
31	Elevated temperature inhibits SARS-CoV-2 replication in respiratory epithelium independently of IFN-mediated innate immune defenses. <i>PLoS Biology</i> , 2021, 19, e3001065.	5.6	26
32	Epidemiology and biology of a herpesvirus in rabies endemic vampire bat populations. <i>Nature Communications</i> , 2020, 11, 5951.	12.8	18
33	Population genomics of louping ill virus provide new insights into the evolution of tick-borne flaviviruses. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008133.	3.0	11
34	“Frozen evolution” of an RNA virus suggests accidental release as a potential cause of arbovirus re-emergence. <i>PLoS Biology</i> , 2020, 18, e3000673.	5.6	15
35	Development of a Reverse Genetics System for Toscana Virus (Lineage A). <i>Viruses</i> , 2020, 12, 411.	3.3	5
36	Title is missing!. , 2020, 14, e0008133.		0

#	ARTICLE	IF	CITATIONS
37	Title is missing!. , 2020, 14, e0008133.		0
38	Title is missing!. , 2020, 14, e0008133.		0
39	Title is missing!. , 2020, 14, e0008133.		0
40	Title is missing!. , 2020, 14, e0008133.		0
41	Title is missing!. , 2020, 14, e0008133.		0
42	Metagenomic next-generation sequencing aids the diagnosis of viral infections in febrile returning travellers. <i>Journal of Infection</i> , 2019, 79, 383-388.	3.3	45
43	Suboptimal SVR rates in African patients with atypical genotype 1 subtypes: Implications for global elimination of hepatitis C. <i>Journal of Hepatology</i> , 2019, 71, 1099-1105.	3.7	52
44	Amino Acid Substitutions in Genotype 3a Hepatitis C Virus Polymerase Protein Affect Responses to Sofosbuvir. <i>Gastroenterology</i> , 2019, 157, 692-704.e9.	1.3	27
45	Convalescent plasma therapy for persistent hepatitis E virus infection. <i>Journal of Hepatology</i> , 2019, 71, 434-438.	3.7	17
46	Development of a World Health Organization International Reference Panel for different genotypes of hepatitis E virus for nucleic acid amplification testing. <i>Journal of Clinical Virology</i> , 2019, 119, 60-67.	3.1	14
47	Interpreting Viral Deep Sequencing Data with GLUE. <i>Viruses</i> , 2019, 11, 323.	3.3	29
48	The histone chaperone HIRA promotes the induction of host innate immune defences in response to HSV-1 infection. <i>PLoS Pathogens</i> , 2019, 15, e1007667.	4.7	47
49	Highly Diverse Hepatitis C Strains Detected in Sub-Saharan Africa Have Unknown Susceptibility to Direct-Acting Antiviral Treatments. <i>Hepatology</i> , 2019, 69, 1426-1441.	7.3	36
50	Using noninvasive metagenomics to characterize viral communities from wildlife. <i>Molecular Ecology Resources</i> , 2019, 19, 128-143.	4.8	53
51	Interferon lambda 4 impacts the genetic diversity of hepatitis C virus. <i>ELife</i> , 2019, 8, .	6.0	28
52	Reply to: "Reply to: "Response to DAA therapy in the NHS England Early Access Programme for rare HCV subtypes from low and middle income countries" Journal of Hepatology, 2018, 68, 864-866.	3.7	2
53	Genome Sequences of Five African Swine Fever Virus Genotype IX Isolates from Domestic Pigs in Uganda. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	26
54	A polymorphic residue that attenuates the antiviral potential of interferon lambda 4 in hominid lineages. <i>PLoS Pathogens</i> , 2018, 14, e1007307.	4.7	25

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55	Development of reverse genetics systems and investigation of host response antagonism and reassortment potential for Cache Valley and Kairi viruses, two emerging orthobunyaviruses of the Americas. PLoS Neglected Tropical Diseases, 2018, 12, e0006884.	3.0	12
56	Response to DAA therapy in the NHS England Early Access Programme for rare HCV subtypes from low and middle income countries. Journal of Hepatology, 2017, 67, 1348-1350.	3.7	31
57	Hepatitis C Virus NS5A Targets Nucleosome Assembly Protein NAP1L1 To Control the Innate Cellular Response. Journal of Virology, 2017, 91, .	3.4	21
58	Comparison of Next-Generation Sequencing Technologies for Comprehensive Assessment of Full-Length Hepatitis C Viral Genomes. Journal of Clinical Microbiology, 2016, 54, 2470-2484.	3.9	112
59	Late Ebola virus relapse causing meningoencephalitis: a case report. Lancet, The, 2016, 388, 498-503.	13.7	291
60	Full Genome Sequence and sfRNA Interferon Antagonist Activity of Zika Virus from Recife, Brazil. PLoS Neglected Tropical Diseases, 2016, 10, e0005048.	3.0	193
61	Viral genotype correlates with distinct liver gene transcription signatures in chronic hepatitis C virus infection. Liver International, 2015, 35, 2256-2264.	3.9	13
62	Structural Analysis of Hepatitis C Virus Core-E1 Signal Peptide and Requirements for Cleavage of the Genotype 3a Signal Sequence by Signal Peptide Peptidase. Journal of Virology, 2012, 86, 7818-7828.	3.4	21
63	A Polymorphic Residue That Attenuates Interferon Lambda 4 Activity in Hominid Lineages. SSRN Electronic Journal, 0, , .	0.4	0