

# 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	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
2	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
3	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
4	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
5	Late Ebola virus relapse causing meningoencephalitis: a case report. <i>Lancet</i> , The, 2016, 388, 498-503.	13.7	291
6	SARS-CoV-2 within-host diversity and transmission. <i>Science</i> , 2021, 372, .	12.6	278
7	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> , The, 2021, 6, e335-e345.	10.0	269
8	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</i> , The, 2021, 2, e354-e365.	7.3	216
9	Full Genome Sequence and sfRNA Interferon Antagonist Activity of Zika Virus from Recife, Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0005048.	3.0	193
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	Development and validation of the ISARIC 4C Deterioration model for adults hospitalised with COVID-19: a prospective cohort study. <i>Lancet Respiratory Medicine</i> , the, 2021, 9, 349-359.	10.7	161
12	A prenylated dsRNA sensor protects against severe COVID-19. <i>Science</i> , 2021, 374, eabj3624.	12.6	124
13	Comparison of Next-Generation Sequencing Technologies for Comprehensive Assessment of Full-Length Hepatitis C Viral Genomes. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2470-2484.	3.9	112
14	Characterisation of in-hospital complications associated with COVID-19 using the ISARIC WHO Clinical Characterisation Protocol UK: a prospective, multicentre cohort study. <i>Lancet</i> , The, 2021, 398, 223-237.	13.7	110
15	In vitro selection of Remdesivir resistance suggests evolutionary predictability of SARS-CoV-2. <i>PLoS Pathogens</i> , 2021, 17, e1009929.	4.7	108
16	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
17	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> , the, 2021, 9, 773-785.	10.7	78
18	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</i> , The, 2021, 3, e498-e506.	3.9	58

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19	The impact of viral mutations on recognition by SARS-CoV-2 specific T cells. <i>IScience</i> , 2021, 24, 103353.	4.1	57
20	Using noninvasive metagenomics to characterize viral communities from wildlife. <i>Molecular Ecology Resources</i> , 2019, 19, 128-143.	4.8	53
21	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
22	Subgenomic RNA identification in SARS-CoV-2 genomic sequencing data. <i>Genome Research</i> , 2021, 31, 645-658.	5.5	48
23	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
24	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
25	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
26	Response to DAA therapy in the NHS England Early Access Programme for rare HCV subtypes from low and middle income countries. <i>Journal of Hepatology</i> , 2017, 67, 1348-1350.	3.7	31
27	Interpreting Viral Deep Sequencing Data with GLUE. <i>Viruses</i> , 2019, 11, 323.	3.3	29
28	Interferon lambda 4 impacts the genetic diversity of hepatitis C virus. <i>ELife</i> , 2019, 8, .	6.0	28
29	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
30	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
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	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
33	Structural Analysis of Hepatitis C Virus Core-E1 Signal Peptide and Requirements for Cleavage of the Genotype 3a Signal Sequence by Signal Peptide Peptidase. <i>Journal of Virology</i> , 2012, 86, 7818-7828.	3.4	21
34	Hepatitis C Virus NS5A Targets Nucleosome Assembly Protein NAP1L1 To Control the Innate Cellular Response. <i>Journal of Virology</i> , 2017, 91, .	3.4	21
35	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
36	Epidemiology and biology of a herpesvirus in rabies endemic vampire bat populations. <i>Nature Communications</i> , 2020, 11, 5951.	12.8	18

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37	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
38	Convalescent plasma therapy for persistent hepatitis E virus infection. <i>Journal of Hepatology</i> , 2019, 71, 434-438.	3.7	17
39	Zika Virus Infection Leads to Demyelination and Axonal Injury in Mature CNS Cultures. <i>Viruses</i> , 2021, 13, 91.	3.3	17
40	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
41	“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
42	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
43	Viral genotype correlates with distinct liver gene transcription signatures in chronic hepatitis C virus infection. <i>Liver International</i> , 2015, 35, 2256-2264.	3.9	13
44	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. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006884.	3.0	12
45	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
46	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
47	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission. <i>Nature Communications</i> , 2022, 13, 1012.	12.8	10
48	Longitudinal deep sequencing informs vector selection and future deployment strategies for transmissible vaccines. <i>PLoS Biology</i> , 2022, 20, e3001580.	5.6	10
49	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
50	Development of a Reverse Genetics System for Toscana Virus (Lineage A). <i>Viruses</i> , 2020, 12, 411.	3.3	5
51	Seoul Virus Associated with Pet Rats, Scotland, UK, 2019. <i>Emerging Infectious Diseases</i> , 2021, 27, 2677-2680.	4.3	5
52	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
53	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
54	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”” <i>Journal of Hepatology</i> , 2018, 68, 864-866.	3.7	2

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55	Modified recombinant human IgG1 $\alpha$ Fc is superior to natural intravenous immunoglobulin at inhibiting immune-mediated demyelination. Immunology, 2021, 164, 90-105.	4.4	2
56	A clinical and molecular epidemiological survey of hepatitis C in Blantyre, Malawi, suggests a historic mechanism of transmission. Journal of Viral Hepatitis, 2022, , .	2.0	2
57	A Polymorphic Residue That Attenuates Interferon Lambda 4 Activity in Hominid Lineages. SSRN Electronic Journal, 0, , .	0.4	0
58	Title is missing!. , 2020, 14, e0008133.		0
59	Title is missing!. , 2020, 14, e0008133.		0
60	Title is missing!. , 2020, 14, e0008133.		0
61	Title is missing!. , 2020, 14, e0008133.		0
62	Title is missing!. , 2020, 14, e0008133.		0
63	Title is missing!. , 2020, 14, e0008133.		0