

Jose Lourenco

List of Publications by Citations

Source: <https://exaly.com/author-pdf/6854139/jose-lourenco-publications-by-citations.pdf>

Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

81
papers

3,163
citations

24
h-index

56
g-index

98
ext. papers

4,496
ext. citations

10.5
avg, IF

5.25
L-index

#	Paper	IF	Citations
81	Zika virus in the Americas: Early epidemiological and genetic findings. <i>Science</i> , 2016 , 352, 345-349	33.3	703
80	Detection of a SARS-CoV-2 variant of concern in South Africa. <i>Nature</i> , 2021 , 592, 438-443	50.4	685
79	Sixteen novel lineages of SARS-CoV-2 in South Africa. <i>Nature Medicine</i> , 2021 , 27, 440-446	50.5	206
78	Genomic and epidemiological monitoring of yellow fever virus transmission potential. <i>Science</i> , 2018 , 361, 894-899	33.3	184
77	The Long-Term Safety, Public Health Impact, and Cost-Effectiveness of Routine Vaccination with a Recombinant, Live-Attenuated Dengue Vaccine (Dengvaxia): A Model Comparison Study. <i>PLoS Medicine</i> , 2016 , 13, e1002181	11.6	127
76	Fundamental principles of epidemic spread highlight the immediate need for large-scale serological surveys to assess the stage of the SARS-CoV-2 epidemic		109
75	A32 Genomic surveillance of Zika virus transmission in the Amazonas State, Brazil. <i>Virus Evolution</i> , 2019 , 5,	3.7	78
74	Estimating the false-negative test probability of SARS-CoV-2 by RT-PCR. <i>Eurosurveillance</i> , 2020 , 25,	19.8	76
73	The 2012 Madeira dengue outbreak: epidemiological determinants and future epidemic potential. <i>PLoS Neglected Tropical Diseases</i> , 2014 , 8, e3083	4.8	69
72	Epidemiological and ecological determinants of Zika virus transmission in an urban setting. <i>ELife</i> , 2017 , 6,	8.9	55
71	Spread of Chikungunya Virus East/Central/South African Genotype in Northeast Brazil. <i>Emerging Infectious Diseases</i> , 2017 , 23, 1742-1744	10.2	51
70	Epidemiology of Chikungunya Virus in Bahia, Brazil, 2014-2015. <i>PLOS Currents</i> , 2016 , 8,		48
69	Genomic, epidemiological and digital surveillance of Chikungunya virus in the Brazilian Amazon. <i>PLoS Neglected Tropical Diseases</i> , 2019 , 13, e0007065	4.8	37
68	Early transmission of SARS-CoV-2 in South Africa: An epidemiological and phylogenetic report. <i>International Journal of Infectious Diseases</i> , 2021 , 103, 234-241	10.5	37
67	Natural, persistent oscillations in a spatial multi-strain disease system with application to dengue. <i>PLoS Computational Biology</i> , 2013 , 9, e1003308	5	34
66	Genomic and epidemiological characterisation of a dengue virus outbreak among blood donors in Brazil. <i>Scientific Reports</i> , 2017 , 7, 15216	4.9	33
65	Viral and epidemiological determinants of the invasion dynamics of novel dengue genotypes. <i>PLoS Neglected Tropical Diseases</i> , 2010 , 4, e894	4.8	32

64	Vaccination Drives Changes in Metabolic and Virulence Profiles of <i>Streptococcus pneumoniae</i> . <i>PLoS Pathogens</i> , 2015 , 11, e1005034	7.6	31
63	Epidemiology of the Zika Virus Outbreak in the Cabo Verde Islands, West Africa. <i>PLOS Currents</i> , 2018 , 10,		29
62	The ongoing COVID-19 epidemic in Minas Gerais, Brazil: insights from epidemiological data and SARS-CoV-2 whole genome sequencing. <i>Emerging Microbes and Infections</i> , 2020 , 9, 1824-1834	18.9	26
61	High residual carriage of vaccine-serotype <i>Streptococcus pneumoniae</i> after introduction of pneumococcal conjugate vaccine in Malawi. <i>Nature Communications</i> , 2020 , 11, 2222	17.4	25
60	Distinct rates and patterns of spread of the major HIV-1 subtypes in Central and East Africa. <i>PLoS Pathogens</i> , 2019 , 15, e1007976	7.6	25
59	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. <i>Cell Reports</i> , 2020 , 30, 2275-2283.e7	10.6	24
58	The generation of a simian adenoviral vectored HCV vaccine encoding genetically conserved gene segments to target multiple HCV genotypes. <i>Vaccine</i> , 2018 , 36, 313-321	4.1	24
57	Competing species leave many potential niches unfilled. <i>Nature Ecology and Evolution</i> , 2017 , 1, 1495-1501	12.3	23
56	A naturally protective epitope of limited variability as an influenza vaccine target. <i>Nature Communications</i> , 2018 , 9, 3859	17.4	23
55	Vaccination can drive an increase in frequencies of antibiotic resistance among nonvaccine serotypes of. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 3102-3107	11.5	22
54	Dengue serotype immune-interactions and their consequences for vaccine impact predictions. <i>Epidemics</i> , 2016 , 16, 40-8	5.1	21
53	Hospital discharges in urban sanitation systems: Long-term monitoring of wastewater resistome and microbiota in relationship to their eco-exposome. <i>Water Research X</i> , 2020 , 7, 100045	8.1	20
52	Early transmission of SARS-CoV-2 in South Africa: An epidemiological and phylogenetic report 2020 ,		20
51	Zika virus complete genome from Salvador, Bahia, Brazil. <i>Infection, Genetics and Evolution</i> , 2016 , 41, 142-145	14.5	20
50	Determinants of high residual post-PCV13 pneumococcal vaccine-type carriage in Blantyre, Malawi: a modelling study. <i>BMC Medicine</i> , 2019 , 17, 219	11.4	18
49	The global impact of the COVID-19 pandemic on the prevention, diagnosis and treatment of hepatitis B virus (HBV) infection. <i>BMJ Global Health</i> , 2021 , 6,	6.6	18
48	The impact of host resistance on cumulative mortality and the threshold of herd immunity for SARS-CoV-2		17
47	MVSE: An R-package that estimates a climate-driven mosquito-borne viral suitability index. <i>Methods in Ecology and Evolution</i> , 2019 , 10, 1357-1370	7.7	16

46	Hepatitis B virus seroepidemiology data for Africa: Modelling intervention strategies based on a systematic review and meta-analysis. <i>PLoS Medicine</i> , 2020 , 17, e1003068	11.6	15
45	Challenges in dengue research: A computational perspective. <i>Evolutionary Applications</i> , 2018 , 11, 516-533	3.8	15
44	Lineage structure of <i>Streptococcus pneumoniae</i> may be driven by immune selection on the groEL heat-shock protein. <i>Scientific Reports</i> , 2017 , 7, 9023	4.9	14
43	Reducing HIV infection in people who inject drugs is impossible without targeting recently-infected subjects. <i>Aids</i> , 2016 , 30, 2885-2890	3.5	13
42	SARS-CoV-2 shifting transmission dynamics and hidden reservoirs potentially limit efficacy of public health interventions in Italy. <i>Communications Biology</i> , 2021 , 4, 489	6.7	13
41	A multi-country study of dengue vaccination strategies with Dengvaxia and a future vaccine candidate in three dengue-endemic countries: Vietnam, Thailand, and Colombia. <i>Vaccine</i> , 2018 , 36, 2346-2355	4.1	12
40	Identifying genes associated with invasive disease in <i>S. pneumoniae</i> by applying a machine learning approach to whole genome sequence typing data. <i>Scientific Reports</i> , 2019 , 9, 4049	4.9	10
39	Asynchronicity of endemic and emerging mosquito-borne disease outbreaks in the Dominican Republic. <i>Nature Communications</i> , 2021 , 12, 151	17.4	9
38	MANTIS: an R package that simulates multilocus models of pathogen evolution. <i>BMC Bioinformatics</i> , 2015 , 16, 176	3.6	7
37	Return of the founder Chikungunya virus to its place of introduction into Brazil is revealed by genomic characterization of exanthematic disease cases. <i>Emerging Microbes and Infections</i> , 2020 , 9, 53-57	18.9	7
36	Genomic evidence of SARS-CoV-2 reinfection case with the emerging B.1.2 variant in Brazil. <i>Journal of Infection</i> , 2021 , 83, 237-279	18.9	7
35	Characterising West Nile virus epidemiology in Israel using a transmission suitability index. <i>Eurosurveillance</i> , 2020 , 25,	19.8	6
34	Malaria infection and severe disease risks in Africa. <i>Science</i> , 2021 , 373, 926-931	33.3	6
33	Modeling Combinations of Pre-erythrocytic <i>Plasmodium falciparum</i> Malaria Vaccines. <i>American Journal of Tropical Medicine and Hygiene</i> , 2015 , 93, 1254-1259	3.2	5
32	Measuring Mosquito-borne Viral Suitability in Myanmar and Implications for Local Zika Virus Transmission. <i>PLOS Currents</i> , 2018 , 10,		5
31	Short Report: Early genomic detection of SARS-CoV-2 P.1 variant in Northeast Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2021 , 15, e0009591	4.8	5
30	Effects of neutralizing antibodies on escape from CD8+ T-cell responses in HIV-1 infection. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015 , 370,	5.8	4
29	Phylogenetic Analysis of in Portugal. <i>Viruses</i> , 2021 , 13,	6.2	4

28	Potential impact of individual exposure histories to endemic human coronaviruses on age-dependent severity of COVID-19. <i>BMC Medicine</i> , 2021 , 19, 19	11.4	4
27	SARS-CoV-2 epidemic in Brazil: how variants displacement have driven distinct epidemic waves.. <i>Virus Research</i> , 2022 , 198785	6.4	4
26	West Nile virus transmission potential in Portugal.. <i>Communications Biology</i> , 2022 , 5, 6	6.7	3
25	Determinants of high residual post-PCV13 pneumococcal vaccine type carriage in Blantyre, Malawi: a modelling study		3
24	Classification of hospital and urban wastewater resistome and microbiota over time and their relationship to the eco-exposome		3
23	Field and classroom initiatives for portable sequence-based monitoring of dengue virus in Brazil. <i>Nature Communications</i> , 2021 , 12, 2296	17.4	3
22	West Nile Virus in Brazil. <i>Pathogens</i> , 2021 , 10,	4.5	3
21	Identifying <i>Streptococcus pneumoniae</i> associated with invasive disease using pangenome-based whole genome sequence typing		2
20	Short report: Introduction of chikungunya virus ECSA genotype into the Brazilian Midwest and its dispersion through the Americas. <i>PLoS Neglected Tropical Diseases</i> , 2021 , 15, e0009290	4.8	2
19	Reverse immunodynamics: a new method for identifying targets of protective immunity. <i>Scientific Reports</i> , 2019 , 9, 2164	4.9	2
18	Malaria hospitalisation in East Africa: age, phenotype and transmission intensity.. <i>BMC Medicine</i> , 2022 , 20, 28	11.4	1
17	Malaria elimination on Hainan Island despite climate change. <i>Communications Medicine</i> , 2022 , 2,		1
16	Genomic epidemiology reveals the impact of national and international restrictions measures on the SARS-CoV-2 epidemic in Brazil. 2022 ,		1
15	MVSE: an R-package that estimates a climate-driven mosquito-borne viral suitability index		1
14	Lineage structure of <i>Streptococcus pneumoniae</i> driven by immune selection on the groEL heat-shock protein		1
13	Machine learning models exploring characteristic single-nucleotide signatures in Yellow Fever Virus		1
12	Analysis and visualization of epidemics on the timescale of burden: derivation and application of Epidemic Resistance Lines (ERLs) to COVID-19 outbreaks in the US		1
11	West Nile virus in Portugal		1

10	Replacement of the Gamma by the Delta variant in Brazil: Impact of lineage displacement on the ongoing pandemic.. <i>Virus Evolution</i> , 2022 , 8, veac024	3.7	1
9	Real-time seroprevalence and exposure levels of emerging pathogens in infection-naive host populations. <i>Scientific Reports</i> , 2021 , 11, 5825	4.9	0
8	Molecular Identification and Ecology of Portuguese Wild-Caught Phlebotomine Sandfly Specimens 2022 , 2, 19-31		0
7	A Retrospective Overview of Zika Virus Evolution in the Midwest of Brazil.. <i>Microbiology Spectrum</i> , 2022 , e0015522	8.9	0
6	Spacer Domain in Hepatitis B Virus Polymerase: Plugging a Hole or Performing a Role?. <i>Journal of Virology</i> , 2022 , e0005122	6.6	0
5	First detection of human T-lymphotropic virus in blood donors in Benin shows that testing is required to improve blood safety. <i>ISBT Science Series</i> , 2019 , 14, 163-168	1.1	
4	Hepatitis B virus seroepidemiology data for Africa: Modelling intervention strategies based on a systematic review and meta-analysis 2020 , 17, e1003068		
3	Hepatitis B virus seroepidemiology data for Africa: Modelling intervention strategies based on a systematic review and meta-analysis 2020 , 17, e1003068		
2	Hepatitis B virus seroepidemiology data for Africa: Modelling intervention strategies based on a systematic review and meta-analysis 2020 , 17, e1003068		
1	Hepatitis B virus seroepidemiology data for Africa: Modelling intervention strategies based on a systematic review and meta-analysis 2020 , 17, e1003068		