

Jose Lourenco

List of Publications by Year in Descending Order

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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	West Nile virus transmission potential in Portugal.. <i>Communications Biology</i> , 2022 , 5, 6	6.7	3
80	Malaria hospitalisation in East Africa: age, phenotype and transmission intensity.. <i>BMC Medicine</i> , 2022 , 20, 28	11.4	1
79	Malaria elimination on Hainan Island despite climate change. <i>Communications Medicine</i> , 2022 , 2,		1
78	Genomic epidemiology reveals the impact of national and international restrictions measures on the SARS-CoV-2 epidemic in Brazil. 2022 ,		1
77	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
76	Molecular Identification and Ecology of Portuguese Wild-Caught Phlebotomine Sandfly Specimens 2022 , 2, 19-31		0
75	A Retrospective Overview of Zika Virus Evolution in the Midwest of Brazil.. <i>Microbiology Spectrum</i> , 2022 , e0015522	8.9	0
74	Spacer Domain in Hepatitis B Virus Polymerase: Plugging a Hole or Performing a Role?. <i>Journal of Virology</i> , 2022 , e0005122	6.6	0
73	SARS-CoV-2 epidemic in Brazil: how variants displacement have driven distinct epidemic waves.. <i>Virus Research</i> , 2022 , 198785	6.4	4
72	Detection of a SARS-CoV-2 variant of concern in South Africa. <i>Nature</i> , 2021 , 592, 438-443	50.4	685
71	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
70	Field and classroom initiatives for portable sequence-based monitoring of dengue virus in Brazil. <i>Nature Communications</i> , 2021 , 12, 2296	17.4	3
69	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
68	West Nile Virus in Brazil. <i>Pathogens</i> , 2021 , 10,	4.5	3
67	Phylogenetic Analysis of in Portugal. <i>Viruses</i> , 2021 , 13,	6.2	4
66	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
65	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

64	Asynchronicity of endemic and emerging mosquito-borne disease outbreaks in the Dominican Republic. <i>Nature Communications</i> , 2021 , 12, 151	17.4	9
63	Sixteen novel lineages of SARS-CoV-2 in South Africa. <i>Nature Medicine</i> , 2021 , 27, 440-446	50.5	206
62	Real-time seroprevalence and exposure levels of emerging pathogens in infection-naive host populations. <i>Scientific Reports</i> , 2021 , 11, 5825	4.9	0
61	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
60	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
59	Malaria infection and severe disease risks in Africa. <i>Science</i> , 2021 , 373, 926-931	33.3	6
58	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
57	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
56	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. <i>Cell Reports</i> , 2020 , 30, 2275-2283.e7	10.6	24
55	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
54	Characterising West Nile virus epidemiology in Israel using a transmission suitability index. <i>Eurosurveillance</i> , 2020 , 25,	19.8	6
53	Estimating the false-negative test probability of SARS-CoV-2 by RT-PCR. <i>Eurosurveillance</i> , 2020 , 25,	19.8	76
52	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
51	Early transmission of SARS-CoV-2 in South Africa: An epidemiological and phylogenetic report 2020 ,		20
50	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
49	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
48	Hepatitis B virus seroepidemiology data for Africa: Modelling intervention strategies based on a systematic review and meta-analysis 2020 , 17, e1003068		
47	Hepatitis B virus seroepidemiology data for Africa: Modelling intervention strategies based on a systematic review and meta-analysis 2020 , 17, e1003068		

46	Hepatitis B virus seroepidemiology data for Africa: Modelling intervention strategies based on a systematic review and meta-analysis 2020 , 17, e1003068		
45	Hepatitis B virus seroepidemiology data for Africa: Modelling intervention strategies based on a systematic review and meta-analysis 2020 , 17, e1003068		
44	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
43	Genomic, epidemiological and digital surveillance of Chikungunya virus in the Brazilian Amazon. <i>PLoS Neglected Tropical Diseases</i> , 2019 , 13, e0007065	4.8	37
42	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
41	A32 Genomic surveillance of Zika virus transmission in the Amazonas State, Brazil. <i>Virus Evolution</i> , 2019 , 5,	3.7	78
40	Reverse immunodynamics: a new method for identifying targets of protective immunity. <i>Scientific Reports</i> , 2019 , 9, 2164	4.9	2
39	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
38	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
37	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	
36	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
35	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
34	Challenges in dengue research: A computational perspective. <i>Evolutionary Applications</i> , 2018 , 11, 516-533	4.8	15
33	Genomic and epidemiological monitoring of yellow fever virus transmission potential. <i>Science</i> , 2018 , 361, 894-899	33.3	184
32	Epidemiology of the Zika Virus Outbreak in the Cabo Verde Islands, West Africa. <i>PLOS Currents</i> , 2018 , 10,		29
31	Measuring Mosquito-borne Viral Suitability in Myanmar and Implications for Local Zika Virus Transmission. <i>PLOS Currents</i> , 2018 , 10,		5
30	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
29	A naturally protective epitope of limited variability as an influenza vaccine target. <i>Nature Communications</i> , 2018 , 9, 3859	17.4	23

28	Competing species leave many potential niches unfilled. <i>Nature Ecology and Evolution</i> , 2017 , 1, 1495-1501.	2.3	23
27	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
26	Genomic and epidemiological characterisation of a dengue virus outbreak among blood donors in Brazil. <i>Scientific Reports</i> , 2017 , 7, 15216	4.9	33
25	Spread of Chikungunya Virus East/Central/South African Genotype in Northeast Brazil. <i>Emerging Infectious Diseases</i> , 2017 , 23, 1742-1744	10.2	51
24	Epidemiological and ecological determinants of Zika virus transmission in an urban setting. <i>ELife</i> , 2017 , 6,	8.9	55
23	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
22	Zika virus in the Americas: Early epidemiological and genetic findings. <i>Science</i> , 2016 , 352, 345-349	33.3	703
21	Epidemiology of Chikungunya Virus in Bahia, Brazil, 2014-2015. <i>PLOS Currents</i> , 2016 , 8,		48
20	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
19	Zika virus complete genome from Salvador, Bahia, Brazil. <i>Infection, Genetics and Evolution</i> , 2016 , 41, 142-145	4.5	20
18	Dengue serotype immune-interactions and their consequences for vaccine impact predictions. <i>Epidemics</i> , 2016 , 16, 40-8	5.1	21
17	MANTIS: an R package that simulates multilocus models of pathogen evolution. <i>BMC Bioinformatics</i> , 2015 , 16, 176	3.6	7
16	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
15	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
14	Vaccination Drives Changes in Metabolic and Virulence Profiles of <i>Streptococcus pneumoniae</i> . <i>PLoS Pathogens</i> , 2015 , 11, e1005034	7.6	31
13	The 2012 Madeira dengue outbreak: epidemiological determinants and future epidemic potential. <i>PLoS Neglected Tropical Diseases</i> , 2014 , 8, e3083	4.8	69
12	Natural, persistent oscillations in a spatial multi-strain disease system with application to dengue. <i>PLoS Computational Biology</i> , 2013 , 9, e1003308	5	34
11	Viral and epidemiological determinants of the invasion dynamics of novel dengue genotypes. <i>PLoS Neglected Tropical Diseases</i> , 2010 , 4, e894	4.8	32

10	MVSE: an R-package that estimates a climate-driven mosquito-borne viral suitability index	1
9	Lineage structure of <i>Streptococcus pneumoniae</i> driven by immune selection on the groEL heat-shock protein	1
8	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
7	The impact of host resistance on cumulative mortality and the threshold of herd immunity for SARS-CoV-2	17
6	Identifying <i>Streptococcus pneumoniae</i> genes associated with invasive disease using pangenome-based whole genome sequence typing	2
5	Determinants of high residual post-PCV13 pneumococcal vaccine type carriage in Blantyre, Malawi: a modelling study	3
4	Classification of hospital and urban wastewater resistome and microbiota over time and their relationship to the eco-exposome	3
3	Machine learning models exploring characteristic single-nucleotide signatures in Yellow Fever Virus	1
2	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
1	West Nile virus in Portugal	1