

VÃ-tor Borges

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8984549/publications.pdf>

Version: 2024-02-01

50
papers

2,316
citations

304743

22
h-index

254184

43
g-index

65
all docs

65
docs citations

65
times ranked

3221
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative Effectiveness of Coronavirus Vaccine in Preventing Breakthrough Infections among Vaccinated Persons Infected with Delta and Alpha Variants. <i>Emerging Infectious Diseases</i> , 2022, 28, 331-337.	4.3	32
2	SARS-CoV-2 introductions and early dynamics of the epidemic in Portugal. <i>Communications Medicine</i> , 2022, 2, .	4.2	5
3	Mutation rate of SARS-CoV-2 and emergence of mutators during experimental evolution. <i>Evolution, Medicine and Public Health</i> , 2022, 10, 142-155.	2.5	101
4	Insights on catheter-related bloodstream infections: a prospective observational study on the catheter colonization and multidrug resistance. <i>Journal of Hospital Infection</i> , 2022, 123, 43-51.	2.9	3
5	Clinical and epidemiological characterization of lymphogranuloma venereum in a sexually transmitted diseases clinic in Lisbon, 2001-2020. <i>Sexually Transmitted Diseases</i> , 2022, Publish Ahead of Print, .	1.7	1
6	Unraveling the hurdles of a large COVID-19 epidemiological investigation by viral genomics. <i>Journal of Infection</i> , 2022, 85, 64-74.	3.3	0
7	A Search for Novel <i>Legionella pneumophila</i> Effector Proteins Reveals a Strain Specific Nucleotropic Effector. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, .	3.9	0
8	Phylogenomic characterization and signs of microevolution in the 2022 multi-country outbreak of monkeypox virus. <i>Nature Medicine</i> , 2022, 28, 1569-1572.	30.7	429
9	<i>Neisseria gonorrhoeae</i> clustering to reveal major European whole-genome-sequencing-based genogroups in association with antimicrobial resistance. <i>Microbial Genomics</i> , 2021, 7, .	2.0	9
10	Tracking SARS-CoV-2 lineage B.1.1.7 dissemination: insights from nationwide spike gene target failure (SGTF) and spike gene late detection (SGTL) data, Portugal, week 49 2020 to week 3 2021. <i>Eurosurveillance</i> , 2021, 26, .	7.0	64
11	Characteristics of SARS-CoV-2 variants of concern B.1.1.7, B.1.351 or P.1: data from seven EU/EEA countries, weeks 38/2020 to 10/2021. <i>Eurosurveillance</i> , 2021, 26, .	7.0	216
12	Nosocomial Outbreak of SARS-CoV-2 in a "Non-COVID-19" Hospital Ward: Virus Genome Sequencing as a Key Tool to Understand Cryptic Transmission. <i>Viruses</i> , 2021, 13, 604.	3.3	45
13	Long-Term Evolution of SARS-CoV-2 in an Immunocompromised Patient with Non-Hodgkin Lymphoma. <i>MSphere</i> , 2021, 6, e0024421.	2.9	63
14	Potential recurrence of COVID-19 in a healthcare professional: SARS-CoV-2 genome sequencing confirms contagiousness after re-positivity. <i>International Journal of Infectious Diseases</i> , 2021, 112, 318-320.	3.3	2
15	Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2 with grinch. <i>Wellcome Open Research</i> , 2021, 6, 121.	1.8	129
16	Emergence and global spread of <i>Listeria monocytogenes</i> main clinical clonal complex. <i>Science Advances</i> , 2021, 7, eabj9805.	10.3	23
17	Towards a rapid sequencing-based molecular surveillance and mosaicism investigation of <i>Toxoplasma gondii</i> . <i>Parasitology Research</i> , 2020, 119, 587-599.	1.6	2
18	Mitogenome diversity of <i>Aedes (Stegomyia) albopictus</i> : Detection of multiple introduction events in Portugal. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008657.	3.0	12

#	ARTICLE	IF	CITATIONS
19	Massive dissemination of a SARS-CoV-2 Spike Y839 variant in Portugal. <i>Emerging Microbes and Infections</i> , 2020, 9, 2488-2496.	6.5	20
20	Virulence and antibiotic resistance plasticity of <i>Arcobacter butzleri</i> : Insights on the genomic diversity of an emerging human pathogen. <i>Infection, Genetics and Evolution</i> , 2020, 80, 104213.	2.3	38
21	Congenital SARS-CoV-2 Infection in a Neonate With Severe Acute Respiratory Syndrome. <i>Pediatric Infectious Disease Journal</i> , 2020, 39, e439-e443.	2.0	19
22	Proficiency Testing of Virus Diagnostics Based on Bioinformatics Analysis of Simulated <i>In Silico</i> High-Throughput Sequencing Data Sets. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	34
23	Multimiomics Assessment of Gene Expression in a Clinical Strain of CTX-M-15-Producing ST131 <i>Escherichia coli</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 831.	3.5	6
24	Nontuberculous Mycobacteria Persistence in a Cell Model Mimicking Alveolar Macrophages. <i>Microorganisms</i> , 2019, 7, 113.	3.6	12
25	CteG is a <i>Chlamydia trachomatis</i> effector protein that associates with the Golgi complex of infected host cells. <i>Scientific Reports</i> , 2019, 9, 6133.	3.3	17
26	Evaluation of a gene-by-gene approach for prospective whole-genome sequencing-based surveillance of multidrug resistant <i>Mycobacterium tuberculosis</i> . <i>Tuberculosis</i> , 2019, 115, 81-88.	1.9	10
27	<i>Chlamydia trachomatis</i> : when the virulence-associated genome backbone imports a prevalence-associated major antigen signature. <i>Microbial Genomics</i> , 2019, 5, .	2.0	18
28	Genetic Determinants of High-Level Oxacillin Resistance in Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	16
29	INNUENDO: A cross-sectoral platform for the integration of genomics in the surveillance of foodborne pathogens. <i>EFSA Supporting Publications</i> , 2018, 15, 1498E.	0.7	56
30	Genomic Study of a <i>Clostridium difficile</i> Multidrug Resistant Outbreak-Related Clone Reveals Novel Determinants of Resistance. <i>Frontiers in Microbiology</i> , 2018, 9, 2994.	3.5	25
31	Imipenem Resistance in <i>Clostridium difficile</i> Ribotype 017, Portugal. <i>Emerging Infectious Diseases</i> , 2018, 24, 741-745.	4.3	24
32	INSaFLU: an automated open web-based bioinformatics suite "from-reads" for influenza whole-genome-sequencing-based surveillance. <i>Genome Medicine</i> , 2018, 10, 46.	8.2	55
33	The Environmental <i>Acinetobacter baumannii</i> Isolate DSM30011 Reveals Clues into the Preantibiotic Era Genome Diversity, Virulence Potential, and Niche Range of a Predominant Nosocomial Pathogen. <i>Genome Biology and Evolution</i> , 2017, 9, 2292-2307.	2.5	61
34	Global survey of mRNA levels and decay rates of <i>Chlamydia trachomatis</i> trachoma and lymphogranuloma venereum biovars. <i>Heliyon</i> , 2017, 3, e00364.	3.2	10
35	Genome-scale analysis of the non-cultivable <i>Treponema pallidum</i> reveals extensive within-patient genetic variation. <i>Nature Microbiology</i> , 2017, 2, 16190.	13.3	81
36	Insights on <i>Klebsiella pneumoniae</i> Biofilms Assembled on Different Surfaces Using Phenotypic and Genotypic Approaches. <i>Microorganisms</i> , 2017, 5, 16.	3.6	24

#	ARTICLE	IF	CITATIONS
37	Legionella pneumophila strain associated with the first evidence of person-to-person transmission of Legionnairesâ€™ disease: a unique mosaic genetic backbone. Scientific Reports, 2016, 6, 26261.	3.3	49
38	Probable Person-to-Person Transmission of Legionnairesâ€™ Disease. New England Journal of Medicine, 2016, 374, 497-498.	27.0	165
39	In Silico Scrutiny of Genes Revealing Phylogenetic Congruence with Clinical Prevalence or Tropism Properties of Chlamydia trachomatis Strains. G3: Genes, Genomes, Genetics, 2015, 5, 9-19.	1.8	14
40	Differential Role of the T6SS in Acinetobacter baumannii Virulence. PLoS ONE, 2015, 10, e0138265.	2.5	114
41	Deep comparative genomics among Chlamydia trachomatis lymphogranuloma venereum isolates highlights genes potentially involved in pathoadaptation. Infection, Genetics and Evolution, 2015, 32, 74-88.	2.3	17
42	Chlamydia trachomatis In Vivo to In Vitro Transition Reveals Mechanisms of Phase Variation and Down-Regulation of Virulence Factors. PLoS ONE, 2015, 10, e0133420.	2.5	14
43	Complete Genome Sequence of Chlamydia trachomatis Ocular Serovar C Strain TW-3. Genome Announcements, 2014, 2, .	0.8	8
44	Identification of type III secretion substrates of Chlamydia trachomatis using Yersinia enterocolitica as a heterologous system. BMC Microbiology, 2014, 14, 40.	3.3	56
45	Assessment of the load and transcriptional dynamics of Chlamydia trachomatis plasmid according to strainsâ€™ tissue tropism. Microbiological Research, 2013, 168, 333-339.	5.3	28
46	Effect of long-term laboratory propagation on Chlamydia trachomatis genome dynamics. Infection, Genetics and Evolution, 2013, 17, 23-32.	2.3	29
47	Directional Evolution of Chlamydia trachomatis towards Niche-Specific Adaptation. Journal of Bacteriology, 2012, 194, 6143-6153.	2.2	41
48	Polymorphisms in Inc Proteins and Differential Expression of <i>inc</i> Genes among Chlamydia trachomatis Strains Correlate with Invasiveness and Tropism of Lymphogranuloma Venereum Isolates. Journal of Bacteriology, 2012, 194, 6574-6585.	2.2	49
49	INSaFLU-TELE-Vir: an open web-based bioinformatics suite for influenza and SARS-CoV-2 genome-based surveillance. ARPHA Conference Abstracts, 0, 4, .	0.0	0
50	The Type III Secretion Effector CteG Mediates Host Cell Lytic Exit of Chlamydia trachomatis. Frontiers in Cellular and Infection Microbiology, 0, 12, .	3.9	7