

# Joao Andre Carrico

## List of Publications by Year in descending order

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Version: 2024-02-01

74  
papers

5,192  
citations

136950

32  
h-index

91884

69  
g-index

81  
all docs

81  
docs citations

81  
times ranked

6220  
citing authors

#	ARTICLE	IF	CITATIONS
1	EPIDEMIOLOGIA E FATORES DE RISCO PARA MORTALIDADE EM BACTEREMIAS OCASIONADAS POR MRSA DE PORTO ALEGRE, RS. Brazilian Journal of Infectious Diseases, 2022, 26, 102239.	0.6	0
2	Genome analysis of <i>Legionella pneumophila</i> ST23 from various countries reveals highly similar strains. Life Science Alliance, 2022, 5, e202101117.	2.8	6
3	Distance-based phylogenetic inference from typing data: a unifying view. Briefings in Bioinformatics, 2021, 22, .	6.5	8
4	Chewie Nomenclature Server (chewie-NS): a deployable nomenclature server for easy sharing of core and whole genome MLST schemas. Nucleic Acids Research, 2021, 49, D660-D666.	14.5	21
5	Heterogeneity of penicillin-non-susceptible group B streptococci isolated from a single patient in Germany. Journal of Antimicrobial Chemotherapy, 2020, 75, 296-299.	3.0	16
6	BacPipe: A Rapid, User-Friendly Whole-Genome Sequencing Pipeline for Clinical Diagnostic Bacteriology. IScience, 2020, 23, 100769.	4.1	31
7	Lactobacillus mulieris sp. nov., a new species of Lactobacillus delbrueckii group. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1522-1527.	1.7	36
8	Two multi-fragment recombination events resulted in the $\beta$ -lactam-resistant serotype 11A-ST6521 related to Spain9V-ST156 pneumococcal clone spreading in south-western Europe, 2008 to 2016. Eurosurveillance, 2020, 25, .	7.0	12
9	DEN-IM: dengue virus genotyping from amplicon and shotgun metagenomic sequencing. Microbial Genomics, 2020, 6, .	2.0	0
10	Natural Occurrence of Escherichia coli-Infecting Bacteriophages in Clinical Samples. Frontiers in Microbiology, 2019, 10, 2484.	3.5	21
11	Distinct Phenotypic and Genomic Signatures Underlie Contrasting Pathogenic Potential of Staphylococcus epidermidis Clonal Lineages. Frontiers in Microbiology, 2019, 10, 1971.	3.5	32
12	Insights into the population structure and pan-genome of Haemophilus influenzae. Infection, Genetics and Evolution, 2019, 67, 126-135.	2.3	38
13	Plasmid ATLAS: plasmid visual analytics and identification in high-throughput sequencing data. Nucleic Acids Research, 2019, 47, D188-D194.	14.5	34
14	Streptococcus pneumoniae Serotype 3 in Mexico (1994 to 2017): Decrease of the Unusual Clonal Complex 4909 Lineage following PCV13 Introduction. Journal of Clinical Microbiology, 2019, 57, .	3.9	8
15	Draft Genome Sequence of Escherichia coli DSM 12242, a Highly Efficient Host Strain for the Isolation of Somatic Coliphages. Microbiology Resource Announcements, 2019, 8, .	0.6	0
16	Origin, evolution, and distribution of the molecular machinery for biosynthesis of sialylated lipooligosaccharide structures in Campylobacter coli. Scientific Reports, 2018, 8, 3028.	3.3	13
17	A primer on microbial bioinformatics for nonbioinformaticians. Clinical Microbiology and Infection, 2018, 24, 342-349.	6.0	52
18	INNUENDO: A cross-sectoral platform for the integration of genomics in the surveillance of food-borne pathogens. EFSA Supporting Publications, 2018, 15, 1498E.	0.7	56

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19	Increasing macrolide resistance among <i>Streptococcus agalactiae</i> causing invasive disease in non-pregnant adults was driven by a single capsular-transformed lineage, Portugal, 2009 to 2015. <i>Eurosurveillance</i> , 2018, 23, .	7.0	37
20	Critical steps in clinical shotgun metagenomics for the concomitant detection and typing of microbial pathogens. <i>Scientific Reports</i> , 2018, 8, 13767.	3.3	70
21	GrapeTree: visualization of core genomic relationships among 100,000 bacterial pathogens. <i>Genome Research</i> , 2018, 28, 1395-1404.	5.5	553
22	Large-Scale Simulations of Bacterial Populations Over Complex Networks. <i>Journal of Computational Biology</i> , 2018, 25, 850-861.	1.6	1
23	Fast phylogenetic inference from typing data. <i>Algorithms for Molecular Biology</i> , 2018, 13, 4.	1.2	14
24	chewBBACA: A complete suite for gene-by-gene schema creation and strain identification. <i>Microbial Genomics</i> , 2018, 4, .	2.0	201
25	Clinical and molecular epidemiology of <i>Acinetobacter baumannii</i> bloodstream infections in an endemic setting. <i>Future Microbiology</i> , 2017, 12, 271-283.	2.0	19
26	Serum lipid alterations in GBA-associated Parkinson's disease. <i>Parkinsonism and Related Disorders</i> , 2017, 44, 58-65.	2.2	73
27	Using Spark and GraphX to Parallelize Large-Scale Simulations of Bacterial Populations over Host Contact Networks. <i>Lecture Notes in Computer Science</i> , 2017, , 591-600.	1.3	2
28	PHYLOViZ 2.0: providing scalable data integration and visualization for multiple phylogenetic inference methods. <i>Bioinformatics</i> , 2017, 33, 128-129.	4.1	336
29	Epidemiological Surveillance and Typing Methods to Track Antibiotic Resistant Strains Using High Throughput Sequencing. <i>Methods in Molecular Biology</i> , 2017, 1520, 331-356.	0.9	9
30	Food Safety in the Age of Next Generation Sequencing, <i>Bioinformatics</i> , and Open Data Access. <i>Frontiers in Microbiology</i> , 2017, 8, 909.	3.5	87
31	Clonal and serotype dynamics of serogroup 6 isolates causing invasive pneumococcal disease in Portugal: 1999-2012. <i>PLoS ONE</i> , 2017, 12, e0170354.	2.5	8
32	A widespread family of polymorphic toxins encoded by temperate phages. <i>BMC Biology</i> , 2017, 15, 75.	3.8	33
33	<i>Citrobacter portucalensis</i> sp. nov., isolated from an aquatic sample. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 3513-3517.	1.7	40
34	Beta-hemolytic <i>Streptococcus dysgalactiae</i> strains isolated from horses are a genetically distinct population within the <i>Streptococcus dysgalactiae</i> taxon. <i>Scientific Reports</i> , 2016, 6, 31736.	3.3	16
35	PHYLOViZ Online: web-based tool for visualization, phylogenetic inference, analysis and sharing of minimum spanning trees. <i>Nucleic Acids Research</i> , 2016, 44, W246-W251.	14.5	152
36	Not Seeing the Forest for the Trees: Size of the Minimum Spanning Trees (MSTs) Forest and Branch Significance in MST-Based Phylogenetic Analysis. <i>PLoS ONE</i> , 2015, 10, e0119315.	2.5	15

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37	Emergence of the Same Successful Clade among Distinct Populations of <i>Streptococcus pyogenes</i> in Multiple Geographic Regions. <i>MBio</i> , 2015, 6, e01780-15.	4.1	33
38	Molecular Epidemiology of <i>Streptococcus pneumoniae</i> . , 2015, , 3-19.		11
39	Automatic determination of NET (neutrophil extracellular traps) coverage in fluorescent microscopy images. <i>Bioinformatics</i> , 2015, 31, 2364-2370.	4.1	26
40	Comparing Matrix-Assisted Laser Desorption Ionization–Time of Flight Mass Spectrometry and Phenotypic and Molecular Methods for Identification of Species within the <i>Streptococcus anginosus</i> Group. <i>Journal of Clinical Microbiology</i> , 2015, 53, 3580-3588.	3.9	21
41	Phylogenetic and clonality analysis of <i>Bacillus pumilus</i> isolates uncovered a highly heterogeneous population of different closely related species and clones. <i>FEMS Microbiology Ecology</i> , 2014, 90, 689-698.	2.7	24
42	TypOn: the microbial typing ontology. <i>Journal of Biomedical Semantics</i> , 2014, 5, 43.	1.6	7
43	<i>Bacillus invictae</i> sp. nov., isolated from a health product. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 3867-3876.	1.7	20
44	Scarlet Fever Is Caused By a Limited Number of <i>Streptococcus pyogenes</i> Lineages and Is Associated with the Exotoxin Genes <i>ssa</i> , <i>speA</i> and <i>speC</i> . <i>Pediatric Infectious Disease Journal</i> , 2014, 33, 306-310.	2.0	28
45	The Use of Machine Learning Methodologies to Analyse Antibiotic and Biocide Susceptibility in <i>Staphylococcus aureus</i> . <i>PLoS ONE</i> , 2013, 8, e55582.	2.5	40
46	Bioinformatics in bacterial molecular epidemiology and public health: databases, tools and the next-generation sequencing revolution. <i>Eurosurveillance</i> , 2013, 18, 20382.	7.0	52
47	PHYLOViZ: phylogenetic inference and data visualization for sequence based typing methods. <i>BMC Bioinformatics</i> , 2012, 13, 87.	2.6	492
48	An Ontology and a REST API for Sequence Based Microbial Typing Data. <i>Lecture Notes in Computer Science</i> , 2012, , 21-28.	1.3	0
49	Evaluation of Jackknife and Bootstrap for Defining Confidence Intervals for Pairwise Agreement Measures. <i>PLoS ONE</i> , 2011, 6, e19539.	2.5	49
50	Prognostic Prediction through Biclustering-Based Classification of Clinical Gene Expression Time Series. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, 73-89.	1.5	12
51	Analysis of Invasiveness of Pneumococcal Serotypes and Clones Circulating in Portugal before Widespread Use of Conjugate Vaccines Reveals Heterogeneous Behavior of Clones Expressing the Same Serotype. <i>Journal of Clinical Microbiology</i> , 2011, 49, 1369-1375.	3.9	92
52	Adjusted Wallace Coefficient as a Measure of Congruence between Typing Methods. <i>Journal of Clinical Microbiology</i> , 2011, 49, 3997-4000.	3.9	146
53	Biclustering-Based Classification of Clinical Expression Time Series: A Case Study in Patients with Multiple Sclerosis. <i>Advances in Intelligent and Soft Computing</i> , 2011, , 229-239.	0.2	4
54	Baiacu: A Tool for the Visual Analysis of the <i>Saccharomyces Cerevisiae</i> Regulatory Network. <i>Advances in Intelligent and Soft Computing</i> , 2011, , 49-56.	0.2	0

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55	Prognostic prediction through biclustering-based classification of clinical gene expression time series. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, 175.	1.5	10
56	Highly Penicillin-Resistant Multidrug-Resistant Pneumococcus-Like Strains Colonizing Children in Oeiras, Portugal: Genomic Characteristics and Implications for Surveillance. <i>Journal of Clinical Microbiology</i> , 2010, 48, 238-246.	3.9	41
57	Global optimal eBURST analysis of multilocus typing data using a graphic matroid approach. <i>BMC Bioinformatics</i> , 2009, 10, 152.	2.6	522
58	ccrB typing tool: an online resource for staphylococci ccrB sequence typing. <i>Journal of Antimicrobial Chemotherapy</i> , 2008, 61, 959-960.	3.0	16
59	Analysis of Typing Methods for Epidemiological Surveillance of both Methicillin-Resistant and Methicillin-Susceptible <i>Staphylococcus aureus</i> Strains. <i>Journal of Clinical Microbiology</i> , 2008, 46, 136-144.	3.9	108
60	High Rates of Transmission of and Colonization by <i>Streptococcus pneumoniae</i> and <i>Haemophilus influenzae</i> within a Day Care Center Revealed in a Longitudinal Study. <i>Journal of Clinical Microbiology</i> , 2008, 46, 225-234.	3.9	96
61	Comparison of Molecular Typing Methods for Characterization of <i>Staphylococcus epidermidis</i> : Proposal for Clone Definition. <i>Journal of Clinical Microbiology</i> , 2008, 46, 118-129.	3.9	104
62	Ranked Adjusted Rand: integrating distance and partition information in a measure of clustering agreement. <i>BMC Bioinformatics</i> , 2007, 8, 44.	2.6	15
63	Illustration of a Common Framework for Relating Multiple Typing Methods by Application to Macrolide-Resistant <i>Streptococcus pyogenes</i> . <i>Journal of Clinical Microbiology</i> , 2006, 44, 2524-2532.	3.9	277
64	Data integration gets 'Sloppy'. <i>Nature Biotechnology</i> , 2006, 24, 1070-1071.	17.5	17
65	Trends in Drug Resistance, Serotypes, and Molecular Types of <i>Streptococcus pneumoniae</i> Colonizing Preschool-Age Children Attending Day Care Centers in Lisbon, Portugal: a Summary of 4 Years of Annual Surveillance. <i>Journal of Clinical Microbiology</i> , 2005, 43, 1285-1293.	3.9	50
66	Effect of the Seven-Valent Conjugate Pneumococcal Vaccine on Carriage and Drug Resistance of <i>Streptococcus pneumoniae</i> in Healthy Children Attending Day-Care Centers in Lisbon. <i>Pediatric Infectious Disease Journal</i> , 2005, 24, 243-252.	2.0	102
67	Assessment of Band-Based Similarity Coefficients for Automatic Type and Subtype Classification of Microbial Isolates Analyzed by Pulsed-Field Gel Electrophoresis. <i>Journal of Clinical Microbiology</i> , 2005, 43, 5483-5490.	3.9	102
68	Natural History of Drug-Resistant Clones of <i>Streptococcus pneumoniae</i> Colonizing Healthy Children in Portugal. <i>Microbial Drug Resistance</i> , 2005, 11, 309-322.	2.0	25
69	Properties of Novel International Drug-Resistant Pneumococcal Clones Identified in Day-Care Centers of Lisbon, Portugal. <i>Journal of Clinical Microbiology</i> , 2005, 43, 4696-4703.	3.9	22
70	Characterization of the Genetic Lineages Responsible for Pneumococcal Invasive Disease in Portugal. <i>Journal of Clinical Microbiology</i> , 2005, 43, 1706-1715.	3.9	44
71	Building the national health information infrastructure for personal health, health care services, public health, and research. <i>BMC Medical Informatics and Decision Making</i> , 2003, 3, 1.	3.0	188
72	EURISWEB – Web-based epidemiological surveillance of antibiotic-resistant pneumococci in Day Care Centers. <i>BMC Medical Informatics and Decision Making</i> , 2003, 3, 9.	3.0	10

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73	Molecular Characterization of Methicillin-Resistant <i>Staphylococcus epidermidis</i> Clones: Evidence of Geographic Dissemination. <i>Journal of Clinical Microbiology</i> , 2002, 40, 430-438.	3.9	87
74	Analysis of genomic sequences by Chaos Game Representation. <i>Bioinformatics</i> , 2001, 17, 429-437.	4.1	210