Joao Andre Carrico

List of Publications by Year
in descending order

74	5,192	136950	91884
papers	citations	32	69
		h-index	g-index

81	81	81	6220
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	GrapeTree: visualization of core genomic relationships among 100,000 bacterial pathogens. Genome Research, 2018, 28, 1395-1404.	5.5	553
2	Global optimal eBURST analysis of multilocus typing data using a graphic matroid approach. BMC Bioinformatics, 2009, 10, 152.	2.6	522
3	PHYLOViZ: phylogenetic inference and data visualization for sequence based typing methods. BMC Bioinformatics, 2012, 13, 87.	2.6	492
4	PHYLOViZ 2.0: providing scalable data integration and visualization for multiple phylogenetic inference methods. Bioinformatics, 2017, 33, 128-129.	4.1	336
5	Illustration of a Common Framework for Relating Multiple Typing Methods by Application to Macrolide-Resistant Streptococcus pyogenes. Journal of Clinical Microbiology, 2006, 44, 2524-2532.	3.9	277
6	Analysis of genomic sequences by Chaos Game Representation. Bioinformatics, 2001, 17, 429-437.	4.1	210
7	chewBBACA: A complete suite for gene-by-gene schema creation and strain identification. Microbial Genomics, 2018, 4, .	2.0	201
8	Building the national health information infrastructure for personal health, health care services, public health, and research. BMC Medical Informatics and Decision Making, 2003, 3, 1.	3.0	188
9	PHYLOViZ Online: web-based tool for visualization, phylogenetic inference, analysis and sharing of minimum spanning trees. Nucleic Acids Research, 2016, 44, W246-W251.	14.5	152
10	Adjusted Wallace Coefficient as a Measure of Congruence between Typing Methods. Journal of Clinical Microbiology, 2011, 49, 3997-4000.	3.9	146
11	Analysis of Typing Methods for Epidemiological Surveillance of both Methicillin-Resistant and Methicillin-Susceptible <i>Staphylococcus aureus</i> Strains. Journal of Clinical Microbiology, 2008, 46, 136-144.	3.9	108
12	Comparison of Molecular Typing Methods for Characterization of <i>Staphylococcus epidermidis</i> : Proposal for Clone Definition. Journal of Clinical Microbiology, 2008, 46, 118-129.	3.9	104
13	Effect of the Seven-Valent Conjugate Pneumococcal Vaccine on Carriage and Drug Resistance of Streptococcus pneumoniae in Healthy Children Attending Day-Care Centers in Lisbon. Pediatric Infectious Disease Journal, 2005, 24, 243-252.	2.0	102
14	Assessment of Band-Based Similarity Coefficients for Automatic Type and Subtype Classification of Microbial Isolates Analyzed by Pulsed-Field Gel Electrophoresis. Journal of Clinical Microbiology, 2005, 43, 5483-5490.	3.9	102
15	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. Journal of Clinical Microbiology, 2008, 46, 225-234.	3.9	96
16	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. Journal of Clinical Microbiology, 2011, 49, 1369-1375.	3.9	92
17	Molecular Characterization of Methicillin-Resistant <i>Staphylococcus epidermidis</i> Clones: Evidence of Geographic Dissemination. Journal of Clinical Microbiology, 2002, 40, 430-438.	3.9	87
18	Food Safety in the Age of Next Generation Sequencing, Bioinformatics, and Open Data Access. Frontiers in Microbiology, 2017, 8, 909.	3.5	87

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19	Serum lipid alterations in GBA-associated Parkinson's disease. Parkinsonism and Related Disorders, 2017, 44, 58-65.	2.2	73
20	Critical steps in clinical shotgun metagenomics for the concomitant detection and typing of microbial pathogens. Scientific Reports, 2018, 8, 13767.	3.3	70
21	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
22	A primer on microbial bioinformatics for nonbioinformaticians. Clinical Microbiology and Infection, 2018, 24, 342-349.	6.0	52
23	Bioinformatics in bacterial molecular epidemiology and public health: databases, tools and the next-generation sequencing revolution. Eurosurveillance, 2013, 18, 20382.	7.0	52
24	Trends in Drug Resistance, Serotypes, and Molecular Types of Streptococcus pneumoniae Colonizing Preschool-Age Children Attending Day Care Centers in Lisbon, Portugal: a Summary of 4 Years of Annual Surveillance. Journal of Clinical Microbiology, 2005, 43, 1285-1293.	3.9	50
25	Evaluation of Jackknife and Bootstrap for Defining Confidence Intervals for Pairwise Agreement Measures. PLoS ONE, 2011, 6, e19539.	2.5	49
26	Characterization of the Genetic Lineages Responsible for Pneumococcal Invasive Disease in Portugal. Journal of Clinical Microbiology, 2005, 43, 1706-1715.	3.9	44
27	Highly Penicillin-Resistant Multidrug-Resistant Pneumococcus-Like Strains Colonizing Children in Oeiras, Portugal: Genomic Characteristics and Implications for Surveillance. Journal of Clinical Microbiology, 2010, 48, 238-246.	3.9	41
28	Citrobacter portucalensis sp. nov., isolated from an aquatic sample. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 3513-3517.	1.7	40
29	The Use of Machine Learning Methodologies to Analyse Antibiotic and Biocide Susceptibility in Staphylococcus aureus. PLoS ONE, 2013, 8, e55582.	2.5	40
30	Insights into the population structure and pan-genome of Haemophilus influenzae. Infection, Genetics and Evolution, 2019, 67, 126-135.	2.3	38
31	Increasing macrolide resistance among Streptococcus agalactiae causing invasive disease in non-pregnant adults was driven by a single capsular-transformed lineage, Portugal, 2009 to 2015. Eurosurveillance, 2018, 23, .	7.0	37
32	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
33	Plasmid ATLAS: plasmid visual analytics and identification in high-throughput sequencing data. Nucleic Acids Research, 2019, 47, D188-D194.	14.5	34
34	Emergence of the Same Successful Clade among Distinct Populations of <i>emm</i> 89 Streptococcus pyogenes in Multiple Geographic Regions. MBio, 2015, 6, e01780-15.	4.1	33
35	A widespread family of polymorphic toxins encoded by temperate phages. BMC Biology, 2017, 15, 75.	3.8	33
36	Distinct Phenotypic and Genomic Signatures Underlie Contrasting Pathogenic Potential of Staphylococcus epidermidis Clonal Lineages. Frontiers in Microbiology, 2019, 10, 1971.	3.5	32

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37	BacPipe: A Rapid, User-Friendly Whole-Genome Sequencing Pipeline for Clinical Diagnostic Bacteriology. IScience, 2020, 23, 100769.	4.1	31
38	Scarlet Fever Is Caused By a Limited Number of Streptococcus pyogenes Lineages and Is Associated with the Exotoxin Genes ssa, speA and speC. Pediatric Infectious Disease Journal, 2014, 33, 306-310.	2.0	28
39	Automatic determination of NET (neutrophil extracellular traps) coverage in fluorescent microscopy images. Bioinformatics, 2015, 31, 2364-2370.	4.1	26
40	Natural History of Drug-Resistant Clones ofStreptococcus pneumoniaeColonizing Healthy Children in Portugal. Microbial Drug Resistance, 2005, 11, 309-322.	2.0	25
41	Phylogenetic and clonality analysis ofBacillus pumilusisolates uncovered a highly heterogeneous population of different closely related species and clones. FEMS Microbiology Ecology, 2014, 90, 689-698.	2.7	24
42	Properties of Novel International Drug-Resistant Pneumococcal Clones Identified in Day-Care Centers of Lisbon, Portugal. Journal of Clinical Microbiology, 2005, 43, 4696-4703.	3.9	22
43	Comparing Matrix-Assisted Laser Desorption Ionization–Time of Flight Mass Spectrometry and Phenotypic and Molecular Methods for Identification of Species within the Streptococcus anginosus Group. Journal of Clinical Microbiology, 2015, 53, 3580-3588.	3.9	21
44	Natural Occurrence of Escherichia coli-Infecting Bacteriophages in Clinical Samples. Frontiers in Microbiology, 2019, 10, 2484.	3.5	21
45	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
46	Bacillus invictae sp. nov., isolated from a health product. International Journal of Systematic and Evolutionary Microbiology, 2014, 64, 3867-3876.	1.7	20
47	Clinical and molecular epidemiology of<i>Acinetobacter baumannii</i>bloodstream infections in an endemic setting. Future Microbiology, 2017, 12, 271-283.	2.0	19
48	Data integration gets 'Sloppy'. Nature Biotechnology, 2006, 24, 1070-1071.	17.5	17
49	ccrB typing tool: an online resource for staphylococci ccrB sequence typing. Journal of Antimicrobial Chemotherapy, 2008, 61, 959-960.	3.0	16
50	Beta-hemolytic Streptococcus dysgalactiae strains isolated from horses are a genetically distinct population within the Streptococcus dysgalactiae taxon. Scientific Reports, 2016, 6, 31736.	3.3	16
51	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
52	Ranked Adjusted Rand: integrating distance and partition information in a measure of clustering agreement. BMC Bioinformatics, 2007, 8, 44.	2.6	15
53	Not Seeing the Forest for the Trees: Size of the Minimum Spanning Trees (MSTs) Forest and Branch Significance in MST-Based Phylogenetic Analysis. PLoS ONE, 2015, 10, e0119315.	2.5	15
54	Fast phylogenetic inference from typing data. Algorithms for Molecular Biology, 2018, 13, 4.	1.2	14

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55	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
56	Prognostic Prediction through Biclustering-Based Classification of Clinical Gene Expression Time Series. Journal of Integrative Bioinformatics, 2011, 8, 73-89.	1.5	12
57	Two multi-fragment recombination events resulted in the Î²-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
58	Molecular Epidemiology of Streptococcus pneumoniae. , 2015, , 3-19.		11
59	EURISWEB â€" Web-based epidemiological surveillance of antibiotic-resistant pneumococci in Day Care Centers. BMC Medical Informatics and Decision Making, 2003, 3, 9.	3.0	10
60	Prognostic prediction through biclustering-based classification of clinical gene expression time series. Journal of Integrative Bioinformatics, 2011, 8, 175.	1.5	10
61	Epidemiological Surveillance and Typing Methods to Track Antibiotic Resistant Strains Using High Throughput Sequencing. Methods in Molecular Biology, 2017, 1520, 331-356.	0.9	9
62	Clonal and serotype dynamics of serogroup 6 isolates causing invasive pneumococcal disease in Portugal: 1999-2012. PLoS ONE, 2017, 12, e0170354.	2.5	8
63	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
64	Distance-based phylogenetic inference from typing data: a unifying view. Briefings in Bioinformatics, 2021, 22, .	6.5	8
65	TypOn: the microbial typing ontology. Journal of Biomedical Semantics, 2014, 5, 43.	1.6	7
66	Genome analysis of <i>Legionella pneumophila</i> ST23 from various countries reveals highly similar strains. Life Science Alliance, 2022, 5, e202101117.	2.8	6
67	Biclustering-Based Classification of Clinical Expression Time Series: A Case Study in Patients with Multiple Sclerosis. Advances in Intelligent and Soft Computing, 2011, , 229-239.	0.2	4
68	Using Spark and GraphX to Parallelize Large-Scale Simulations of Bacterial Populations over Host Contact Networks. Lecture Notes in Computer Science, 2017, , 591-600.	1.3	2
69	Large-Scale Simulations of Bacterial Populations Over Complex Networks. Journal of Computational Biology, 2018, 25, 850-861.	1.6	1
70	Baiacu: A Tool for the Visual Analysis of the Saccharomyces Cerevisiae Regulatory Network. Advances in Intelligent and Soft Computing, 2011, , 49-56.	0.2	0
71	An Ontology and a REST API for Sequence Based Microbial Typing Data. Lecture Notes in Computer Science, 2012, , 21-28.	1.3	0
72	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

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73	DEN-IM: dengue virus genotyping from amplicon and shotgun metagenomic sequencing. Microbial Genomics, 2020, 6, .	2.0	0
74	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