

Gustavo C Cerqueira

List of Publications by Year in descending order

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Version: 2024-02-01

42
papers

6,624
citations

186265
28
h-index

315739
38
g-index

43
all docs

43
docs citations

43
times ranked

9558
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterization of tumor mutation burden, PD-L1 and DNA repair genes to assess relationship to immune checkpoint inhibitors response in metastatic renal cell carcinoma. , 2020, 8, e000319.		67
2	ProphET, prophage estimation tool: A stand-alone prophage sequence prediction tool with self-updating reference database. PLoS ONE, 2019, 14, e0223364.	2.5	45
3	Simultaneous detection of genotype and phenotype enables rapid and accurate antibiotic susceptibility determination. Nature Medicine, 2019, 25, 1858-1864.	30.7	85
4	Abstract 1665: Development of standardized assay and software systems to deliver concordant results across sequencing platforms. , 2019, , .		0
5	Abstract 3515: Functional antigen presentation is required to interpret the tumor mutation burden (TMB) test. , 2019, , .		0
6	RNA-Seq Profile Reveals Th-1 and Th-17-Type of Immune Responses in Mice Infected Systemically with <i>Aspergillus fumigatus</i> . Mycopathologia, 2018, 183, 645-658.	3.1	14
7	Multi-institute analysis of carbapenem resistance reveals remarkable diversity, unexplained mechanisms, and limited clonal outbreaks. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 1135-1140.	7.1	158
8	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus <i>Aspergillus</i> . Genome Biology, 2017, 18, 28.	8.8	417
9	Longitudinal genomic surveillance of <i>Plasmodium falciparum</i> malaria parasites reveals complex genomic architecture of emerging artemisinin resistance. Genome Biology, 2017, 18, 78.	8.8	120
10	A mechanism for a single nucleotide intron shift. Nucleic Acids Research, 2017, 45, 9085-9092.	14.5	12
11	Discovery of McrA, a master regulator of <i>Aspergillus</i> secondary metabolism. Molecular Microbiology, 2017, 103, 347-365.	2.5	73
12	Emergence and loss of spliceosomal twin introns. Fungal Biology and Biotechnology, 2017, 4, 7.	5.1	6
13	Quantifying connectivity between local <i>Plasmodium falciparum</i> malaria parasite populations using identity by descent. PLoS Genetics, 2017, 13, e1007065.	3.5	98
14	Complete genome sequences and analysis of the <i>Fusobacterium nucleatum</i> subspecies <i>animalis</i> 7-1 bacteriophage Φ_{Funu1} and Φ_{Funu2} . Anaerobe, 2016, 38, 125-129.	2.1	11
15	The <i>Aspergillus</i> Genome Database: multispecies curation and incorporation of RNA-Seq data to improve structural gene annotations. Nucleic Acids Research, 2014, 42, D705-D710.	14.5	254
16	Origin in <i>Acinetobacter guillouiae</i> and Dissemination of the Aminoglycoside-Modifying Enzyme Aph(3a ²)-VI. MBio, 2014, 5, e01972-14.	4.1	49
17	The Genomic Diversification of the Whole <i>Acinetobacter</i> Genus: Origins, Mechanisms, and Consequences. Genome Biology and Evolution, 2014, 6, 2866-2882.	2.5	269
18	Identification of 50 Class D β -Lactamases and 65 <i>Acinetobacter</i> -Derived Cephalosporinases in <i>Acinetobacter</i> spp. Antimicrobial Agents and Chemotherapy, 2014, 58, 936-949.	3.2	81

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19	Comprehensive annotation of secondary metabolite biosynthetic genes and gene clusters of <i>Aspergillus nidulans</i> , <i>A. fumigatus</i> , <i>A. niger</i> and <i>A. oryzae</i> . <i>BMC Microbiology</i> , 2013, 13, 91.	3.3	258
20	Genetic loci associated with delayed clearance of <i>Plasmodium falciparum</i> following artemisinin treatment in Southeast Asia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 240-245.	7.1	242
21	The Genome of <i>Anopheles darlingi</i> , the main neotropical malaria vector. <i>Nucleic Acids Research</i> , 2013, 41, 7387-7400.	14.5	102
22	Genomics of <i>Loa loa</i> , a <i>Wolbachia</i> -free filarial parasite of humans. <i>Nature Genetics</i> , 2013, 45, 495-500.	21.4	173
23	Transcript Expression Analysis of Putative <i>Trypanosoma brucei</i> GPI-Anchored Surface Proteins during Development in the Tsetse and Mammalian Hosts. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1708.	3.0	22
24	Genomic epidemiology of the <i>Escherichia coli</i> O104:H4 outbreaks in Europe, 2011. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 3065-3070.	7.1	262
25	<i>Plasmodium falciparum</i> merozoite surface protein 1 blocks the proinflammatory protein S100P. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5429-5434.	7.1	20
26	The <i>Aspergillus</i> Genome Database (AspGD): recent developments in comprehensive multispecies curation, comparative genomics and community resources. <i>Nucleic Acids Research</i> , 2012, 40, D653-D659.	14.5	164
27	DIVERGEMOME: A Bioinformatics Platform to Assist Population Genetics and Genetic Epidemiology Studies. <i>Genetic Epidemiology</i> , 2012, 36, 360-367.	1.3	6
28	Identification of <i>Schistosoma mansoni</i> microRNAs. <i>BMC Genomics</i> , 2011, 12, 47.	2.8	62
29	New resources for functional analysis of omics data for the genus <i>Aspergillus</i> . <i>BMC Genomics</i> , 2011, 12, 486.	2.8	28
30	Genome-Wide Analysis Reveals Novel Genes Essential for Heme Homeostasis in <i>Caenorhabditis elegans</i> . <i>PLoS Genetics</i> , 2010, 6, e1001044.	3.5	32
31	Genomic organization and expression profile of the mucin-associated surface protein (masp) family of the human pathogen <i>Trypanosoma cruzi</i> . <i>Nucleic Acids Research</i> , 2009, 37, 3407-3417.	14.5	111
32	The genome of the blood fluke <i>Schistosoma mansoni</i> . <i>Nature</i> , 2009, 460, 352-358.	27.8	945
33	Sequences involved in mRNA processing in <i>Trypanosoma cruzi</i> . <i>International Journal for Parasitology</i> , 2008, 38, 1383-1389.	3.1	26
34	Sequence diversity and evolution of multigene families in <i>Trypanosoma cruzi</i> . <i>Molecular and Biochemical Parasitology</i> , 2008, 157, 65-72.	1.1	47
35	Genomic organization and transcription analysis of the 195-bp satellite DNA in <i>Trypanosoma cruzi</i> . <i>Molecular and Biochemical Parasitology</i> , 2008, 160, 60-64.	1.1	30
36	Microarray analysis of gene expression induced by sexual contact in <i>Schistosoma mansoni</i> . <i>BMC Genomics</i> , 2007, 8, 181.	2.8	37

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37	Trypanosoma cruzi mitochondrial maxicircles display species- and strain-specific variation and a conserved element in the non-coding region. BMC Genomics, 2006, 7, 60.	2.8	69
38	The Genome Sequence of <i>Trypanosoma cruzi</i> , Etiologic Agent of Chagas Disease. Science, 2005, 309, 409-415.	12.6	1,273
39	Comparative Genomics of Trypanosomatid Parasitic Protozoa. Science, 2005, 309, 404-409.	12.6	713
40	Analysis of expressed sequence tags from Trypanosoma cruzi amastigotes. Memorias Do Instituto Oswaldo Cruz, 2005, 100, 385-389.	1.6	8
41	Simulating the response of land-cover changes to road paving and governance along a major Amazon highway: the Santarém-Cuiabá corridor. Global Change Biology, 2004, 10, 745-764.	9.5	231
42	<title>New approach for old movie restoration</title>. , 2001, 4308, 67.		2