Gustavo C Cerqueira

List of Publications by Year in descending order

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		186265	315739
42	6,624	28	38
papers	citations	h-index	g-index
43	43	43	9558
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	The Genome Sequence of <i>Trypanosoma cruzi</i> , Etiologic Agent of Chagas Disease. Science, 2005, 309, 409-415.	12.6	1,273
2	The genome of the blood fluke Schistosoma mansoni. Nature, 2009, 460, 352-358.	27.8	945
3	Comparative Genomics of Trypanosomatid Parasitic Protozoa. Science, 2005, 309, 404-409.	12.6	713
4	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus Aspergillus. Genome Biology, 2017, 18, 28.	8.8	417
5	The Genomic Diversification of the Whole Acinetobacter Genus: Origins, Mechanisms, and Consequences. Genome Biology and Evolution, 2014, 6, 2866-2882.	2.5	269
6	Genomic epidemiology of the <i>Escherichia coli</i> O104:H4 outbreaks in Europe, 2011. Proceedings of the United States of America, 2012, 109, 3065-3070.	7.1	262
7	Comprehensive annotation of secondary metabolite biosynthetic genes and gene clusters of Aspergillus nidulans, A. fumigatus, A. niger and A. oryzae. BMC Microbiology, 2013, 13, 91.	3.3	258
8	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
9	Genetic loci associated with delayed clearance of <i>Plasmodium falciparum</i> following artemisinin treatment in Southeast Asia. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 240-245.	7.1	242
10	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
11	Genomics of Loa loa, a Wolbachia-free filarial parasite of humans. Nature Genetics, 2013, 45, 495-500.	21.4	173
12	The Aspergillus Genome Database (AspGD): recent developments in comprehensive multispecies curation, comparative genomics and community resources. Nucleic Acids Research, 2012, 40, D653-D659.	14.5	164
13	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
14	Longitudinal genomic surveillance of Plasmodium falciparum malaria parasites reveals complex genomic architecture of emerging artemisinin resistance. Genome Biology, 2017, 18, 78.	8.8	120
15	Genomic organization and expression profile of the mucin-associated surface protein (masp) family of the human pathogen Trypanosoma cruzi. Nucleic Acids Research, 2009, 37, 3407-3417.	14.5	111
16	The Genome of Anopheles darlingi , the main neotropical malaria vector. Nucleic Acids Research, 2013, 41, 7387-7400.	14.5	102
17	Quantifying connectivity between local Plasmodium falciparum malaria parasite populations using identity by descent. PLoS Genetics, 2017, 13, e1007065.	3.5	98
18	Simultaneous detection of genotype and phenotype enables rapid and accurate antibiotic susceptibility determination. Nature Medicine, 2019, 25, 1858-1864.	30.7	85

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19	Identification of 50 Class D β-Lactamases and 65 Acinetobacter-Derived Cephalosporinases in Acinetobacter spp. Antimicrobial Agents and Chemotherapy, 2014, 58, 936-949.	3.2	81
20	Discovery of McrA, a master regulator of <i>Aspergillus</i> secondary metabolism. Molecular Microbiology, 2017, 103, 347-365.	2.5	73
21	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
22	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
23	Identification of Schistosoma mansoni microRNAs. BMC Genomics, 2011, 12, 47.	2.8	62
24	Origin in Acinetobacter guillouiae and Dissemination of the Aminoglycoside-Modifying Enzyme Aph(3′)-VI. MBio, 2014, 5, e01972-14.	4.1	49
25	Sequence diversity and evolution of multigene families in Trypanosoma cruzi. Molecular and Biochemical Parasitology, 2008, 157, 65-72.	1.1	47
26	ProphET, prophage estimation tool: A stand-alone prophage sequence prediction tool with self-updating reference database. PLoS ONE, 2019, 14, e0223364.	2.5	45
27	Microarray analysis of gene expression induced by sexual contact in Schistosoma mansoni. BMC Genomics, 2007, 8, 181.	2.8	37
28	Genome-Wide Analysis Reveals Novel Genes Essential for Heme Homeostasis in Caenorhabditis elegans. PLoS Genetics, 2010, 6, e1001044.	3.5	32
29	Genomic organization and transcription analysis of the 195-bp satellite DNA in Trypanosoma cruzi. Molecular and Biochemical Parasitology, 2008, 160, 60-64.	1.1	30
30	New resources for functional analysis of omics data for the genus Aspergillus. BMC Genomics, 2011, 12, 486.	2.8	28
31	Sequences involved in mRNA processing in Trypanosoma cruzi. International Journal for Parasitology, 2008, 38, 1383-1389.	3.1	26
32	Transcript Expression Analysis of Putative Trypanosoma brucei GPI-Anchored Surface Proteins during Development in the Tsetse and Mammalian Hosts. PLoS Neglected Tropical Diseases, 2012, 6, e1708.	3.0	22
33	<i>Plasmodium falciparum</i> merozoite surface protein 1 blocks the proinflammatory protein S100P. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 5429-5434.	7.1	20
34	RNA-Seq Profile Reveals Th-1 and Th-17-Type of Immune Responses in Mice Infected Systemically with Aspergillus fumigatus. Mycopathologia, 2018, 183, 645-658.	3.1	14
35	A mechanism for a single nucleotide intron shift. Nucleic Acids Research, 2017, 45, 9085-9092.	14.5	12
36	Complete genome sequences and analysis of the Fusobacterium nucleatum subspecies animalis 7-1 bacteriophage É,Funu1 and É,Funu2. Anaerobe, 2016, 38, 125-129.	2.1	11

#	Article	IF	CITATIONS
37	Analysis of expressed sequence tags from Trypanosoma cruzi amastigotes. Memorias Do Instituto Oswaldo Cruz, 2005, 100, 385-389.	1.6	8
38	DIVERGENOME: A Bioinformatics Platform to Assist Population Genetics and Genetic Epidemiology Studies. Genetic Epidemiology, 2012, 36, 360-367.	1.3	6
39	Emergence and loss of spliceosomal twin introns. Fungal Biology and Biotechnology, 2017, 4, 7.	5.1	6
40	<title>New approach for old movie restoration</title> ., 2001, 4308, 67.		2
41	Abstract 1665: Development of standardized assay and software systems to deliver concordant results across sequencing platforms. , 2019, , .		0
42	Abstract 3515: Functional antigen presentation is required to interpret the tumor mutation burden (TMB) test. , 2019, , .		0