

Anderson R Santos

List of Publications by Year in descending order

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41
papers

1,096
citations

430843

18
h-index

414395

32
g-index

43
all docs

43
docs citations

43
times ranked

1282
citing authors

#	ARTICLE	IF	CITATIONS
1	In silico subtractive genomics for target identification in human bacterial pathogens. Drug Development Research, 2011, 72, 162-177.	2.9	115
2	Exoproteome and Secretome Derived Broad Spectrum Novel Drug and Vaccine Candidates in <i>Vibrio cholerae</i> Targeted by Piper betel Derived Compounds. PLoS ONE, 2013, 8, e52773.	2.5	95
3	The Pan-Genome of the Animal Pathogen <i>Corynebacterium pseudotuberculosis</i> Reveals Differences in Genome Plasticity between the Biovar <i>ovis</i> and <i>equi</i> Strains. PLoS ONE, 2013, 8, e53818.	2.5	92
4	Evidence for Reductive Genome Evolution and Lateral Acquisition of Virulence Functions in Two <i>Corynebacterium pseudotuberculosis</i> Strains. PLoS ONE, 2011, 6, e18551.	2.5	75
5	Genome Sequence of <i>Exiguobacterium antarcticum</i> B7, Isolated from a Biofilm in Ginger Lake, King George Island, Antarctica. Journal of Bacteriology, 2012, 194, 6689-6690.	2.2	60
6	A combined approach for comparative exoproteome analysis of <i>Corynebacterium pseudotuberculosis</i> . BMC Microbiology, 2011, 11, 12.	3.3	52
7	A Novel Comparative Genomics Analysis for Common Drug and Vaccine Targets in <i>Corynebacterium pseudotuberculosis</i> and other CMN Group of Human Pathogens. Chemical Biology and Drug Design, 2011, 78, 73-84.	3.2	48
8	Complete Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> 119, a Strain Isolated from a Cow in Israel with Bovine Mastitis. Journal of Bacteriology, 2011, 193, 323-324.	2.2	45
9	Genome sequence of <i>Corynebacterium pseudotuberculosis</i> biovar <i>equi</i> strain 258 and prediction of antigenic targets to improve biotechnological vaccine production. Journal of Biotechnology, 2013, 167, 135-141.	3.8	41
10	Complete genome sequence of <i>Streptococcus agalactiae</i> strain SA20-06, a fish pathogen associated to meningoencephalitis outbreaks. Standards in Genomic Sciences, 2013, 8, 188-197.	1.5	33
11	<i>Campylobacter fetus</i> subspecies: Comparative genomics and prediction of potential virulence targets. Gene, 2012, 508, 145-156.	2.2	32
12	Genome Sequence of <i>Lactococcus lactis</i> subsp. <i>lactis</i> NCDO 2118, a GABA-Producing Strain. Genome Announcements, 2014, 2, .	0.8	31
13	DNA repair in <i>Corynebacterium</i> model. Gene, 2011, 482, 1-7.	2.2	26
14	Conserved host-pathogen PPIs Globally conserved inter-species bacterial PPIs based conserved host-pathogen interactome derived novel target in <i>C. pseudotuberculosis</i> , <i>C. diphtheriae</i> , <i>M. tuberculosis</i> , <i>C. ulcerans</i> , <i>Y. pestis</i> , and <i>E. coli</i> targeted by <i>Piper betel</i> compounds. Integrative Biology (United Kingdom), 2013, 5, 495-509.	1.3	24
15	In silico prediction of conserved vaccine targets in <i>Streptococcus agalactiae</i> strains isolated from fish, cattle, and human samples. Genetics and Molecular Research, 2013, 12, 2902-2912.	0.2	22
16	PANNOTATOR: an automated tool for annotation of pan-genomes. Genetics and Molecular Research, 2013, 12, 2982-2989.	0.2	22
17	Mature Epitope Density - A strategy for target selection based on immunoinformatics and exported prokaryotic proteins. BMC Genomics, 2013, 14, S4.	2.8	21
18	Whole-Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> PAT10 Strain Isolated from Sheep in Patagonia, Argentina. Journal of Bacteriology, 2011, 193, 6420-6421.	2.2	19

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19	Identification of 11 new exoproteins in <i>Corynebacterium pseudotuberculosis</i> by a comparative analysis of the exoproteome. <i>Microbial Pathogenesis</i> , 2013, 61-62, 37-42.	2.9	19
20	Complete Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> Strain CIP 52.97, Isolated from a Horse in Kenya. <i>Journal of Bacteriology</i> , 2011, 193, 7025-7026.	2.2	18
21	Complete Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> Strain Cp267, Isolated from a Llama. <i>Journal of Bacteriology</i> , 2012, 194, 3567-3568.	2.2	18
22	Complete Genome Sequence of Type Strain <i>Campylobacter fetus</i> subsp. <i>venerealis</i> NCTC 10354T. <i>Journal of Bacteriology</i> , 2011, 193, 5871-5872.	2.2	16
23	The <i>Corynebacterium pseudotuberculosis</i> in silico predicted pan-exoproteome. <i>BMC Genomics</i> , 2012, 13, S6.	2.8	16
24	In silico identification of <i>Corynebacterium pseudotuberculosis</i> antigenic targets and application in immunodiagnosis. <i>Journal of Medical Microbiology</i> , 2016, 65, 521-529.	1.8	15
25	Recombinant esterase from <i>Corynebacterium pseudotuberculosis</i> in DNA and subunit recombinant vaccines partially protects mice against challenge. <i>Journal of Medical Microbiology</i> , 2017, 66, 635-642.	1.8	15
26	Complete Genome Sequences of <i>Corynebacterium pseudotuberculosis</i> Strains 3/99-5 and 42/02-A, Isolated from Sheep in Scotland and Australia, Respectively. <i>Journal of Bacteriology</i> , 2012, 194, 4736-4737.	2.2	14
27	Tips and tricks for the assembly of a <i>Corynebacterium pseudotuberculosis</i> genome using a semiconductor sequencer. <i>Microbial Biotechnology</i> , 2013, 6, 150-156.	4.2	14
28	Complete Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> Strain 1/06-A, Isolated from a Horse in North America. <i>Journal of Bacteriology</i> , 2012, 194, 4476-4476.	2.2	13
29	Complete Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> Cp31, Isolated from an Egyptian Buffalo. <i>Journal of Bacteriology</i> , 2012, 194, 6663-6664.	2.2	13
30	Genome Sequence of the <i>Corynebacterium pseudotuberculosis</i> Cp316 Strain, Isolated from the Abscess of a Californian Horse. <i>Journal of Bacteriology</i> , 2012, 194, 6620-6621.	2.2	11
31	Whole-Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> Strain Cp162, Isolated from Camel. <i>Journal of Bacteriology</i> , 2012, 194, 5718-5719.	2.2	10
32	Microbial Comparative Genomics: An Overview of Tools and Insights Into The Genus <i>Corynebacterium</i> . <i>Journal of Bacteriology & Parasitology</i> , 2013, 04, .	0.2	9
33	Complete genome sequence of <i>Corynebacterium pseudotuberculosis</i> biovar <i>ovis</i> strain P54B96 isolated from antelope in South Africa obtained by rapid next generation sequencing technology. <i>Standards in Genomic Sciences</i> , 2012, 7, 189-199.	1.5	8
34	Preliminary Characterization of Mitochondrial Genome of <i>Melipona scutellaris</i> , a Brazilian Stingless Bee. <i>BioMed Research International</i> , 2014, 2014, 1-6.	1.9	7
35	Reannotation of the <i>Corynebacterium diphtheriae</i> NCTC13129 genome as a new approach to studying gene targets connected to virulence and pathogenicity in diphtheria. <i>Open Access Bioinformatics</i> , 2012, , 1.	0.9	6
36	Complete mitochondrial genome sequence of <i>Melipona scutellaris</i> , a Brazilian stingless bee. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3387-3388.	0.7	5

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37	Multiplex PCR assay for correct identification of the fish pathogenic species of Edwardsiella genus reveals the presence of E. anguillarum in South America in strains previously characterized as E. tarda. Journal of Applied Microbiology, 2022, 132, 4225-4235.	3.1	5
38	A singular value decomposition approach for improved taxonomic classification of biological sequences. BMC Genomics, 2011, 12, S11.	2.8	4
39	Using the Gene Ontology tool to produce de novo protein-protein interaction networks with IS_A relationship. Genetics and Molecular Research, 2016, 15, .	0.2	4
40	A Bridging Centrality Plugin for GEPHI and a Case Study for <i>Mycobacterium Tuberculosis</i> H37Rv. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2741-2746.	3.0	2
41	GENPPI: standalone software for creating protein interaction networks from genomes. BMC Bioinformatics, 2021, 22, 596.	2.6	1