

Sintia S Almeida

List of Publications by Year in descending order

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44
papers

1,379
citations

361296

20
h-index

345118

36
g-index

46
all docs

46
docs citations

46
times ranked

1699
citing authors

#	ARTICLE	IF	CITATIONS
1	Two-Component Signal Transduction Systems of Pathogenic Bacteria As Targets for Antimicrobial Therapy: An Overview. <i>Frontiers in Microbiology</i> , 2017, 8, 1878.	1.5	176
2	Exoproteome and Secretome Derived Broad Spectrum Novel Drug and Vaccine Candidates in <i>Vibrio cholerae</i> Targeted by Piper betel Derived Compounds. <i>PLoS ONE</i> , 2013, 8, e52773.	1.1	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. <i>PLoS ONE</i> , 2013, 8, e53818.	1.1	92
4	Comparative analysis of two complete <i>Corynebacterium ulcerans</i> genomes and detection of candidate virulence factors. <i>BMC Genomics</i> , 2011, 12, 383.	1.2	85
5	Evidence for Reductive Genome Evolution and Lateral Acquisition of Virulence Functions in Two <i>Corynebacterium pseudotuberculosis</i> Strains. <i>PLoS ONE</i> , 2011, 6, e18551.	1.1	75
6	Genome Sequence of <i>Exiguobacterium antarcticum</i> B7, Isolated from a Biofilm in Ginger Lake, King George Island, Antarctica. <i>Journal of Bacteriology</i> , 2012, 194, 6689-6690.	1.0	60
7	<i>Helicobacter pylori</i> in dental plaque and stomach of patients from Northern Brazil. <i>World Journal of Gastroenterology</i> , 2010, 16, 3033.	1.4	50
8	Complete Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> I19, a Strain Isolated from a Cow in Israel with Bovine Mastitis. <i>Journal of Bacteriology</i> , 2011, 193, 323-324.	1.0	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. <i>Journal of Biotechnology</i> , 2013, 167, 135-141.	1.9	41
10	Metagenomic Approaches to Analyze Antimicrobial Resistance: An Overview. <i>Frontiers in Genetics</i> , 2020, 11, 575592.	1.1	41
11	Rapid hybrid de novo assembly of a microbial genome using only short reads: <i>Corynebacterium pseudotuberculosis</i> I19 as a case study. <i>Journal of Microbiological Methods</i> , 2011, 86, 218-223.	0.7	40
12	Fine-tuned characterization of <i>Staphylococcus aureus</i> Newbould 305, a strain associated with mild and chronic mastitis in bovines. <i>Veterinary Research</i> , 2014, 45, 106.	1.1	34
13	Complete genome sequence of <i>Streptococcus agalactiae</i> strain SA20-06, a fish pathogen associated to meningoencephalitis outbreaks. <i>Standards in Genomic Sciences</i> , 2013, 8, 188-197.	1.5	33
14	<i>Staphylococcus aureus</i> -Induced G2/M Phase Transition Delay in Host Epithelial Cells Increases Bacterial Infective Efficiency. <i>PLoS ONE</i> , 2013, 8, e63279.	1.1	33
15	<i>Campylobacter fetus</i> subspecies: Comparative genomics and prediction of potential virulence targets. <i>Gene</i> , 2012, 508, 145-156.	1.0	32
16	Genome Sequence of <i>Lactococcus lactis</i> subsp. <i>lactis</i> NCDO 2118, a GABA-Producing Strain. <i>Genome Announcements</i> , 2014, 2, .	0.8	31
17	Proteome scale comparative modeling for conserved drug and vaccine targets identification in <i>Corynebacterium pseudotuberculosis</i> . <i>BMC Genomics</i> , 2014, 15, S3.	1.2	30
18	Mutations and genomic islands can explain the strain dependency of sugar utilization in 21 strains of <i>Propionibacterium freudenreichii</i> . <i>BMC Genomics</i> , 2015, 16, 296.	1.2	30

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19	Genome Sequence of <i>Staphylococcus aureus</i> Newbould 305, a Strain Associated with Mild Bovine Mastitis. <i>Journal of Bacteriology</i> , 2012, 194, 6292-6293.	1.0	29
20	Molecular characterization of the <i>Corynebacterium pseudotuberculosis</i> hsp60-hsp10 operon, and evaluation of the immune response and protective efficacy induced by hsp60 DNA vaccination in mice. <i>BMC Research Notes</i> , 2011, 4, 243.	0.6	22
21	In silico prediction of conserved vaccine targets in <i>Streptococcus agalactiae</i> strains isolated from fish, cattle, and human samples. <i>Genetics and Molecular Research</i> , 2013, 12, 2902-2912.	0.3	22
22	The genome anatomy of <i>Corynebacterium pseudotuberculosis</i> VD57 a highly virulent strain causing Caseous lymphadenitis. <i>Standards in Genomic Sciences</i> , 2016, 11, 29.	1.5	20
23	Whole-Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> PAT10 Strain Isolated from Sheep in Patagonia, Argentina. <i>Journal of Bacteriology</i> , 2011, 193, 6420-6421.	1.0	19
24	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.	1.0	18
25	Complete Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> Strain Cp267, Isolated from a Llama. <i>Journal of Bacteriology</i> , 2012, 194, 3567-3568.	1.0	18
26	<i>C. pseudotuberculosis</i> Phop confers virulence and may be targeted by natural compounds. <i>Integrative Biology (United Kingdom)</i> , 2014, 6, 1088-1099.	0.6	17
27	DISMIRA: Prioritization of disease candidates in miRNA-disease associations based on maximum weighted matching inference model and motif-based analysis. <i>BMC Genomics</i> , 2015, 16, S12.	1.2	17
28	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.	1.0	16
29	The <i>Corynebacterium pseudotuberculosis</i> in silico predicted pan-exoproteome. <i>BMC Genomics</i> , 2012, 13, S6.	1.2	16
30	Quadruplex PCR assay for identification of <i>Corynebacterium pseudotuberculosis</i> differentiating biovar <i>Ovis</i> and <i>Equi</i> . <i>BMC Veterinary Research</i> , 2017, 13, 290.	0.7	15
31	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.	1.0	14
32	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.	2.0	14
33	Exploration of Nitrate Reductase Metabolic Pathway in <i>Corynebacterium pseudotuberculosis</i> . <i>International Journal of Genomics</i> , 2017, 2017, 1-12.	0.8	14
34	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.	1.0	13
35	Complete Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> Cp31, Isolated from an Egyptian Buffalo. <i>Journal of Bacteriology</i> , 2012, 194, 6663-6664.	1.0	13
36	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.	1.0	11

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37	Corynebacterium pseudotuberculosis may be under anagenesis and biovar Equi forms biovar Ovis: a phylogenetic inference from sequence and structural analysis. BMC Microbiology, 2016, 16, 100.	1.3	11
38	Whole-Genome Sequence of Corynebacterium pseudotuberculosis Strain Cp162, Isolated from Camel. Journal of Bacteriology, 2012, 194, 5718-5719.	1.0	10
39	Complete genome sequence of Corynebacterium pseudotuberculosis biovar ovis strain P54B96 isolated from antelope in South Africa obtained by rapid next generation sequencing technology. Standards in Genomic Sciences, 2012, 7, 189-199.	1.5	8
40	CMRegNetâ€“An interspecies reference database for corynebacterial and mycobacterial regulatory networks. BMC Genomics, 2015, 16, 452.	1.2	5
41	Complete Genome Sequence of the Attenuated Corynebacterium pseudotuberculosis Strain T1. Genome Announcements, 2016, 4, .	0.8	5
42	The Phage Display Technique: Advantages and Recent Patents. Recent Patents on DNA & Gene Sequences, 2011, 5, 136-148.	0.7	4
43	Complete Genome Sequence of Corynebacterium pseudotuberculosis Strain 12C. Genome Announcements, 2015, 3, .	0.8	3
44	Whole Genome Annotation: In Silico Analysis. , 0, , .		1