

# Artur Silva

## List of Publications by Year in descending order

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214  
papers

5,501  
citations

145106

33  
h-index

124990

64  
g-index

216  
all docs

216  
docs citations

216  
times ranked

8321  
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene expression in cell lines from human ameloblastoma immortalized using hTERT and HPV16. Oral Diseases, 2022, 28, 2230-2238.	1.5	5
2	Evidence of episodic positive selection in <i>Corynebacterium diphtheriae</i> complex of species and its implementations in identification of drug and vaccine targets. PeerJ, 2022, 10, e12662.	0.9	1
3	Characterization of the first vaginal <i>Lactobacillus crispatus</i> genomes isolated in Brazil. PeerJ, 2021, 9, e11079.	0.9	5
4	Genome analysis of two multidrug-resistant Escherichia coli O8:H9-ST48 strains isolated from lettuce. Gene, 2021, 785, 145603.	1.0	6
5	Influence of FPGS, ABCC4, SLC29A1, and MTHFR genes on the pharmacogenomics of fluoropyrimidines in patients with gastrointestinal cancer from the Brazilian Amazon. Cancer Chemotherapy and Pharmacology, 2021, 88, 837-844.	1.1	4
6	A journey through the <i>Corynebacterium pseudotuberculosis</i> proteome promotes insights into its functional genome. PeerJ, 2021, 9, e12456.	0.9	3
7	HIF-1 $\alpha$ Is Associated with Resistance to Hypoxia-Induced Apoptosis in Ameloblastoma. International Journal of Dentistry, 2021, 2021, 1-10.	0.5	8
8	Occurrence of carbapenemase-producing Enterobacteriaceae in a Portuguese river: blaNDM, blaKPC and blaGES among the detected genes. Environmental Pollution, 2020, 260, 113913.	3.7	45
9	First Steps in the Analysis of Prokaryotic Pan-Genomes. Bioinformatics and Biology Insights, 2020, 14, 117793222093806.	1.0	48
10	Co-Expression Networks for Causal Gene Identification Based on RNA-Seq Data of Corynebacterium pseudotuberculosis. Genes, 2020, 11, 794.	1.0	3
11	Occurrence, antibiotic-resistance and virulence of E. coli strains isolated from mangrove oysters (Crassostrea gasar) farmed in estuaries of Amazonia. Marine Pollution Bulletin, 2020, 157, 111302.	2.3	15
12	Characterization of pharmacogenetic markers related to Acute Lymphoblastic Leukemia toxicity in Amazonian native Americans population. Scientific Reports, 2020, 10, 10292.	1.6	11
13	Resistome in Lake Bolonha, Brazilian Amazon: Identification of Genes Related to Resistance to Broad-Spectrum Antibiotics. Frontiers in Microbiology, 2020, 11, 67.	1.5	19
14	Bacterial diversity in deep-sea sediments under influence of asphalt seep at the São Paulo Plateau. Antonie Van Leeuwenhoek, 2020, 113, 707-717.	0.7	17
15	Comparative genomic analysis and identification of pathogenicity islands of hypervirulent ST-17 Streptococcus agalactiae Brazilian strain. Infection, Genetics and Evolution, 2020, 80, 104195.	1.0	9
16	Bioinformatics approaches applied in pan-genomics and their challenges. , 2020, , 43-64.		1
17	Genomic analysis of Chromobacterium haemolyticum: insights into the species resistome, virulence determinants and genome plasticity. Molecular Genetics and Genomics, 2020, 295, 1001-1012.	1.0	7
18	Amazonia Seasons Have an Influence in the Composition of Bacterial Gut Microbiota of Mangrove Oysters (Crassostrea gasar). Frontiers in Genetics, 2020, 11, 602608.	1.1	8

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19	In silico functional prediction of hypothetical proteins from the core genome of <i>Corynebacterium pseudotuberculosis</i> biovar <i>ovis</i> . PeerJ, 2020, 8, e9643.	0.9	10
20	Taxonomic classification of strain PO100/5 shows a broader geographic distribution and genetic markers of the recently described <i>Corynebacterium silvaticum</i> . PLoS ONE, 2020, 15, e0244210.	1.1	6
21	Redundancy Treatment of NGS Contigs in Microbial Genome Finishing with Hashing-Based Approach. Lecture Notes in Computer Science, 2020, , 13-24.	1.0	0
22	A Clustering Approach to Identify Candidates to Housekeeping Genes Based on RNA-seq Data. Lecture Notes in Computer Science, 2020, , 83-95.	1.0	1
23	Polymorphisms of ADME-related genes and their implications for drug safety and efficacy in Amazonian Amerindians. Scientific Reports, 2019, 9, 7201.	1.6	23
24	Prediction of new vaccine targets in the core genome of <i>Corynebacterium pseudotuberculosis</i> through omics approaches and reverse vaccinology. Gene, 2019, 702, 36-45.	1.0	31
25	Extended Spectrum Beta-Lactamase-Producing Gram-Negative Bacteria Recovered From an Amazonian Lake Near the City of Belém, Brazil. Frontiers in Microbiology, 2019, 10, 364.	1.5	38
26	Re-sequencing and optical mapping reveals misassemblies and real inversions on <i>Corynebacterium pseudotuberculosis</i> genomes. Scientific Reports, 2019, 9, 16387.	1.6	6
27	Linking the Environmental Microbial Diversity and Antibiotic Resistance. , 2019, , 451-457.		0
28	Structure of Hierridin C, Synthesis of Hierridins B and C, and Evidence for Prevalent Alkylresorcinol Biosynthesis in Picocyanobacteria. Journal of Natural Products, 2019, 82, 393-402.	1.5	17
29	GO FEAT: a rapid web-based functional annotation tool for genomic and transcriptomic data. Scientific Reports, 2018, 8, 1794.	1.6	99
30	Genomic Architecture of the Two Cold-Adapted Genera <i>Exiguobacterium</i> and <i>Psychrobacter</i> : Evidence of Functional Reduction in the <i>Exiguobacterium antarcticum</i> B7 Genome. Genome Biology and Evolution, 2018, 10, 731-741.	1.1	17
31	Heat shock stress: Profile of differential expression in <i>Corynebacterium pseudotuberculosis</i> biovar <i>Equi</i> . Gene, 2018, 645, 124-130.	1.0	10
32	PhageWeb – Web Interface for Rapid Identification and Characterization of Prophages in Bacterial Genomes. Frontiers in Genetics, 2018, 9, 644.	1.1	30
33	Genome of <i>Leptospira borgpetersenii</i> strain 4E, a highly virulent isolate obtained from <i>Mus musculus</i> in southern Brazil. Memórias Do Instituto Oswaldo Cruz, 2018, 113, 137-141.	0.8	2
34	Dynamics and diversity of the bacterial community during the spontaneous decay of a <i>Sai</i> (Euterpe) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.8	4
35	Pan4Draft: A Computational Tool to Improve the Accuracy of Pan-Genomic Analysis Using Draft Genomes. Scientific Reports, 2018, 8, 9670.	1.6	14
36	Functional annotation of hypothetical proteins from the <i>Exiguobacterium antarcticum</i> strain B7 reveals proteins involved in adaptation to extreme environments, including high arsenic resistance. PLoS ONE, 2018, 13, e0198965.	1.1	52

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37	The Druggable Pocketome of <i>Corynebacterium diphtheriae</i> : A New Approach for in silico Putative Druggable Targets. <i>Frontiers in Genetics</i> , 2018, 9, 44.	1.1	8
38	Searching whole genome sequences for biochemical identification features of emerging and reemerging pathogenic <i>Corynebacterium</i> species. <i>Functional and Integrative Genomics</i> , 2018, 18, 593-610.	1.4	18
39	Transcriptome analysis of <i>Corynebacterium pseudotuberculosis</i> biovar <i>Equi</i> in two conditions of the environmental stress. <i>Gene</i> , 2018, 677, 349-360.	1.0	5
40	Improving Metagenomic Assemblies Through Data Partitioning: A GC Content Approach. <i>Lecture Notes in Computer Science</i> , 2018, , 415-425.	1.0	11
41	Gel-Based Approaches in Genomic and Proteomic Sciences. <i>Gels Horizons: From Science To Smart Materials</i> , 2018, , 185-195.	0.3	0
42	Efficient detection of differentially methylated regions using DiMmeR. <i>Bioinformatics</i> , 2017, 33, 549-551.	1.8	9
43	The assembly and annotation of the complete Rufous-bellied thrush mitochondrial genome. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 231-232.	0.7	4
44	Draft Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> Strain PA06 Isolated from a Subauricular Abscess in an Ovine Host. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
45	Draft Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> Strain PA07 Biovar <i>ovis</i> , Isolated from a Sheep Udder in Amazonia. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
46	Whole-Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> PA04, Isolated from the Lymph Node of a Sheep in the Amazon, Brazil. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
47	A shift in the virulence potential of <i>Corynebacterium pseudotuberculosis</i> biovar <i>ovis</i> after passage in a murine host demonstrated through comparative proteomics. <i>BMC Microbiology</i> , 2017, 17, 55.	1.3	16
48	Draft Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> Strain PA05 Isolated from an Ovine Host in Pará State, Brazil. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
49	Transcriptional profiling by RNA sequencing of black pepper ( <i>Piper nigrum</i> L.) roots infected by <i>Fusarium solani</i> f. sp. <i>piperis</i> . <i>Acta Physiologiae Plantarum</i> , 2017, 39, 1.	1.0	2
50	Efficient differentiation of <i>Corynebacterium striatum</i> , <i>Corynebacterium amycolatum</i> and <i>Corynebacterium xerosis</i> clinical isolates by multiplex PCR using novel species-specific primers. <i>Journal of Microbiological Methods</i> , 2017, 142, 33-35.	0.7	8
51	Label-free quantitative proteomics of <i>Corynebacterium pseudotuberculosis</i> isolates reveals differences between Biovars <i>ovis</i> and <i>equi</i> strains. <i>BMC Genomics</i> , 2017, 18, 451.	1.2	17
52	Genomic analysis of four strains of <i>Corynebacterium pseudotuberculosis</i> bv. <i>Equi</i> isolated from horses showing distinct signs of infection. <i>Standards in Genomic Sciences</i> , 2017, 12, 16.	1.5	4
53	A Proteomic Perspective on the Bacterial Adaptation to Cold: Integrating OMICs Data of the Psychrotrophic Bacterium <i>Exiguobacterium antarcticum</i> B7. <i>Proteomes</i> , 2017, 5, 9.	1.7	29
54	BARHL1 Is Downregulated in Alzheimer's Disease and May Regulate Cognitive Functions through ESR1 and Multiple Pathways. <i>Genes</i> , 2017, 8, 245.	1.0	57

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55	Quantitative Proteomic Analysis Reveals Changes in the Benchmark <i>Corynebacterium pseudotuberculosis</i> Biovar <i>Equi</i> Exoproteome after Passage in a Murine Host. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 325.	1.8	12
56	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
57	Comparative genomic analysis between <i>Corynebacterium pseudotuberculosis</i> strains isolated from buffalo. <i>PLoS ONE</i> , 2017, 12, e0176347.	1.1	30
58	An integrative in-silico approach for therapeutic target identification in the human pathogen <i>Corynebacterium diphtheriae</i> . <i>PLoS ONE</i> , 2017, 12, e0186401.	1.1	35
59	Assessing the Genotypic Differences between Strains of <i>Corynebacterium pseudotuberculosis</i> biovar <i>equi</i> through Comparative Genomics. <i>PLoS ONE</i> , 2017, 12, e0170676.	1.1	26
60	PanWeb: A web interface for pan-genomic analysis. <i>PLoS ONE</i> , 2017, 12, e0178154.	1.1	23
61	CDH1 mutations in gastric cancer patients from northern Brazil identified by Next- Generation Sequencing (NGS). <i>Genetics and Molecular Biology</i> , 2016, 39, 189-198.	0.6	11
62	Reconstruction of the Fatty Acid Biosynthetic Pathway of <i>Exiguobacterium antarcticum</i> B7 Based on Genomic and Bibliomic Data. <i>BioMed Research International</i> , 2016, 2016, 1-9.	0.9	5
63	<i>Corynebacterium pseudotuberculosis</i> may be under anagenesis and biovar <i>Equi</i> forms biovar <i>Ovis</i> : a phylogenetic inference from sequence and structural analysis. <i>BMC Microbiology</i> , 2016, 16, 100.	1.3	11
64	Draft Genome Sequence of Toxigenic <i>Corynebacterium ulcerans</i> Strain 04-7514, Isolated from a Dog in France. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
65	Draft Genome Sequence of the N <sub>2</sub> -Fixing Cyanobacterium <i>Nostoc piscinale</i> CENA21, Isolated from the Brazilian Amazon Floodplain. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
66	Complete Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> Strain PA01, Isolated from Sheep in Pará, Brazil. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
67	Draft Genome Sequence of <i>Corynebacterium ulcerans</i> Strain 04-3911, Isolated from Humans. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
68	Whole-Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> Strain 226, Isolated from the Abscess of a Goat in California. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
69	Whole-Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> 262 Biovar <i>equi</i> Isolated from Cow Milk. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
70	Whole-Genome Sequence of <i>Corynebacterium auriscanis</i> Strain CIP 106629 Isolated from a Dog with Bilateral Otitis from the United Kingdom. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
71	Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> Strain PA02 Isolated from an Ovine Host in the Amazon. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
72	Draft Genome Sequence of Toxigenic <i>Corynebacterium ulcerans</i> Strain 03-8664 Isolated from a Human Throat. <i>Genome Announcements</i> , 2016, 4, .	0.8	2

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73	Draft genome sequence of <i>Psychrobacter</i> sp. ENNN9_III, a strain isolated from water in a polluted temperate estuarine system ( Ria de Aveiro , Portugal). <i>Genomics Data</i> , 2016, 8, 21-24.	1.3	0
74	De novo assembly and characterization of the <i>Trichuris trichiura</i> adult worm transcriptome using Ion Torrent sequencing. <i>Acta Tropica</i> , 2016, 159, 132-141.	0.9	14
75	Bartolosides Eâ€™K from a Marine Coccoid Cyanobacterium. <i>Journal of Natural Products</i> , 2016, 79, 2504-2513.	1.5	23
76	In silico identification of essential proteins in <i>Corynebacterium pseudotuberculosis</i> based on protein-protein interaction networks. <i>BMC Systems Biology</i> , 2016, 10, 103.	3.0	24
77	SIMBA: a web tool for managing bacterial genome assembly generated by Ion PGM sequencing technology. <i>BMC Bioinformatics</i> , 2016, 17, 456.	1.2	8
78	Whole-genome optical mapping reveals a mis-assembly between two rRNA operons of <i>Corynebacterium pseudotuberculosis</i> strain 1002. <i>BMC Genomics</i> , 2016, 17, 315.	1.2	17
79	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
80	GIPSy: Genomic island prediction software. <i>Journal of Biotechnology</i> , 2016, 232, 2-11.	1.9	128
81	GapBlasterâ€™A Graphical Gap Filler for Prokaryote Genomes. <i>PLoS ONE</i> , 2016, 11, e0155327.	1.1	22
82	PetriScape - A plugin for discrete Petri net simulations in Cytoscape. <i>Journal of Integrative Bioinformatics</i> , 2016, 13, 284.	1.0	3
83	Illumina - A comprehensive Java-based API for statistical Illumina Infinium HumanMethylation450 and MethylationEPIC data processing. <i>Journal of Integrative Bioinformatics</i> , 2016, 13, 294.	1.0	4
84	<i>Corynebacterium pseudotuberculosis</i> RNA-seq data from abiotic stresses. <i>Data in Brief</i> , 2015, 5, 963-966.	0.5	1
85	High-Throughput miRNA Sequencing Reveals a Field Effect in Gastric Cancer and Suggests an Epigenetic Network Mechanism. <i>Bioinformatics and Biology Insights</i> , 2015, 9, BBI.S24066.	1.0	39
86	miRegulome: a knowledge-base of miRNA regulomics and analysis. <i>Scientific Reports</i> , 2015, 5, 12832.	1.6	12
87	Complete Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> Strain E19, Isolated from a Horse in Chile. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
88	Genome informatics and vaccine targets in <i>Corynebacterium urealyticum</i> using two whole genomes, comparative genomics, and reverse vaccinology. <i>BMC Genomics</i> , 2015, 16, S7.	1.2	10
89	Draft Genome Sequence of the Picocyanobacterium <i>Synechococcus</i> sp. Strain GFB01, Isolated from a Freshwater Lagoon in the Brazilian Amazon. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
90	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

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91	An integrated structural proteomics approach along the druggable genome of <i>Corynebacterium pseudotuberculosis</i> species for putative druggable targets. <i>BMC Genomics</i> , 2015, 16, S9.	1.2	25
92	High-Throughput Sequencing of miRNAs Reveals a Tissue Signature in Gastric Cancer and Suggests Novel Potential Biomarkers. <i>Bioinformatics and Biology Insights</i> , 2015, 9s1, BBI.S23773.	1.0	20
93	Pan-Genome Analysis of Human Gastric Pathogen <i>H. pylori</i> : Comparative Genomics and Pathogenomics Approaches to Identify Regions Associated with Pathogenicity and Prediction of Potential Core Therapeutic Targets. <i>BioMed Research International</i> , 2015, 2015, 1-17.	0.9	47
94	Inside the Pan-genome - Methods and Software Overview. <i>Current Genomics</i> , 2015, 16, 245-252.	0.7	79
95	Exposure to an extremely low-frequency electromagnetic field only slightly modifies the proteome of <i>Chromobacterium violaceum</i> ATCC 12472. <i>Genetics and Molecular Biology</i> , 2015, 38, 227-230.	0.6	5
96	Genome Sequence of <i>Corynebacterium ulcerans</i> Strain FRC11. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
97	Complete Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> Strain 12C. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
98	Draft Genome Sequences of <i>Vibrio fluvialis</i> Strains 560 and 539, Isolated from Environmental Samples. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
99	The impact of quality filter for RNA-Seq. <i>Gene</i> , 2015, 563, 165-171.	1.0	7
100	CMRegNet—An interspecies reference database for corynebacterial and mycobacterial regulatory networks. <i>BMC Genomics</i> , 2015, 16, 452.	1.2	5
101	Draft Genome Sequence of <i>Corynebacterium striatum</i> 1961 BR-RJ/09, a Multidrug-Susceptible Strain Isolated from the Urine of a Hospitalized 37-Year-Old Female Patient. <i>Genome Announcements</i> , 2015, 3, .	0.8	8
102	In Silico Protein-Protein Interactions: Avoiding Data and Method Biases Over Sensitivity and Specificity. <i>Current Protein and Peptide Science</i> , 2015, 16, 689-700.	0.7	8
103	MapRepeat: an approach for effective assembly of repetitive regions in prokaryotic genomes. <i>Bioinformatics</i> , 2015, 11, 276-279.	0.2	12
104	Lack of evidence for human infection with Xenotropic murine leukemia virus-related virus in the Brazilian Amazon basin. <i>Revista Da Sociedade Brasileira De Medicina Tropical</i> , 2014, 47, 302-306.	0.4	1
105	Reference genes for RT-qPCR studies in <i>Corynebacterium pseudotuberculosis</i> identified through analysis of RNA-seq data. <i>Antonie Van Leeuwenhoek</i> , 2014, 106, 605-614.	0.7	19
106	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
107	Characterization of the Opp Peptide Transporter of <i>Corynebacterium pseudotuberculosis</i> and Its Role in Virulence and Pathogenicity. <i>BioMed Research International</i> , 2014, 2014, 1-7.	0.9	27
108	Draft Genome Sequence of <i>Haloferax</i> sp. Strain ATB1, Isolated from a Semi-Arid Region in the Brazilian Caatinga. <i>Genome Announcements</i> , 2014, 2, .	0.8	6

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109	Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> MB20 bv. equi Isolated from a Pectoral Abscess of an Oldenburg Horse in California. <i>Genome Announcements</i> , 2014, 2, .	0.8	5
110	Genome Sequence of <i>Corynebacterium ulcerans</i> Strain 210932. <i>Genome Announcements</i> , 2014, 2, .	0.8	4
111	Draft Genome Sequence of <i>Corynebacterium ulcerans</i> FRC58, Isolated from the Bronchitic Aspiration of a Patient in France. <i>Genome Announcements</i> , 2014, 2, .	0.8	6
112	An improved interolog mapping-based computational prediction of protein-protein interactions with increased network coverage. <i>Integrative Biology (United Kingdom)</i> , 2014, 6, 1080-1087.	0.6	32
113	An iron-acquisition-deficient mutant of <i>Corynebacterium pseudotuberculosis</i> efficiently protects mice against challenge. <i>Veterinary Research</i> , 2014, 45, 28.	1.1	17
114	Label-free proteomic analysis to confirm the predicted proteome of <i>Corynebacterium pseudotuberculosis</i> under nitrosative stress mediated by nitric oxide. <i>BMC Genomics</i> , 2014, 15, 1065.	1.2	29
115	Omics profiles used to evaluate the gene expression of <i>Exiguobacterium antarcticum</i> B7 during cold adaptation. <i>BMC Genomics</i> , 2014, 15, 986.	1.2	21
116	ECF factors of gram-positive bacteria. <i>Virulence</i> , 2014, 5, 587-600.	1.8	18
117	<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
118	Brazilian Microbiome Project: Revealing the Unexplored Microbial Diversity—Challenges and Prospects. <i>Microbial Ecology</i> , 2014, 67, 237-241.	1.4	119
119	Differential transcriptional profile of <i>Corynebacterium pseudotuberculosis</i> in response to abiotic stresses. <i>BMC Genomics</i> , 2014, 15, 14.	1.2	45
120	Serological proteome analysis of <i>Corynebacterium pseudotuberculosis</i> isolated from different hosts reveals novel candidates for prophylactics to control caseous lymphadenitis. <i>Veterinary Microbiology</i> , 2014, 174, 255-260.	0.8	13
121	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
122	A Protocol for mtGenome Analysis on Large Sample Numbers. <i>Bioinformatics and Biology Insights</i> , 2014, 8, BBI.S14623.	1.0	1
123	Draft Genome Sequence of Non-O1 and Non-O139 <i>Vibrio cholerae</i> Strain VCC19. <i>Genome Announcements</i> , 2014, 2, .	0.8	0
124	MiRNA Expression Profile for the Human Gastric Antrum Region Using Ultra-Deep Sequencing. <i>PLoS ONE</i> , 2014, 9, e92300.	1.1	25
125	<i>Chromobacterium violaceum</i> : Important Insights for Virulence and Biotechnological Potential by Exoproteomic Studies. <i>Current Microbiology</i> , 2013, 67, 100-106.	1.0	16
126	Mature Epitope Density - A strategy for target selection based on immunoinformatics and exported prokaryotic proteins. <i>BMC Genomics</i> , 2013, 14, S4.	1.2	21



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127	A novel in silico reverse-transcriptomics-based identification and blood-based validation of a panel of sub-type specific biomarkers in lung cancer. BMC Genomics, 2013, 14, S5.	1.2	22
128	Tips and tricks for the assembly of a <i>Corynebacterium pseudotuberculosis</i> genome using a semiconductor sequencer. Microbial Biotechnology, 2013, 6, 150-156.	2.0	14
129	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.	0.6	24
130	Genome sequence of <i>Corynebacterium pseudotuberculosis</i> biovar equi strain 258 and prediction of antigenic targets to improve biotechnological vaccine production. Journal of Biotechnology, 2013, 167, 135-141.	1.9	41
131	on <i>Corynebacterium pseudotuberculosis</i> based transcriptional assessment of a <i>C. pseudotuberculosis</i> equi strain reveals denaturing high-performance liquid chromatography a promising rRNA depletion method. Microbial Biotechnology, 2013, 6, 168-177.	2.0	11
132	Identification of 11 new exoproteins in <i>Corynebacterium pseudotuberculosis</i> by a comparative analysis of the exoproteome. Microbial Pathogenesis, 2013, 61-62, 37-42.	1.3	19
133	Differential Exoproteome Analysis of Two <i>Corynebacterium pseudotuberculosis</i> Biovar Ovis Strains Isolated from Goat (1002) and Sheep (C231). Current Microbiology, 2013, 67, 460-465.	1.0	15
134	High efficiency application of a mate-paired library from next-generation sequencing to postlight sequencing: <i>Corynebacterium pseudotuberculosis</i> as a case study for microbial de novo genome assembly. Journal of Microbiological Methods, 2013, 95, 441-447.	0.7	6
135	PROGRESSION OF OMICS™ METHODOLOGIES FOR UNDERSTANDING THE PATHOGENICITY OF CORYNEBACTERIUM PSEUDOTUBERCULOSIS: THE BRAZILIAN EXPERIENCE. Computational and Structural Biotechnology Journal, 2013, 6, e201303013.	1.9	14
136	Complete Genome of a <i>Methanosarcina mazei</i> Strain Isolated from Sediment Samples from an Amazonian Flooded Area. Genome Announcements, 2013, 1, .	0.8	8
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