

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	A Molecular Phylogeny of Living Primates. <i>PLoS Genetics</i> , 2011, 7, e1001342.	1.5	1,130
2	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
3	Pangenomic Study of <i>Corynebacterium diphtheriae</i> That Provides Insights into the Genomic Diversity of Pathogenic Isolates from Cases of Classical Diphtheria, Endocarditis, and Pneumonia. <i>Journal of Bacteriology</i> , 2012, 194, 3199-3215.	1.0	142
4	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 May 2009â€“31 July 2009. <i>Molecular Ecology Resources</i> , 2009, 9, 1460-1466.	2.2	128
5	GIPSy: Genomic island prediction software. <i>Journal of Biotechnology</i> , 2016, 232, 2-11.	1.9	128
6	Brazilian Microbiome Project: Revealing the Unexplored Microbial Diversityâ€”Challenges and Prospects. <i>Microbial Ecology</i> , 2014, 67, 237-241.	1.4	119
7	The Genome of <i>Anopheles darlingi</i> , the main neotropical malaria vector. <i>Nucleic Acids Research</i> , 2013, 41, 7387-7400.	6.5	102
8	GO FEAT: a rapid web-based functional annotation tool for genomic and transcriptomic data. <i>Scientific Reports</i> , 2018, 8, 1794.	1.6	99
9	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
10	The Pan-Genome of the Animal Pathogen <i>Corynebacterium pseudotuberculosis</i> Reveals Differences in Genome Plasticity between the Biovar ovis and equi Strains. <i>PLoS ONE</i> , 2013, 8, e53818.	1.1	92
11	The complete genome sequence of <i>Corynebacterium pseudotuberculosis</i> FRC41 isolated from a 12-year-old girl with necrotizing lymphadenitis reveals insights into gene-regulatory networks contributing to virulence. <i>BMC Genomics</i> , 2010, 11, 728.	1.2	89
12	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
13	Inside the Pan-genome - Methods and Software Overview. <i>Current Genomics</i> , 2015, 16, 245-252.	0.7	79
14	Analysis of mitochondrial D-loop region casts new light on domestic water buffalo (<i>Bubalus bubalis</i>) phylogeny. <i>Molecular Phylogenetics and Evolution</i> , 2004, 30, 308-324.	1.2	78
15	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
16	PIPS: Pathogenicity Island Prediction Software. <i>PLoS ONE</i> , 2012, 7, e30848.	1.1	70
17	Ultra-Deep Sequencing Reveals the microRNA Expression Pattern of the Human Stomach. <i>PLoS ONE</i> , 2010, 5, e13205.	1.1	67
18	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

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19	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
20	High-throughput sequencing of black pepper root transcriptome. <i>BMC Plant Biology</i> , 2012, 12, 168.	1.6	55
21	Genetic structure of red-handed howler monkey populations in the fragmented landscape of Eastern Brazilian Amazonia. <i>Genetics and Molecular Biology</i> , 2010, 33, 774-780.	0.6	54
22	A combined approach for comparative exoproteome analysis of <i>Corynebacterium pseudotuberculosis</i> . <i>BMC Microbiology</i> , 2011, 11, 12.	1.3	52
23	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. <i>PLoS ONE</i> , 2018, 13, e0198965.	1.1	52
24	A Novel Comparative Genomics Analysis for Common Drug and Vaccine Targets in <i>Corynebacterium pseudotuberculosis</i> and other CMN Group of Human Pathogens. <i>Chemical Biology and Drug Design</i> , 2011, 78, 73-84.	1.5	48
25	First Steps in the Analysis of Prokaryotic Pan-Genomes. <i>Bioinformatics and Biology Insights</i> , 2020, 14, 117793222093806.	1.0	48
26	Guarana (<i>Paullinia cupana</i> var. <i>sorbilis</i>), an anciently consumed stimulant from the Amazon rain forest: the seeded-fruit transcriptome. <i>Plant Cell Reports</i> , 2008, 27, 117-124.	2.8	47
27	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
28	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
29	Differential transcriptional profile of <i>Corynebacterium pseudotuberculosis</i> in response to abiotic stresses. <i>BMC Genomics</i> , 2014, 15, 14.	1.2	45
30	Occurrence of carbapenemase-producing Enterobacteriaceae in a Portuguese river: blaNDM, blaKPC and blaGES among the detected genes. <i>Environmental Pollution</i> , 2020, 260, 113913.	3.7	45
31	Genome sequence of <i>Corynebacterium pseudotuberculosis</i> biovar equi strain 258 and prediction of antigenic targets to improve biotechnological vaccine production. <i>Journal of Biotechnology</i> , 2013, 167, 135-141.	1.9	41
32	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
33	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
34	Extended Spectrum Beta-Lactamase-Producing Gram-Negative Bacteria Recovered From an Amazonian Lake Near the City of Belém, Brazil. <i>Frontiers in Microbiology</i> , 2019, 10, 364.	1.5	38
35	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
36	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

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37	An alternative genotyping method using dye-labeled universal primer to reduce unspecific amplifications. <i>Molecular Biology Reports</i> , 2010, 37, 2031-2036.	1.0	32
38	<i>Campylobacter fetus</i> subspecies: Comparative genomics and prediction of potential virulence targets. <i>Gene</i> , 2012, 508, 145-156.	1.0	32
39	The Detection and Sequencing of a Broad-Host-Range Conjugative IncP-1 ⁺ Plasmid in an Epidemic Strain of <i>Mycobacterium abscessus</i> subsp. <i>bolletii</i> . <i>PLoS ONE</i> , 2013, 8, e60746.	1.1	32
40	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
41	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
42	Prediction of new vaccine targets in the core genome of <i>Corynebacterium pseudotuberculosis</i> through omics approaches and reverse vaccinology. <i>Gene</i> , 2019, 702, 36-45.	1.0	31
43	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
44	Comparative genomic analysis between <i>Corynebacterium pseudotuberculosis</i> strains isolated from buffalo. <i>PLoS ONE</i> , 2017, 12, e0176347.	1.1	30
45	PhageWeb – Web Interface for Rapid Identification and Characterization of Prophages in Bacterial Genomes. <i>Frontiers in Genetics</i> , 2018, 9, 644.	1.1	30
46	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
47	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
48	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
49	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
50	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
51	MiRNA Expression Profile for the Human Gastric Antrum Region Using Ultra-Deep Sequencing. <i>PLoS ONE</i> , 2014, 9, e92300.	1.1	25
52	Evolutionary inferences on the diversity of the genus <i>Aotus</i> (Platyrrhini, Cebidae) from mitochondrial cytochrome c oxidase subunit II gene sequences. <i>Molecular Phylogenetics and Evolution</i> , 2009, 51, 382-387.	1.2	24
53	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. <i>Integrative Biology (United Kingdom)</i> . 2013, 5, 495-509.	0.6	24
54	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

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55	Whole genome sequencing of environmental <i>Vibrio cholerae</i> O1 from 10 nanograms of DNA using short reads. <i>Journal of Microbiological Methods</i> , 2011, 87, 208-212.	0.7	23
56	Bartolosides Eâ€“K from a Marine Coccoid Cyanobacterium. <i>Journal of Natural Products</i> , 2016, 79, 2504-2513.	1.5	23
57	Polymorphisms of ADME-related genes and their implications for drug safety and efficacy in Amazonian Amerindians. <i>Scientific Reports</i> , 2019, 9, 7201.	1.6	23
58	PanWeb: A web interface for pan-genomic analysis. <i>PLoS ONE</i> , 2017, 12, e0178154.	1.1	23
59	Analysis of quality raw data of second generation sequencers with Quality Assessment Software. <i>BMC Research Notes</i> , 2011, 4, 130.	0.6	22
60	A novel in silico reverse-transcriptomics-based identification and blood-based validation of a panel of sub-type specific biomarkers in lung cancer. <i>BMC Genomics</i> , 2013, 14, S5.	1.2	22
61	GapBlasterâ€“A Graphical Gap Filler for Prokaryote Genomes. <i>PLoS ONE</i> , 2016, 11, e0155327.	1.1	22
62	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
63	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
64	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
65	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
66	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
67	Identification of 11 new exoproteins in <i>Corynebacterium pseudotuberculosis</i> byâ€“comparative analysis of the exoproteome. <i>Microbial Pathogenesis</i> , 2013, 61-62, 37-42.	1.3	19
68	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
69	Resistome in Lake Bolonha, Brazilian Amazon: Identification of Genes Related to Resistance to Broad-Spectrum Antibiotics. <i>Frontiers in Microbiology</i> , 2020, 11, 67.	1.5	19
70	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
71	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
72	ÿf^{ECF}factors of gram-positive bacteria. <i>Virulence</i> , 2014, 5, 587-600.	1.8	18

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73	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
74	Microbial Diversity of an Anoxic Zone of a Hydroelectric Power Station Reservoir in Brazilian Amazonia. <i>Microbial Ecology</i> , 2011, 62, 853-61.	1.4	17
75	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
76	<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
77	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
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	Label-free quantitative proteomics of <i>Corynebacterium pseudotuberculosis</i> isolates reveals differences between <i>Biovars ovis</i> and <i>equi</i> strains. <i>BMC Genomics</i> , 2017, 18, 451.	1.2	17
80	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. <i>Genome Biology and Evolution</i> , 2018, 10, 731-741.	1.1	17
81	Bacterial diversity in deep-sea sediments under influence of asphalt seep at the São Paulo Plateau. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 707-717.	0.7	17
82	Structure of Hierridin C, Synthesis of Hierridins B and C, and Evidence for Prevalent Alkylresorcinol Biosynthesis in Picocyanobacteria. <i>Journal of Natural Products</i> , 2019, 82, 393-402.	1.5	17
83	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
84	The <i>Corynebacterium pseudotuberculosis</i> in silico predicted pan-exoproteome. <i>BMC Genomics</i> , 2012, 13, S6.	1.2	16
85	<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
86	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
87	Differential Exoproteome Analysis of Two <i>Corynebacterium pseudotuberculosis</i> Biovar <i>Ovis</i> Strains Isolated from Goat (1002) and Sheep (C231). <i>Current Microbiology</i> , 2013, 67, 460-465.	1.0	15
88	Occurrence, antibiotic-resistance and virulence of <i>E. coli</i> strains isolated from mangrove oysters (<i>Crassostrea gasar</i>) farmed in estuaries of Amazonia. <i>Marine Pollution Bulletin</i> , 2020, 157, 111302.	2.3	15
89	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
90	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

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91	PROGRESSION OF ÔMICSA™ METHODOLOGIES FOR UNDERSTANDING THE PATHOGENICITY OF CORYNEBACTERIUM PSEUDOTUBERCULOSIS: THE BRAZILIAN EXPERIENCE. Computational and Structural Biotechnology Journal, 2013, 6, e201303013.	1.9	14
92	De novo assembly and characterization of the Trichuris trichiura adult worm transcriptome using Ion Torrent sequencing. Acta Tropica, 2016, 159, 132-141.	0.9	14
93	Pan4Draft: A Computational Tool to Improve the Accuracy of Pan-Genomic Analysis Using Draft Genomes. Scientific Reports, 2018, 8, 9670.	1.6	14
94	Effects of Habitat Fragmentation on the Genetic Variability of Silvery Marmosets, Mico argentatus. , 2003, , 17-28.		13
95	Complete Genome Sequence of Corynebacterium pseudotuberculosis Strain 1/06-A, Isolated from a Horse in North America. Journal of Bacteriology, 2012, 194, 4476-4476.	1.0	13
96	Complete Genome Sequence of Corynebacterium pseudotuberculosis Cp31, Isolated from an Egyptian Buffalo. Journal of Bacteriology, 2012, 194, 6663-6664.	1.0	13
97	Serological proteome analysis of Corynebacterium pseudotuberculosis isolated from different hosts reveals novel candidates for prophylactics to control caseous lymphadenitis. Veterinary Microbiology, 2014, 174, 255-260.	0.8	13
98	Genetic variability and efficiency of DNA microsatellite markers for paternity testing in horse breeds from the Brazilian Marajó archipelago. Genetics and Molecular Biology, 2008, 31, 68-72.	0.6	12
99	Phylogenetic and gene trees of Synechococcus: choice of the right marker to evaluate the population diversity in the Tucuruí Hydroelectric Power Station Reservoir in Brazilian Amazonia. Journal of Plankton Research, 2012, 34, 245-257.	0.8	12
100	miRegulome: a knowledge-base of miRNA regulomics and analysis. Scientific Reports, 2015, 5, 12832.	1.6	12
101	Quantitative Proteomic Analysis Reveals Changes in the Benchmark Corynebacterium pseudotuberculosis Biovar Equi Exoproteome after Passage in a Murine Host. Frontiers in Cellular and Infection Microbiology, 2017, 7, 325.	1.8	12
102	MapRepeat: an approach for effective assembly of repetitive regions in prokaryotic genomes. Bioinformatics, 2015, 11, 276-279.	0.2	12
103	Genome Sequence of the Corynebacterium pseudotuberculosis Cp316 Strain, Isolated from the Abscess of a Californian Horse. Journal of Bacteriology, 2012, 194, 6620-6621.	1.0	11
104	The core stimulon of Corynebacterium pseudotuberculosis strain 1002 identified using ab initio methodologies. Integrative Biology (United Kingdom), 2012, 4, 789.	0.6	11
105	on T-based transcriptional assessment of a Corynebacterium pseudotuberculosis equi strain reveals denaturing high-performance liquid chromatography a promising rRNA depletion method. Microbial Biotechnology, 2013, 6, 168-177.	2.0	11
106	Draft Genome Sequence of the Brazilian Toxic Bloom-Forming Cyanobacterium Microcystis aeruginosa Strain SPC777. Genome Announcements, 2013, 1, .	0.8	11
107	CDH1 mutations in gastric cancer patients from northern Brazil identified by Next- Generation Sequencing (NGS). Genetics and Molecular Biology, 2016, 39, 189-198.	0.6	11
108	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

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109	Improving Metagenomic Assemblies Through Data Partitioning: A GC Content Approach. Lecture Notes in Computer Science, 2018, , 415-425.	1.0	11
110	Characterization of pharmacogenetic markers related to Acute Lymphoblastic Leukemia toxicity in Amazonian native Americans population. Scientific Reports, 2020, 10, 10292.	1.6	11
111	Simplifier: a web tool to eliminate redundant NGS contigs. Bioinformatics, 2012, 8, 996-999.	0.2	11
112	Gene expression of the arsenic resistance operon in Chromobacterium violaceum ATCC 12472. Canadian Journal of Microbiology, 2008, 54, 137-142.	0.8	10
113	Whole-Genome Sequence of Corynebacterium pseudotuberculosis Strain Cp162, Isolated from Camel. Journal of Bacteriology, 2012, 194, 5718-5719.	1.0	10
114	Genome informatics and vaccine targets in Corynebacterium urealyticum using two whole genomes, comparative genomics, and reverse vaccinology. BMC Genomics, 2015, 16, S7.	1.2	10
115	Heat shock stress: Profile of differential expression in Corynebacterium pseudotuberculosis biovar Equi. Gene, 2018, 645, 124-130.	1.0	10
116	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
117	Genetic Diversity of Red-Bellied Titis (<i>Callicebus moloch</i>) from Eastern Amazonia Based on Microsatellite Markers. Biochemical Genetics, 2009, 47, 235-240.	0.8	9
118	Quality of prokaryote genome assembly: Indispensable issues of factors affecting prokaryote genome assembly quality. Gene, 2012, 505, 365-367.	1.0	9
119	High-Throughput Sequencing of a South American Amerindian. PLoS ONE, 2013, 8, e83340.	1.1	9
120	Efficient detection of differentially methylated regions using DiMmeR. Bioinformatics, 2017, 33, 549-551.	1.8	9
121	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
122	A practical teaching course in directed protein evolution using the green fluorescent protein as a model. Biochemistry and Molecular Biology Education, 2011, 39, 21-27.	0.5	8
123	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
124	Complete Genome of a Methanosarcina mazei Strain Isolated from Sediment Samples from an Amazonian Flooded Area. Genome Announcements, 2013, 1, .	0.8	8
125	Draft Genome Sequence of Corynebacterium striatum 1961 BR-RJ/09, a Multidrug-Susceptible Strain Isolated from the Urine of a Hospitalized 37-Year-Old Female Patient. Genome Announcements, 2015, 3, .	0.8	8
126	SIMBA: a web tool for managing bacterial genome assembly generated by Ion PGM sequencing technology. BMC Bioinformatics, 2016, 17, 456.	1.2	8

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127	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
128	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
129	Amazonia Seasons Have an Influence in the Composition of Bacterial Gut Microbiota of Mangrove Oysters (<i>Crassostrea gasar</i>). <i>Frontiers in Genetics</i> , 2020, 11, 602608.	1.1	8
130	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
131	HIF-1 α Is Associated with Resistance to Hypoxia-Induced Apoptosis in Ameloblastoma. <i>International Journal of Dentistry</i> , 2021, 2021, 1-10.	0.5	8
132	Homology modeling, molecular dynamics and QM/MM study of the regulatory protein PhoP from <i>Corynebacterium pseudotuberculosis</i> . <i>Journal of Molecular Modeling</i> , 2012, 18, 1219-1227.	0.8	7
133	Draft Genome Sequence of <i>Serratia fonticola</i> UTAD54, a Carbapenem-Resistant Strain Isolated from Drinking Water. <i>Genome Announcements</i> , 2013, 1, .	0.8	7
134	Draft Genome Sequence of <i>Methylobacterium mesophilicum</i> Strain SR1.6/6, Isolated from Citrus sinensis. <i>Genome Announcements</i> , 2013, 1, .	0.8	7
135	The impact of quality filter for RNA-Seq. <i>Gene</i> , 2015, 563, 165-171.	1.0	7
136	Genomic analysis of <i>Chromobacterium haemolyticum</i> : insights into the species resistome, virulence determinants and genome plasticity. <i>Molecular Genetics and Genomics</i> , 2020, 295, 1001-1012.	1.0	7
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