

Robson Francisco de Souza

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

2,981
citations

304602

22
h-index

302012

39
g-index

48
all docs

48
docs citations

48
times ranked

4100
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparison of the genomes of two <i>Xanthomonas</i> pathogens with differing host specificities. <i>Nature</i> , 2002, 417, 459-463.	13.7	1,074
2	Polymorphic toxin systems: Comprehensive characterization of trafficking modes, processing, mechanisms of action, immunity and ecology using comparative genomics. <i>Biology Direct</i> , 2012, 7, 18.	1.9	440
3	Bioinformatics construction of the human cell surfaceome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 16752-16757.	3.3	119
4	Genealogical Evidence for Positive Selection in the <i>nef</i> Gene of HIV-1. <i>Genetics</i> , 1999, 153, 1077-1089.	1.2	113
5	Assembly of the 373k gene space of the polyploid sugarcane genome reveals reservoirs of functional diversity in the world's leading biomass crop. <i>GigaScience</i> , 2019, 8, .	3.3	106
6	Novel insights into the genomic basis of citrus canker based on the genome sequences of two strains of <i>Xanthomonas fuscans</i> subsp. <i>aurantifolii</i> . <i>BMC Genomics</i> , 2010, 11, 238.	1.2	102
7	The Natural History of ADP-Ribosyltransferases and the ADP-Ribosylation System. <i>Current Topics in Microbiology and Immunology</i> , 2014, 384, 3-32.	0.7	99
8	Gene flow and biological conflict systems in the origin and evolution of eukaryotes. <i>Frontiers in Cellular and Infection Microbiology</i> , 2012, 2, 89.	1.8	67
9	Identification of novel components of NAD-utilizing metabolic pathways and prediction of their biochemical functions. <i>Molecular BioSystems</i> , 2012, 8, 1661.	2.9	63
10	COMPARATIVE GENOMICS ANALYSES OF CITRUS-ASSOCIATED BACTERIA. <i>Annual Review of Phytopathology</i> , 2004, 42, 163-184.	3.5	57
11	Comparative genomics uncovers novel structural and functional features of the heterotrimeric GTPase signaling system. <i>Gene</i> , 2011, 475, 63-78.	1.0	57
12	Diversity and evolution of chromatin proteins encoded by DNA viruses. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2010, 1799, 302-318.	0.9	52
13	Lineage-specific expansions of TET/JBP genes and a new class of DNA transposons shape fungal genomic and epigenetic landscapes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 1676-1683.	3.3	51
14	Cytological Characterization of YpsB, a Novel Component of the <i>Bacillus subtilis</i> Divisome. <i>Journal of Bacteriology</i> , 2008, 190, 7096-7107.	1.0	48
15	Origin and evolution of peptide-modifying dioxygenases and identification of the wybutosine hydroxylase/hydroperoxidase. <i>Nucleic Acids Research</i> , 2010, 38, 5261-5279.	6.5	46
16	Predicted class-I aminoacyl tRNA synthetase-like proteins in non-ribosomal peptide synthesis. <i>Biology Direct</i> , 2010, 5, 48.	1.9	45
17	Complete Genome Sequencing of <i>Mycobacterium bovis</i> SP38 and Comparative Genomics of <i>Mycobacterium bovis</i> and <i>M. tuberculosis</i> Strains. <i>Frontiers in Microbiology</i> , 2017, 8, 2389.	1.5	40
18	Comparative Analyses of <i>Xanthomonas</i> and <i>Xylella</i> Complete Genomes. <i>OMICS A Journal of Integrative Biology</i> , 2005, 9, 43-76.	1.0	39

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19	A Family of T6SS Antibacterial Effectors Related to L,d-Transpeptidases Targets the Peptidoglycan. Cell Reports, 2020, 31, 107813.	2.9	39
20	Global Distribution and Evolution of Mycobacterium bovis Lineages. Frontiers in Microbiology, 2020, 11, 843.	1.5	37
21	Polyvalent Proteins, a Pervasive Theme in the Intergenomic Biological Conflicts of Bacteriophages and Conjugative Elements. Journal of Bacteriology, 2017, 199, .	1.0	33
22	Phylogenetic inference and SSR characterization of tropical woody bamboos tribe Bambuseae (Poaceae: Bambusoideae) based on complete plastid genome sequences. Current Genetics, 2016, 62, 443-453.	0.8	26
23	Profiling the rainbow trout hepatic miRNAome under diet-induced hyperglycemia. Physiological Genomics, 2019, 51, 411-431.	1.0	26
24	Structural and Enzymatic Characterization of a cAMP-Dependent Diguanylate Cyclase from Pathogenic Leptospira Species. Journal of Molecular Biology, 2017, 429, 2337-2352.	2.0	24
25	UMA and MABP domains throw light on receptor endocytosis and selection of endosomal cargoes. Bioinformatics, 2010, 26, 1477-1480.	1.8	23
26	The World of Cyclic Dinucleotides in Bacterial Behavior. Molecules, 2020, 25, 2462.	1.7	21
27	Molecular Epidemiology of Multidrug-Resistant Klebsiella pneumoniae Isolates in a Brazilian Tertiary Hospital. Frontiers in Microbiology, 2019, 10, 1669.	1.5	20
28	Molecular Dynamics Reveals Complex Compensatory Effects of Ionic Strength on the Severe Acute Respiratory Syndrome Coronavirus 2 Spike/Human Angiotensin-Converting Enzyme 2 Interaction. Journal of Physical Chemistry Letters, 2020, 11, 10446-10453.	2.1	20
29	AMIN domains have a predicted role in localization of diverse periplasmic protein complexes. Bioinformatics, 2008, 24, 2423-2426.	1.8	16
30	Functional and evolutionary characterization of Ohr proteins in eukaryotes reveals many active homologs among pathogenic fungi. Redox Biology, 2017, 12, 600-609.	3.9	15
31	Severe Acute Respiratory Syndrome Coronavirus 2 Variants of Concern: A Perspective for Emerging More Transmissible and Vaccine-Resistant Strains. Viruses, 2022, 14, 827.	1.5	14
32	Genome Sequence of <i>Streptomyces olindensis</i> DAUFPE 5622, Producer of the Antitumoral Anthracycline Cosmomycin D. Genome Announcements, 2014, 2, .	0.8	8
33	First Genome Sequences of Two Multidrug-Resistant Candida haemulonii var. vulnera Isolates From Pediatric Patients With Candidemia. Frontiers in Microbiology, 2020, 11, 1535.	1.5	8
34	The Anabaena sensory rhodopsin transducer defines a novel superfamily of prokaryotic small-molecule binding domains. Biology Direct, 2009, 4, 25.	1.9	7
35	Quantitative structure-activity relationships, molecular docking and molecular dynamics simulations reveal drug repurposing candidates as potent SARS-CoV-2 main protease inhibitors. Journal of Biomolecular Structure and Dynamics, 2021, , 1-18.	2.0	6
36	Comparative Phylogenomic Analysis Reveals Evolutionary Genomic Changes and Novel Toxin Families in Endophytic <i>Liberibacter</i> Pathogens. Microbiology Spectrum, 2021, 9, e0050921.	1.2	6

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37	Development and validation of a <i>Xanthomonas axonopodis</i> pv. <i>citri</i> DNA microarray platform (XACarray) generated from the shotgun libraries previously used in the sequencing of this bacterial genome. <i>BMC Research Notes</i> , 2010, 3, 150.	0.6	3
38	A bipartite periplasmic receptor–diguanylate cyclase pair (XAC2383–XAC2382) in the bacterium <i>Xanthomonas citri</i> . <i>Journal of Biological Chemistry</i> , 2018, 293, 10767-10781.	1.6	2
39	Tucuxi-BLAST: Enabling fast and accurate record linkage of large-scale health-related administrative databases through a DNA-encoded approach. <i>PeerJ</i> , 0, 10, e13507.	0.9	0