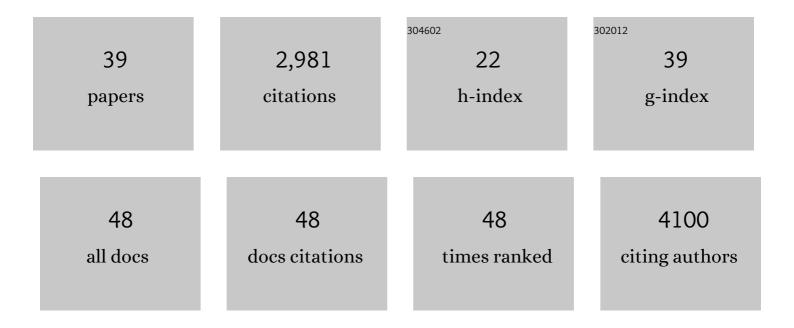
Robson Francisco de Souza

List of Publications by Year in descending order

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Version: 2024-02-01



| # | Article | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | 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 |
| 2 | 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 |
| 3 | 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 |
| 4 | 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 |
| 5 | 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 |
| 6 | Global Distribution and Evolution of Mycobacterium bovis Lineages. Frontiers in Microbiology, 2020, 11, 843. | 1.5 | 37 |
| 7 | The World of Cyclic Dinucleotides in Bacterial Behavior. Molecules, 2020, 25, 2462. | 1.7 | 21 |
| 8 | A Family of T6SS Antibacterial Effectors Related to I,d-Transpeptidases Targets the Peptidoglycan. Cell Reports, 2020, 31, 107813. | 2.9 | 39 |
| 9 | Profiling the rainbow trout hepatic miRNAome under diet-induced hyperglycemia. Physiological Genomics, 2019, 51, 411-431. | 1.0 | 26 |
| 10 | Molecular Epidemiology of Multidrug-Resistant Klebsiella pneumoniae Isolates in a Brazilian Tertiary Hospital. Frontiers in Microbiology, 2019, 10, 1669. | 1.5 | 20 |
| 11 | Assembly of the 373k gene space of the polyploid sugarcane genome reveals reservoirs of functional diversity in the world's leading biomass crop. GigaScience, 2019, 8, . | 3.3 | 106 |
| 12 | A bipartite periplasmic receptor–diguanylate cyclase pair (XAC2383–XAC2382) in the bacterium Xanthomonas citri. Journal of Biological Chemistry, 2018, 293, 10767-10781. | 1.6 | 2 |
| 13 | 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 |
| 14 | 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 |
| 15 | Polyvalent Proteins, a Pervasive Theme in the Intergenomic Biological Conflicts of Bacteriophages and Conjugative Elements. Journal of Bacteriology, 2017, 199, . | 1.0 | 33 |
| 16 | Complete Genome Sequencing of Mycobacterium bovis SP38 and Comparative Genomics of Mycobacterium bovis and M. tuberculosis Strains. Frontiers in Microbiology, 2017, 8, 2389. | 1.5 | 40 |
| 17 | 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 |
| 18 | Lineage-specific expansions of TET/JBP genes and a new class of DNA transposons shape fungal genomic and epigenetic landscapes. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 1676-1683. | 3.3 | 51 |

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|----|--|-----|-----------|
| 19 | Genome Sequence of <i>Streptomyces olindensis</i> DAUFPE 5622, Producer of the Antitumoral Anthracycline Cosmomycin D. Genome Announcements, 2014, 2, . | 0.8 | 8 |
| 20 | The Natural History of ADP-Ribosyltransferases and the ADP-Ribosylation System. Current Topics in Microbiology and Immunology, 2014, 384, 3-32. | 0.7 | 99 |
| 21 | Polymorphic toxin systems: Comprehensive characterization of trafficking modes, processing, mechanisms of action, immunity and ecology using comparative genomics. Biology Direct, 2012, 7, 18. | 1.9 | 440 |
| 22 | Identification of novel components of NAD-utilizing metabolic pathways and prediction of their biochemical functions. Molecular BioSystems, 2012, 8, 1661. | 2.9 | 63 |
| 23 | Gene flow and biological conflict systems in the origin and evolution of eukaryotes. Frontiers in Cellular and Infection Microbiology, 2012, 2, 89. | 1.8 | 67 |
| 24 | Comparative genomics uncovers novel structural and functional features of the heterotrimeric GTPase signaling system. Gene, 2011, 475, 63-78. | 1.0 | 57 |
| 25 | Novel insights into the genomic basis of citrus canker based on the genome sequences of two strains of Xanthomonas fuscans subsp. aurantifolii. BMC Genomics, 2010, 11, 238. | 1.2 | 102 |
| 26 | Predicted class-I aminoacyl tRNA synthetase-like proteins in non-ribosomal peptide synthesis. Biology Direct, 2010, 5, 48. | 1.9 | 45 |
| 27 | Development and validation of a Xanthomonas axonopodis pv. citri DNA microarray platform (XACarray) generated from the shotgun libraries previously used in the sequencing of this bacterial genome. BMC Research Notes, 2010, 3, 150. | 0.6 | 3 |
| 28 | UMA and MABP domains throw light on receptor endocytosis and selection of endosomal cargoes. Bioinformatics, 2010, 26, 1477-1480. | 1.8 | 23 |
| 29 | Origin and evolution of peptide-modifying dioxygenases and identification of the wybutosine hydroxylase/hydroperoxidase. Nucleic Acids Research, 2010, 38, 5261-5279. | 6.5 | 46 |
| 30 | Diversity and evolution of chromatin proteins encoded by DNA viruses. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2010, 1799, 302-318. | 0.9 | 52 |
| 31 | Bioinformatics construction of the human cell surfaceome. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 16752-16757. | 3.3 | 119 |
| 32 | The Anabaena sensory rhodopsin transducer defines a novel superfamily of prokaryotic small-molecule binding domains. Biology Direct, 2009, 4, 25. | 1.9 | 7 |
| 33 | AMIN domains have a predicted role in localization of diverse periplasmic protein complexes. Bioinformatics, 2008, 24, 2423-2426. | 1.8 | 16 |
| 34 | Cytological Characterization of YpsB, a Novel Component of the <i>Bacillus subtilis</i> Divisome. Journal of Bacteriology, 2008, 190, 7096-7107. | 1.0 | 48 |
| 35 | Comparative Analyses ofXanthomonasandXylellaComplete Genomes. OMICS A Journal of Integrative Biology, 2005, 9, 43-76. | 1.0 | 39 |
| 36 | COMPARATIVE GENOMICS ANALYSES OF CITRUS-ASSOCIATED BACTERIA. Annual Review of Phytopathology, 2004, 42, 163-184. | 3.5 | 57 |

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|----|--|------|-----------|
| 37 | Comparison of the genomes of two Xanthomonas pathogens with differing host specificities. Nature, 2002, 417, 459-463. | 13.7 | 1,074 |
| 38 | Genealogical Evidence for Positive Selection in the nef Gene of HIV-1. Genetics, 1999, 153, 1077-1089. | 1.2 | 113 |
| 39 | Tucuxi-BLAST: Enabling fast and accurate record linkage of large-scale health-related administrative databases through a DNA-encoded approach. PeerJ, 0, 10, e13507. | 0.9 | 0 |