

Thiago Motta Venancio

List of Publications by Year in descending order

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Version: 2024-02-01

56
papers

1,699
citations

361388

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330122

37
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78
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78
docs citations

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times ranked

2512
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Genome of <i>Rhodnius prolixus</i> , an insect vector of Chagas disease, reveals unique adaptations to hematophagy and parasite infection. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14936-14941. | 7.1 | 329 |
| 2 | Schistosoma mansoni Tegument Protein Sm29 Is Able to Induce a Th1-Type of Immune Response and Protection against Parasite Infection. PLoS Neglected Tropical Diseases, 2008, 2, e308. | 3.0 | 155 |
| 3 | Interference with Hemozoin Formation Represents an Important Mechanism of Schistosomicidal Action of Antimalarial Quinoline Methanols. PLoS Neglected Tropical Diseases, 2009, 3, e477. | 3.0 | 74 |
| 4 | The <i>Aedes aegypti</i> larval transcriptome: a comparative perspective with emphasis on trypsins and the domain structure of peritrophins. Insect Molecular Biology, 2009, 18, 33-44. | 2.0 | 65 |
| 5 | Transcriptome analysis uncovers key regulatory and metabolic aspects of soybean embryonic axes during germination. Scientific Reports, 2016, 6, 36009. | 3.3 | 64 |
| 6 | Heme Signaling Impacts Global Gene Expression, Immunity and Dengue Virus Infectivity in <i>Aedes aegypti</i> . PLoS ONE, 2015, 10, e0135985. | 2.5 | 60 |
| 7 | Genome sequencing and assessment of plant growth-promoting properties of a <i>Serratia marcescens</i> strain isolated from vermicompost. BMC Genomics, 2018, 19, 750. | 2.8 | 58 |
| 8 | Systematic analysis of 1298 RNA-seq samples and construction of a comprehensive soybean (<i>Glycine</i>) transcriptome. BMC Genomics, 2018, 19, 750. | 3.7 | 54 |
| 9 | CYSTM, a novel cysteine-rich transmembrane module with a role in stress tolerance across eukaryotes. Bioinformatics, 2010, 26, 149-152. | 4.1 | 47 |
| 10 | Uncovering major genomic features of essential genes in <i>Bacteria</i> and a methanogenic <i>Archaea</i> . FEBS Journal, 2015, 282, 3395-3411. | 4.7 | 45 |
| 11 | Effects of <i>Phaseolus vulgaris</i> (Fabaceae) seed coat on the embryonic and larval development of the cowpea weevil <i>Callosobruchus maculatus</i> (Coleoptera: Bruchidae). Journal of Insect Physiology, 2014, 60, 50-57. | 2.0 | 41 |
| 12 | Use of a 44k oligoarray to explore the transcriptome of <i>Schistosoma mansoni</i> adult worms. Experimental Parasitology, 2007, 117, 236-245. | 1.2 | 33 |
| 13 | Identification of the <i>Schistosoma mansoni</i> TNF-Alpha Receptor Gene and the Effect of Human TNF-Alpha on the Parasite Gene Expression Profile. PLoS Neglected Tropical Diseases, 2009, 3, e556. | 3.0 | 33 |
| 14 | Reconstructing the ubiquitin network - cross-talk with other systems and identification of novel functions. Genome Biology, 2009, 10, R33. | 9.6 | 33 |
| 15 | Gender biased differential alternative splicing patterns of the transcriptional cofactor CA150 gene in <i>Schistosoma mansoni</i> . Molecular and Biochemical Parasitology, 2006, 150, 123-131. | 1.1 | 31 |
| 16 | Impact of Whole-Genome and Tandem Duplications in the Expansion and Functional Diversification of the F-Box Family in Legumes (Fabaceae). PLoS ONE, 2013, 8, e55127. | 2.5 | 30 |
| 17 | Transcriptomic analyses uncover emerging roles of mucins, lysosome/secretory addressing and detoxification pathways in insect midguts. Current Opinion in Insect Science, 2018, 29, 34-40. | 4.4 | 30 |
| 18 | Genomic analysis unveils important aspects of population structure, virulence, and antimicrobial resistance in <i>Klebsiella aerogenes</i> . FEBS Journal, 2019, 286, 3797-3810. | 4.7 | 27 |

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|----|--|-----|-----------|
| 19 | SmTRC1, a novel <i>Schistosoma mansoni</i> DNA transposon, discloses new families of animal and fungi transposons belonging to the CACTA superfamily. <i>BMC Evolutionary Biology</i> , 2006, 6, 89. | 3.2 | 25 |
| 20 | Pathogenesis-related protein 1 (PR-1) genes in soybean: Genome-wide identification, structural analysis and expression profiling under multiple biotic and abiotic stresses. <i>Gene</i> , 2022, 809, 146013. | 2.2 | 25 |
| 21 | Evolution and multiple roles of the Pancrustacea specific transcription factor zelda in insects. <i>PLoS Genetics</i> , 2017, 13, e1006868. | 3.5 | 24 |
| 22 | Expansion and diversification of the gibberellin receptor GIBBERELLIN INSENSITIVE DWARF1 (GID1) family in land plants. <i>Plant Molecular Biology</i> , 2018, 97, 435-449. | 3.9 | 22 |
| 23 | BioNERO: an all-in-one R/Bioconductor package for comprehensive and easy biological network reconstruction. <i>Functional and Integrative Genomics</i> , 2022, 22, 131-136. | 3.5 | 22 |
| 24 | Bursts of transposition from non-long terminal repeat retrotransposon families of the RTE clade in <i>Schistosoma mansoni</i> . <i>International Journal for Parasitology</i> , 2010, 40, 743-749. | 3.1 | 21 |
| 25 | Molecular Correlates of Experimental Cerebral Malaria Detectable in Whole Blood. <i>Infection and Immunity</i> , 2011, 79, 1244-1253. | 2.2 | 19 |
| 26 | Transcriptional landscape of soybean (<i>Glycine max</i>) embryonic axes during germination in the presence of paclobutrazol, a gibberellin biosynthesis inhibitor. <i>Scientific Reports</i> , 2019, 9, 9601. | 3.3 | 18 |
| 27 | Synergy of Omeprazole and Praziquantel In Vitro Treatment against <i>Schistosoma mansoni</i> Adult Worms. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0004086. | 3.0 | 17 |
| 28 | Polyploidization events shaped the transcription factor repertoires in legumes (Fabaceae). <i>Plant Journal</i> , 2020, 103, 726-741. | 5.7 | 17 |
| 29 | High-confidence mapping of chemical compounds and protein complexes reveals novel aspects of chemical stress response in yeast. <i>Molecular BioSystems</i> , 2009, 6, 175-181. | 2.9 | 16 |
| 30 | Apprehending multicellularity: Regulatory networks, genomics, and evolution. <i>Birth Defects Research Part C: Embryo Today Reviews</i> , 2009, 87, 143-164. | 3.6 | 15 |
| 31 | Reconstructing prokaryotic transcriptional regulatory networks: lessons from actinobacteria. <i>Journal of Biology</i> , 2009, 8, 29. | 2.7 | 14 |
| 32 | Transcription factors, chromatin proteins and the diversification of Hemiptera. <i>Insect Biochemistry and Molecular Biology</i> , 2016, 69, 1-13. | 2.7 | 14 |
| 33 | Population structure and pangenome analysis of <i>Enterobacter bugandensis</i> uncover the presence of blaCTX-M-55, blaNDM-5 and blaIMI-1, along with sophisticated iron acquisition strategies. <i>Genomics</i> , 2020, 112, 1182-1191. | 2.9 | 14 |
| 34 | Structural and Functional Characterization of the Protein Kinase Mps1 in <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2012, 7, e45707. | 2.5 | 13 |
| 35 | Robustness and evolvability in natural chemical resistance: identification of novel systems properties, biochemical mechanisms and regulatory interactions. <i>Molecular BioSystems</i> , 2010, 6, 1475. | 2.9 | 12 |
| 36 | Development of a Gene-Centered SSR Atlas as a Resource for Papaya (<i>Carica papaya</i>) Marker-Assisted Selection and Population Genetic Studies. <i>PLoS ONE</i> , 2014, 9, e112654. | 2.5 | 12 |

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|----|--|-----|-----------|
| 37 | Phylogenetic analysis and population structure of <i>Pseudomonas alloputida</i> . <i>Genomics</i> , 2021, 113, 3762-3773. | 2.9 | 12 |
| 38 | Analysis of <i>Schistosoma mansoni</i> genes shared with <i>Deuterostomia</i> and with possible roles in host interactions. <i>BMC Genomics</i> , 2007, 8, 407. | 2.8 | 11 |
| 39 | Molecular epidemiology of 16S rRNA methyltransferase in Brazil: RmtG in <i>Klebsiella aerogenes</i> ST93 (CC4). <i>Anais Da Academia Brasileira De Ciencias</i> , 2019, 91, e20180762. | 0.8 | 11 |
| 40 | Genome Sequencing of Four Multidrug-Resistant <i>Enterobacter aerogenes</i> Isolates from Hospitalized Patients in Brazil. <i>Frontiers in Microbiology</i> , 2016, 7, 1649. | 3.5 | 10 |
| 41 | Genome-Wide Analysis of the COBRA-Like Gene Family Supports Gene Expansion through Whole-Genome Duplication in Soybean (<i>Glycine max</i>). <i>Plants</i> , 2021, 10, 167. | 3.5 | 10 |
| 42 | Integration of genome-wide association studies and gene coexpression networks unveils promising soybean resistance genes against five common fungal pathogens. <i>Scientific Reports</i> , 2021, 11, 24453. | 3.3 | 10 |
| 43 | Curupira-1 and Curupira-2, two novel Mutator-like DNA transposons from the genomes of human parasites <i>Schistosoma mansoni</i> and <i>Schistosoma japonicum</i> . <i>Parasitology</i> , 2011, 138, 1124-1133. | 1.5 | 8 |
| 44 | De novo transcriptome sequencing and comparative analysis of midgut tissues of four non-model insects pertaining to Hemiptera, Coleoptera, Diptera and Lepidoptera. <i>Gene</i> , 2017, 627, 85-93. | 2.2 | 8 |
| 45 | Cell wall dynamics and gene expression on soybean embryonic axes during germination. <i>Planta</i> , 2019, 250, 1325-1337. | 3.2 | 8 |
| 46 | Exploring the complexity of soybean (<i>Glycine max</i>) transcriptional regulation using global gene co-expression networks. <i>Planta</i> , 2020, 252, 104. | 3.2 | 8 |
| 47 | Evolutionary and Biochemical Aspects of Chemical Stress Resistance in <i>Saccharomyces cerevisiae</i> . <i>Frontiers in Genetics</i> , 2012, 3, 47. | 2.3 | 7 |
| 48 | Integrating omics approaches to discover and prioritize candidate genes involved in oil biosynthesis in soybean. <i>Gene</i> , 2022, 808, 145976. | 2.2 | 7 |
| 49 | Evolutionary analysis of multidrug resistance genes in fungi—Impact of gene duplication and family conservation. <i>FEBS Journal</i> , 2014, 281, 4967-4977. | 4.7 | 6 |
| 50 | A Chemogenomic Screen Reveals Novel Snf1p/AMPK Independent Regulators of Acetyl-CoA Carboxylase. <i>PLoS ONE</i> , 2017, 12, e0169682. | 2.5 | 6 |
| 51 | New insights about host response to smallpox using microarray data. <i>BMC Systems Biology</i> , 2007, 1, 38. | 3.0 | 5 |
| 52 | Characterization of cellular, biochemical and genomic features of the diazotrophic plant growth-promoting bacterium <i>Azospirillum</i> sp. UENF-412522, a novel member of the <i>Azospirillum</i> genus. <i>Microbiological Research</i> , 2022, 254, 126896. | 5.3 | 5 |
| 53 | The state of the art in soybean transcriptomics resources and gene coexpression networks. <i>In Silico Plants</i> , 2021, 3, . | 1.9 | 4 |
| 54 | Genome sequencing of the vermicompost strain <i>Stenotrophomonas maltophilia</i> UENF-4GII and population structure analysis of the <i>S. maltophilia</i> Sm3 genogroup. <i>Microbiological Research</i> , 2022, 255, 126923. | 5.3 | 4 |

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|----|--|-----|-----------|
| 55 | Zika virus infection drives epigenetic modulation of immunity by the histone acetyltransferase CBP of <i>Aedes aegypti</i> . <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010559. | 3.0 | 2 |
| 56 | Maternal or zygotic: Unveiling the secrets of the Pancrustacea transcription factor zelda. <i>PLoS Genetics</i> , 2018, 14, e1007201. | 3.5 | 1 |