

Thiago Motta Venancio

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

61
papers

1,162
citations

18
h-index

32
g-index

78
ext. papers

1,490
ext. citations

4.6
avg, IF

4.2
L-index

#	Paper	IF	Citations
61	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	3.8	3
60	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	1
59	Integrating omics approaches to discover and prioritize candidate genes involved in oil biosynthesis in soybean. <i>Gene</i> , 2022 , 808, 145976	3.8	0
58	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> , 2021 , 255, 126923	5.3	2
57	BioNERO: an all-in-one R/Bioconductor package for comprehensive and easy biological network reconstruction. <i>Functional and Integrative Genomics</i> , 2021 , 1	3.8	1
56	The state of the art in soybean transcriptomics resources and gene coexpression networks. <i>In Silico Plants</i> , 2021 , 3,	3.2	2
55	Phylogenetic analysis and population structure of <i>Pseudomonas alloputida</i> . <i>Genomics</i> , 2021 , 113, 3762-3773	4.3	1
54	Genome-Wide Analysis of the Gene Family Supports Gene Expansion through Whole-Genome Duplication in Soybean (). <i>Plants</i> , 2021 , 10,	4.5	3
53	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	4.9	0
52	Polyploidization events shaped the transcription factor repertoires in legumes (Fabaceae). <i>Plant Journal</i> , 2020 , 103, 726-741	6.9	5
51	Systematic analysis of 1298 RNA-Seq samples and construction of a comprehensive soybean (<i>Glycine max</i>) expression atlas. <i>Plant Journal</i> , 2020 , 103, 1894-1909	6.9	25
50	Exploring the complexity of soybean (<i>Glycine max</i>) transcriptional regulation using global gene co-expression networks. <i>Planta</i> , 2020 , 252, 104	4.7	4
49	Population structure and pangenome analysis of <i>Enterobacter bugandensis</i> uncover the presence of <i>bla</i> , <i>bla</i> and <i>bla</i> , along with sophisticated iron acquisition strategies. <i>Genomics</i> , 2020 , 112, 1182-1191	4.3	7
48	Genomic analysis unveils important aspects of population structure, virulence, and antimicrobial resistance in <i>Klebsiella aerogenes</i> . <i>FEBS Journal</i> , 2019 , 286, 3797-3810	5.7	11
47	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	4.9	15
46	Cell wall dynamics and gene expression on soybean embryonic axes during germination. <i>Planta</i> , 2019 , 250, 1325-1337	4.7	7
45	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	1.4	6

44	Transcriptomic analyses uncover emerging roles of mucins, lysosome/secretory addressing and detoxification pathways in insect midguts. <i>Current Opinion in Insect Science</i> , 2018 , 29, 34-40	5.1	12
43	Maternal or zygotic: Unveiling the secrets of the Pancrustacea transcription factor zelda. <i>PLoS Genetics</i> , 2018 , 14, e1007201	6	1
42	Genome sequencing and assessment of plant growth-promoting properties of a <i>Serratia marcescens</i> strain isolated from vermicompost. <i>BMC Genomics</i> , 2018 , 19, 750	4.5	34
41	Expansion and diversification of the gibberellin receptor GIBBERELLIN INSENSITIVE DWARF1 (GID1) family in land plants. <i>Plant Molecular Biology</i> , 2018 , 97, 435-449	4.6	13
40	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	3.8	7
39	Evolution and multiple roles of the Pancrustacea specific transcription factor zelda in insects. <i>PLoS Genetics</i> , 2017 , 13, e1006868	6	18
38	A Chemogenomic Screen Reveals Novel Snf1p/AMPK Independent Regulators of Acetyl-CoA Carboxylase. <i>PLoS ONE</i> , 2017 , 12, e0169682	3.7	4
37	Transcription factors, chromatin proteins and the diversification of Hemiptera. <i>Insect Biochemistry and Molecular Biology</i> , 2016 , 69, 1-13	4.5	11
36	Transcriptome analysis uncovers key regulatory and metabolic aspects of soybean embryonic axes during germination. <i>Scientific Reports</i> , 2016 , 6, 36009	4.9	49
35	Genome Sequencing of Four Multidrug-Resistant Isolates from Hospitalized Patients in Brazil. <i>Frontiers in Microbiology</i> , 2016 , 7, 1649	5.7	7
34	Uncovering major genomic features of essential genes in Bacteria and a methanogenic Archaea. <i>FEBS Journal</i> , 2015 , 282, 3395-3411	5.7	23
33	Synergy of Omeprazole and Praziquantel In Vitro Treatment against <i>Schistosoma mansoni</i> Adult Worms. <i>PLoS Neglected Tropical Diseases</i> , 2015 , 9, e0004086	4.8	16
32	Heme Signaling Impacts Global Gene Expression, Immunity and Dengue Virus Infectivity in <i>Aedes aegypti</i> . <i>PLoS ONE</i> , 2015 , 10, e0135985	3.7	35
31	Genome of <i>Rhodnius prolixus</i> , an insect vector of Chagas disease, reveals unique adaptations to hematophagy and parasite infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 14936-41	11.5	220
30	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). <i>Journal of Insect Physiology</i> , 2014 , 60, 50-7	2.4	32
29	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	3.7	10
28	Impact of whole-genome and tandem duplications in the expansion and functional diversification of the F-box family in legumes (Fabaceae). <i>PLoS ONE</i> , 2013 , 8, e55127	3.7	24
27	Structural and functional characterization of the protein kinase Mps1 in <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2012 , 7, e45707	3.7	13

26	Evolutionary and Biochemical Aspects of Chemical Stress Resistance in <i>Saccharomyces cerevisiae</i> . <i>Frontiers in Genetics</i> , 2012 , 3, 47	4.5	7
25	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, 1124-33	2.7	4
24	Molecular correlates of experimental cerebral malaria detectable in whole blood. <i>Infection and Immunity</i> , 2011 , 79, 1244-53	3.7	14
23	CYSTM, a novel cysteine-rich transmembrane module with a role in stress tolerance across eukaryotes. <i>Bioinformatics</i> , 2010 , 26, 149-52	7.2	33
22	Robustness and evolvability in natural chemical resistance: identification of novel systems properties, biochemical mechanisms and regulatory interactions. <i>Molecular BioSystems</i> , 2010 , 6, 1475-91		10
21	High-confidence mapping of chemical compounds and protein complexes reveals novel aspects of chemical stress response in yeast. <i>Molecular BioSystems</i> , 2010 , 6, 175-81		12
20	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, 743-9	4.3	14
19	Interference with hemozoin formation represents an important mechanism of schistosomicidal action of antimalarial quinoline methanols. <i>PLoS Neglected Tropical Diseases</i> , 2009 , 3, e477	4.8	64
18	Identification of the <i>Schistosoma mansoni</i> TNF-alpha receptor gene and the effect of human TNF-alpha on the parasite gene expression profile. <i>PLoS Neglected Tropical Diseases</i> , 2009 , 3, e556	4.8	27
17	Apprehending multicellularity: regulatory networks, genomics, and evolution. <i>Birth Defects Research Part C: Embryo Today Reviews</i> , 2009 , 87, 143-64		13
16	Reconstructing prokaryotic transcriptional regulatory networks: lessons from actinobacteria. <i>Journal of Biology</i> , 2009 , 8, 29		13
15	The <i>Aedes aegypti</i> larval transcriptome: a comparative perspective with emphasis on trypsins and the domain structure of peritrophins. <i>Insect Molecular Biology</i> , 2009 , 18, 33-44	3.4	50
14	Reconstructing the ubiquitin network: cross-talk with other systems and identification of novel functions. <i>Genome Biology</i> , 2009 , 10, R33	18.3	29
13	<i>Schistosoma mansoni</i> tegument protein Sm29 is able to induce a Th1-type of immune response and protection against parasite infection. <i>PLoS Neglected Tropical Diseases</i> , 2008 , 2, e308	4.8	135
12	New insights about host response to smallpox using microarray data. <i>BMC Systems Biology</i> , 2007 , 1, 38	3.5	4
11	Analysis of <i>Schistosoma mansoni</i> genes shared with Deuterostomia and with possible roles in host interactions. <i>BMC Genomics</i> , 2007 , 8, 407	4.5	9
10	Use of a 44k oligoarray to explore the transcriptome of <i>Schistosoma mansoni</i> adult worms. <i>Experimental Parasitology</i> , 2007 , 117, 236-45	2.1	32
9	Gender biased differential alternative splicing patterns of the transcriptional cofactor CA150 gene in <i>Schistosoma mansoni</i> . <i>Molecular and Biochemical Parasitology</i> , 2006 , 150, 123-31	1.9	30

8	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	23
7	Polyplodization events shaped the transcription factor repertoires in legumes (Fabaceae)		1
6	Systematic analysis of 1,298 RNA-Seq samples and construction of a comprehensive soybean (<i>Glycine max</i>) expression atlas		2
5	Exploring the complexity of soybean (<i>Glycine max</i>) transcriptional regulation using global gene co-expression networks		2
4	Phylogenetic and population structure analyses uncover pervasive misclassification and help assessing the biosafety of <i>Pseudomonas alloputida</i> for biotechnological applications		1
3	Pathogenesis-related protein 1 (PR-1) genes in soybean: genome-wide identification, structural analysis and expression profiling under multiple biotic and abiotic stresses		2
2	BioNERO: an all-in-one R/Bioconductor package for comprehensive and easy biological network reconstruction		
1	cageminer: an R/Bioconductor package to prioritize candidate genes by integrating GWAS and gene coexpression networks		1