

Vinicius Maracaja-Coutinho

List of Publications by Year in descending order

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49
papers

1,545
citations

304602

22
h-index

330025

37
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all docs

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docs citations

53
times ranked

2735
citing authors

#	ARTICLE	IF	CITATIONS
1	Insights into agar and secondary metabolite pathways from the genome of the red alga <i>Gracilaria domingensis</i> (Rhodophyta, Gracilariales). <i>Journal of Phycology</i> , 2022, 58, 406-423.	1.0	10
2	Small RNA Expression Profiling Reveals hsa-miR-181d-5p Downregulation Associated With TNF- α Overexpression in Sjögren's Syndrome Patients. <i>Frontiers in Immunology</i> , 2022, 13, 870094.	2.2	6
3	Computational Analysis of and CircRNAs in. <i>Methods in Molecular Biology</i> , 2021, 2362, 147-172.	0.4	1
4	RNAmining: A machine learning stand-alone and web server tool for RNA coding potential prediction. <i>F1000Research</i> , 2021, 10, 323.	0.8	1
5	Deletion of hippocampal Glucocorticoid receptors unveils sex-biased microRNA expression and neuronal morphology alterations in mice. <i>Neurobiology of Stress</i> , 2021, 14, 100306.	1.9	8
6	Development of a Multiplex PCR Assay for Genotyping the Fish Pathogen <i>Piscirickettsia salmonis</i> Through Comparative Genomics. <i>Frontiers in Microbiology</i> , 2021, 12, 673216.	1.5	6
7	RNAmining: A machine learning stand-alone and web server tool for RNA coding potential prediction. <i>F1000Research</i> , 2021, 10, 323.	0.8	7
8	OUTBREAK: a user-friendly georeferencing online tool for disease surveillance. <i>Biological Research</i> , 2021, 54, 20.	1.5	4
9	Sex-Dependent Changes of miRNA Levels in the Hippocampus of Adrenalectomized Rats Following Acute Corticosterone Administration. <i>ACS Chemical Neuroscience</i> , 2021, 12, 2981-3001.	1.7	7
10	Long non-coding RNAs associated with infection and vaccine-induced immunity. <i>Essays in Biochemistry</i> , 2021, 65, 657-669.	2.1	5
11	Novel molecular insights and public omics data in pulmonary hypertension. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2021, 1867, 166200.	1.8	6
12	Genome-wide analysis of in vivo CcpA binding with and without its key cofactor HPr in the major human pathogen group A <i>Streptococcus</i> . <i>Molecular Microbiology</i> , 2021, 115, 1207-1228.	1.2	11
13	Network-Based Approaches Reveal Potential Therapeutic Targets for Host-Directed Antileishmanial Therapy Driving Drug Repurposing. <i>Microbiology Spectrum</i> , 2021, 9, e0101821.	1.2	9
14	Epigenetic Reader BRD4 (Bromodomain-Containing Protein 4) Governs Nucleus-Encoded Mitochondrial Transcriptome to Regulate Cardiac Function. <i>Circulation</i> , 2020, 142, 2356-2370.	1.6	47
15	CORAZON: a web server for data normalization and unsupervised clustering based on expression profiles. <i>BMC Research Notes</i> , 2020, 13, 338.	0.6	5
16	Editorial: User-Friendly Tools Applied to Genetics or Systems Biology. <i>Frontiers in Genetics</i> , 2020, 11, 985.	1.1	1
17	Human adipose-derived mesenchymal stem cell-conditioned medium ameliorates polyneuropathy and foot ulceration in diabetic BKS db/db mice. <i>Stem Cell Research and Therapy</i> , 2020, 11, 168.	2.4	60
18	Angiotensin-(1-9) prevents cardiomyocyte hypertrophy by controlling mitochondrial dynamics via miR-129-3p/PKIA pathway. <i>Cell Death and Differentiation</i> , 2020, 27, 2586-2604.	5.0	29

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19	Mitochondrial transfer from MSCs to T cells induces Treg differentiation and restricts inflammatory response. <i>EMBO Reports</i> , 2020, 21, e48052.	2.0	129
20	Down syndrome and Alzheimer's disease: common molecular traits beyond the amyloid precursor protein. <i>Aging</i> , 2020, 12, 1011-1033.	1.4	48
21	Assessing the Impact of Sample Heterogeneity on Transcriptome Analysis of Human Diseases Using MDP Webtool. <i>Frontiers in Genetics</i> , 2019, 10, 971.	1.1	17
22	Long noncoding RNAs are involved in multiple immunological pathways in response to vaccination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17121-17126.	3.3	58
23	Predicting RNA Families in Nucleotide Sequences Using StructRNAfinder. <i>Methods in Molecular Biology</i> , 2019, 1962, 15-27.	0.4	2
24	webCEMiTool: Co-expression Modular Analysis Made Easy. <i>Frontiers in Genetics</i> , 2019, 10, 146.	1.1	27
25	Prediction of MicroRNAs in the Epstein-Barr Virus Reveals Potential Targets for the Viral Self-Regulation. <i>Indian Journal of Microbiology</i> , 2019, 59, 73-80.	1.5	2
26	Noncoding RNAs Databases: Current Status and Trends. <i>Methods in Molecular Biology</i> , 2019, 1912, 251-285.	0.4	27
27	A regulatory RNA is involved in RNA duplex formation and biofilm regulation in <i>Sulfolobus acidocaldarius</i> . <i>Nucleic Acids Research</i> , 2018, 46, 4794-4806.	6.5	32
28	Genome-wide circulating microRNA expression profiling reveals potential biomarkers for amyotrophic lateral sclerosis. <i>Neurobiology of Aging</i> , 2018, 64, 123-138.	1.5	53
29	StructRNAfinder: an automated pipeline and web server for RNA families prediction. <i>BMC Bioinformatics</i> , 2018, 19, 55.	1.2	42
30	Core non-coding RNAs of <i>Piscirickettsia salmonis</i> . <i>PLoS ONE</i> , 2018, 13, e0197206.	1.1	7
31	Long Non-Coding RNAs Responsive to Salt and Boron Stress in the Hyper-Arid Luteo Maize from Atacama Desert. <i>Genes</i> , 2018, 9, 170.	1.0	53
32	CEMiTool: a Bioconductor package for performing comprehensive modular co-expression analyses. <i>BMC Bioinformatics</i> , 2018, 19, 56.	1.2	215
33	Genomic positional conservation identifies topological anchor point RNAs linked to developmental loci. <i>Genome Biology</i> , 2018, 19, 32.	3.8	114
34	LeishDB: a database of coding gene annotation and non-coding RNAs in <i>Leishmania braziliensis</i> . <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	21
35	Comparative Pan-Genome Analysis of <i>Piscirickettsia salmonis</i> Reveals Genomic Divergences within Genogroups. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 459.	1.8	52
36	miRQuest: integration of tools on a Web server for microRNA research. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	7

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37	A Guide to Scientific Crowdfunding. <i>PLoS Biology</i> , 2016, 14, e1002373.	2.6	39
38	A Novel Method to Predict Genomic Islands Based on Mean Shift Clustering Algorithm. <i>PLoS ONE</i> , 2016, 11, e0146352.	1.1	31
39	Complete Genome Sequence of <i>Salmonella enterica</i> Serovar Enteritidis Bacteriophage f18SE, Isolated in Chile. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
40	Deep Sequencing Reveals the Complete Genome and Evidence for Transcriptional Activity of the First Virus-Like Sequences Identified in <i>Aristotelia chilensis</i> (Maqui Berry). <i>Viruses</i> , 2015, 7, 1685-1699.	1.5	6
41	Draft Genome Sequence of Virulent Strain AUSTRAL-005 of <i>Piscirickettsia salmonis</i> , the Etiological Agent of <i>Piscirickettsiosis</i> . <i>Genome Announcements</i> , 2014, 2, .	0.8	25
42	Draft Genome of Chilean Honeybee (<i>Apis mellifera</i>) Gut Strain <i>Lactobacillus kunkeei</i> MP2. <i>Genome Announcements</i> , 2014, 2, .	0.8	5
43	Expression analysis and in silico characterization of intronic long noncoding RNAs in renal cell carcinoma: emerging functional associations. <i>Molecular Cancer</i> , 2013, 12, 140.	7.9	59
44	Non-coding transcription characterization and annotation. <i>RNA Biology</i> , 2012, 9, 274-282.	1.5	45
45	Non-coding RNAs in schistosomes: an unexplored world. <i>Anais Da Academia Brasileira De Ciencias</i> , 2011, 83, 673-694.	0.3	36
46	Relation of pretreatment sequence diversity in NS5A region of HCV genotype 1 with immune response between pegylated-INF/ribavirin therapy outcomes. <i>Journal of Viral Hepatitis</i> , 2011, 18, 142-148.	1.0	5
47	Long noncoding intronic RNAs are differentially expressed in primary and metastatic pancreatic cancer. <i>Molecular Cancer</i> , 2011, 10, 141.	7.9	153
48	Schizophrenia, brain disease and meta-analyses: Integrating the pieces and testing Fusar-Poliâ€™s hypothesis. <i>Medical Hypotheses</i> , 2010, 74, 142-144.	0.8	2
49	Comparative Profiling of Circulating Exosomal Small RNAs Derived From Peruvian Patients With Tuberculosis and Pulmonary Adenocarcinoma. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	5