Vinicius Maracaja-Coutinho

List of Publications by Year
in descending order

49 papers	1,545 citations	304602 22 h-index	330025 37 g-index
53 all docs	53 docs citations	53 times ranked	2735 citing authors

#	Article	IF	Citations
1	CEMiTool: a Bioconductor package for performing comprehensive modular co-expression analyses. BMC Bioinformatics, 2018, 19, 56.	1.2	215
2	Long noncoding intronic RNAs are differentially expressed in primary and metastatic pancreatic cancer. Molecular Cancer, 2011, 10, 141.	7.9	153
3	Mitochondrial transfer from MSCs to T cells induces Treg differentiation and restricts inflammatory response. EMBO Reports, 2020, 21, e48052.	2.0	129
4	Genomic positional conservation identifies topological anchor point RNAs linked to developmental loci. Genome Biology, 2018, 19, 32.	3.8	114
5	Human adipose-derived mesenchymal stem cell-conditioned medium ameliorates polyneuropathy and foot ulceration in diabetic BKS db/db mice. Stem Cell Research and Therapy, 2020, 11, 168.	2.4	60
6	Expression analysis and in silico characterization of intronic long noncoding RNAs in renal cell carcinoma: emerging functional associations. Molecular Cancer, 2013, 12, 140.	7.9	59
7	Long noncoding RNAs are involved in multiple immunological pathways in response to vaccination. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17121-17126.	3.3	58
8	Genome-wide circulating microRNA expression profiling reveals potential biomarkers for amyotrophic lateral sclerosis. Neurobiology of Aging, 2018, 64, 123-138.	1.5	53
9	Long Non-Coding RNAs Responsive to Salt and Boron Stress in the Hyper-Arid Lluteño Maize from Atacama Desert. Genes, 2018, 9, 170.	1.0	53
10	Comparative Pan-Genome Analysis of Piscirickettsia salmonis Reveals Genomic Divergences within Genogroups. Frontiers in Cellular and Infection Microbiology, 2017, 7, 459.	1.8	52
11	Down syndrome and Alzheimer's disease: common molecular traits beyond the amyloid precursor protein. Aging, 2020, 12, 1011-1033.	1.4	48
12	Epigenetic Reader BRD4 (Bromodomain-Containing Protein 4) Governs Nucleus-Encoded Mitochondrial Transcriptome to Regulate Cardiac Function. Circulation, 2020, 142, 2356-2370.	1.6	47
13	Non-coding transcription characterization and annotation. RNA Biology, 2012, 9, 274-282.	1.5	45
14	StructRNAfinder: an automated pipeline and web server for RNA families prediction. BMC Bioinformatics, 2018, 19, 55.	1.2	42
15	A Guide to Scientific Crowdfunding. PLoS Biology, 2016, 14, e1002373.	2.6	39
16	Non-coding RNAs in schistosomes: an unexplored world. Anais Da Academia Brasileira De Ciencias, 2011, 83, 673-694.	0.3	36
17	A regulatory RNA is involved in RNA duplex formation and biofilm regulation in Sulfolobus acidocaldarius. Nucleic Acids Research, 2018, 46, 4794-4806.	6.5	32
18	A Novel Method to Predict Genomic Islands Based on Mean Shift Clustering Algorithm. PLoS ONE, 2016, 11, e0146352.	1.1	31

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19	Angiotensin-(1–9) prevents cardiomyocyte hypertrophy by controlling mitochondrial dynamics via miR-129-3p/PKIA pathway. Cell Death and Differentiation, 2020, 27, 2586-2604.	5.0	29
20	webCEMiTool: Co-expression Modular Analysis Made Easy. Frontiers in Genetics, 2019, 10, 146.	1.1	27
21	Noncoding RNAs Databases: Current Status and Trends. Methods in Molecular Biology, 2019, 1912, 251-285.	0.4	27
22	Draft Genome Sequence of Virulent Strain AUSTRAL-005 of Piscirickettsia salmonis, the Etiological Agent of Piscirickettsiosis. Genome Announcements, 2014, 2, .	0.8	25
23	LeishDB: a database of coding gene annotation and non-coding RNAs in Leishmania braziliensis. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	21
24	Assessing the Impact of Sample Heterogeneity on Transcriptome Analysis of Human Diseases Using MDP Webtool. Frontiers in Genetics, 2019, 10, 971.	1.1	17
25	Genome-wide analysis of in vivo CcpA binding with and without its key co-factor HPr in the major human pathogen group A *Streptococcus*. Molecular Microbiology, 2021, 115, 1207-1228.	1.2	11
26	Insights into agar and secondary metabolite pathways from the genome of the red alga *Gracilaria domingensis* (Rhodophyta, Gracilariales). Journal of Phycology, 2022, 58, 406-423.	1.0	10
27	Network-Based Approaches Reveal Potential Therapeutic Targets for Host-Directed Antileishmanial Therapy Driving Drug Repurposing. Microbiology Spectrum, 2021, 9, e0101821.	1.2	9
28	Deletion of hippocampal Glucocorticoid receptors unveils sex-biased microRNA expression and neuronal morphology alterations in mice. Neurobiology of Stress, 2021, 14, 100306.	1.9	8
29	miRQuest: integration of tools on a Web server for microRNA research. Genetics and Molecular Research, 2016, 15, .	0.3	7
30	Core non-coding RNAs of Piscirickettsia salmonis. PLoS ONE, 2018, 13, e0197206.	1.1	7
31	RNAmining: A machine learning stand-alone and web server tool for RNA coding potential prediction. F1000Research, 2021, 10, 323.	0.8	7
32	Sex-Dependent Changes of miRNA Levels in the Hippocampus of Adrenalectomized Rats Following Acute Corticosterone Administration. ACS Chemical Neuroscience, 2021, 12, 2981-3001.	1.7	7
33	Deep Sequencing Reveals the Complete Genome and Evidence for Transcriptional Activity of the First Virus-Like Sequences Identified in Aristotelia chilensis (Maqui Berry). Viruses, 2015, 7, 1685-1699.	1.5	6
34	Development of a Multiplex PCR Assay for Genotyping the Fish Pathogen Piscirickettsia salmonis Through Comparative Genomics. Frontiers in Microbiology, 2021, 12, 673216.	1.5	6
35	Novel molecular insights and public omics data in pulmonary hypertension. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2021, 1867, 166200.	1.8	6
36	Small RNA Expression Profiling Reveals hsa-miR-181d-5p Downregulation Associated With TNF-α Overexpression in Sjögren's Syndrome Patients. Frontiers in Immunology, 2022, 13, 870094.	2.2	6

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37	Relation of pretreatment sequence diversity in NS5A region of HCV genotype 1 with immune response between pegylated-INF/ribavirin therapy outcomes. Journal of Viral Hepatitis, 2011, 18, 142-148.	1.0	5
38	Draft Genome of Chilean Honeybee (Apis mellifera) Gut Strain Lactobacillus kunkeei MP2. Genome Announcements, 2014, 2, .	0.8	5
39	Complete Genome Sequence of Salmonella enterica Serovar Enteritidis Bacteriophage f18SE, Isolated in Chile. Genome Announcements, 2015, 3, .	0.8	5
40	CORAZON: a web server for data normalization and unsupervised clustering based on expression profiles. BMC Research Notes, 2020, 13, 338.	0.6	5
41	Long non-coding RNAs associated with infection and vaccine-induced immunity. Essays in Biochemistry, 2021, 65, 657-669.	2.1	5
42	Comparative Profiling of Circulating Exosomal Small RNAs Derived From Peruvian Patients With Tuberculosis and Pulmonary Adenocarcinoma. Frontiers in Cellular and Infection Microbiology, 0, 12, .	1.8	5
43	OUTBREAK: a user-friendly georeferencing online tool for disease surveillance. Biological Research, 2021, 54, 20.	1.5	4
44	Schizophrenia, brain disease and meta-analyses: Integrating the pieces and testing Fusar-Poli's hypothesis. Medical Hypotheses, 2010, 74, 142-144.	0.8	2
45	Predicting RNA Families in Nucleotide Sequences Using StructRNAfinder. Methods in Molecular Biology, 2019, 1962, 15-27.	0.4	2
46	Prediction of MicroRNAs in the Epstein–Barr Virus Reveals Potential Targets for the Viral Self-Regulation. Indian Journal of Microbiology, 2019, 59, 73-80.	1.5	2
47	Editorial: User-Friendly Tools Applied to Genetics or Systems Biology. Frontiers in Genetics, 2020, 11, 985.	1.1	1
48	Computational Analysis of and CircRNAs in. Methods in Molecular Biology, 2021, 2362, 147-172.	0.4	1
49	RNAmining: A machine learning stand-alone and web server tool for RNA coding potential prediction. F1000Research, 2021, 10, 323.	0.8	1