

Eduardo Moraes Rego Reis

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

2,781
citations

201674

27
h-index

175258

52
g-index

54
all docs

54
docs citations

54
times ranked

4199
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptome analysis of the acoelomate human parasite <i>Schistosoma mansoni</i> . <i>Nature Genetics</i> , 2003, 35, 148-157.	21.4	433
2	Genome mapping and expression analyses of human intronic noncoding RNAs reveal tissue-specific patterns and enrichment in genes related to regulation of transcription. <i>Genome Biology</i> , 2007, 8, R43.	9.6	209
3	The Intronic Long Noncoding RNA ANRASSF1 Recruits PRC2 to the RASSF1A Promoter, Reducing the Expression of RASSF1A and Increasing Cell Proliferation. <i>PLoS Genetics</i> , 2013, 9, e1003705.	3.5	180
4	Long noncoding intronic RNAs are differentially expressed in primary and metastatic pancreatic cancer. <i>Molecular Cancer</i> , 2011, 10, 141.	19.2	153
5	Antisense intronic non-coding RNA levels correlate to the degree of tumor differentiation in prostate cancer. <i>Oncogene</i> , 2004, 23, 6684-6692.	5.9	150
6	Perspectives of Long Non-Coding RNAs in Cancer Diagnostics. <i>Frontiers in Genetics</i> , 2012, 3, 32.	2.3	131
7	The contribution of 700,000 ORF sequence tags to the definition of the human transcriptome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 12103-12108.	7.1	123
8	Mitochondrial superoxide dismutase is essential for ethanol tolerance of <i>Saccharomyces cerevisiae</i> in the post-diauxic phase. <i>Microbiology (United Kingdom)</i> , 1997, 143, 1649-1656.	1.8	116
9	The generation and utilization of a cancer-oriented representation of the human transcriptome by using expressed sequence tags. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 13418-13423.	7.1	105
10	Acquisition of Ethanol Tolerance in <i>Saccharomyces cerevisiae</i> : The Key Role of the Mitochondrial Superoxide Dismutase. <i>Archives of Biochemistry and Biophysics</i> , 1993, 300, 608-614.	3.0	75
11	Androgen responsive intronic non-coding RNAs. <i>BMC Biology</i> , 2007, 5, 4.	3.8	73
12	Gene expression arrays in cancer research: methods and applications. <i>Critical Reviews in Oncology/Hematology</i> , 2005, 54, 95-105.	4.4	72
13	Conserved tissue expression signatures of intronic noncoding RNAs transcribed from human and mouse loci. <i>Genomics</i> , 2008, 92, 18-25.	2.9	66
14	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.	19.2	59
15	Global analysis of biogenesis, stability and sub-cellular localization of lncRNAs mapping to intragenic regions of the human genome. <i>RNA Biology</i> , 2015, 12, 877-892.	3.1	59
16	A new tick Kunitz type inhibitor, Amblyomin-X, induces tumor cell death by modulating genes related to the cell cycle and targeting the ubiquitin-proteasome system. <i>Toxicon</i> , 2010, 56, 1145-1154.	1.6	58
17	Large-scale Transcriptome Analyses Reveal New Genetic Marker Candidates of Head, Neck, and Thyroid Cancer. <i>Cancer Research</i> , 2005, 65, 1693-1699.	0.9	55
18	Identification of protein-coding and intronic noncoding RNAs down-regulated in clear cell renal carcinoma. <i>Molecular Carcinogenesis</i> , 2008, 47, 757-767.	2.7	45

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19	Transcriptome of iPSC-derived neuronal cells reveals a module of co-expressed genes consistently associated with autism spectrum disorder. <i>Molecular Psychiatry</i> , 2021, 26, 1589-1605.	7.9	44
20	As Antisense RNA Gets Intronic. <i>OMICS A Journal of Integrative Biology</i> , 2005, 9, 2-12.	2.0	37
21	ESTWeb: bioinformatics services for EST sequencing projects. <i>Bioinformatics</i> , 2003, 19, 1587-1588.	4.1	36
22	Detailed molecular characterization of cord blood-derived endothelial progenitors. <i>Experimental Hematology</i> , 2008, 36, 193.e1-193.e15.	0.4	33
23	Transcriptional profiling of <i>Neurospora crassa</i> \hat{m} ak-2 reveals that mitogen-activated protein kinase MAK-2 participates in the phosphate signaling pathway. <i>Fungal Genetics and Biology</i> , 2013, 60, 140-149.	2.1	33
24	Insights into the Function of Long Noncoding RNAs in Sepsis Revealed by Gene Co-Expression Network Analysis. <i>Non-coding RNA</i> , 2017, 3, 5.	2.6	30
25	Aurora A kinase and its activator TPX2 are potential therapeutic targets in KRAS-induced pancreatic cancer. <i>Cellular Oncology (Dordrecht)</i> , 2020, 43, 445-460.	4.4	30
26	RASL11A, member of a novel small monomeric GTPase gene family, is down-regulated in prostate tumors. <i>Biochemical and Biophysical Research Communications</i> , 2004, 316, 618-627.	2.1	29
27	CIP4 promotes metastasis in triple-negative breast cancer and is associated with poor patient prognosis. <i>Oncotarget</i> , 2015, 6, 9397-9408.	1.8	29
28	Apert p.Ser252Trp Mutation in FGFR2 Alters Osteogenic Potential and Gene Expression of Cranial Periosteal Cells. <i>Molecular Medicine</i> , 2007, 13, 422-442.	4.4	28
29	Septic Shock in Advanced Age: Transcriptome Analysis Reveals Altered Molecular Signatures in Neutrophil Granulocytes. <i>PLoS ONE</i> , 2015, 10, e0128341.	2.5	27
30	Evaluating the Stability of mRNAs and Noncoding RNAs. <i>Methods in Molecular Biology</i> , 2017, 1468, 139-153.	0.9	23
31	Identification of novel biomarkers associated with poor patient outcomes in invasive breast carcinoma. <i>Tumor Biology</i> , 2016, 37, 13855-13870.	1.8	19
32	Zerg: a very fast BLAST parser library. <i>Bioinformatics</i> , 2003, 19, 1035-1036.	4.1	17
33	Evaluation of reference-based two-color methods for measurement of gene expression ratios using spotted cDNA microarrays. <i>BMC Genomics</i> , 2006, 7, 35.	2.8	17
34	Splice variants of TLE family genes and up-regulation of a TLE3 isoform in prostate tumors. <i>Biochemical and Biophysical Research Communications</i> , 2007, 364, 918-923.	2.1	16
35	Gene expression profiling reveals molecular marker candidates of laryngeal squamous cell carcinoma. <i>Oncology Reports</i> , 2009, , .	2.6	14
36	Short-Term Effects of Sepsis and the Impact of Aging on the Transcriptional Profile of Different Brain Regions. <i>Inflammation</i> , 2019, 42, 1023-1031.	3.8	12

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37	N-terminal chimeric constructs improve the expression of sarcoplasmic reticulum Ca ²⁺ -ATPase in yeast. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 1999, 1461, 83-95.	2.6	11
38	Auto-antibodies in prostate cancer: Humoral immune response to antigenic determinants coded by the differentially expressed transcripts FLJ23438 and VAMP3. <i>Prostate</i> , 2006, 66, 1463-1473.	2.3	11
39	Chromatin Landscape Distinguishes the Genomic Loci of Hundreds of Androgen-Receptor-Associated LincRNAs From the Loci of Non-associated LincRNAs. <i>Frontiers in Genetics</i> , 2018, 9, 132.	2.3	10
40	Gene Expression Profiling of Cultured Cells From Brainstem of Newborn Spontaneously Hypertensive and Wistar Kyoto Rats. <i>Cellular and Molecular Neurobiology</i> , 2009, 29, 287-308.	3.3	9
41	Loss of Caspase 7 Expression Is Associated With Poor Prognosis in Renal Cell Carcinoma Clear Cell Subtype. <i>Urology</i> , 2013, 82, 974.e1-974.e7.	1.0	9
42	Gene co-expression and histone modification signatures are associated with melanoma progression, epithelial-to-mesenchymal transition, and metastasis. <i>Clinical Epigenetics</i> , 2020, 12, 127.	4.1	9
43	Heterologous expression of sarcoplasmic reticulum Ca ²⁺ -ATPase. <i>Bioscience Reports</i> , 1996, 16, 107-113.	2.4	5
44	Transcriptional signatures underlying dynamic phenotypic switching and novel disease biomarkers in a linear cellular model of melanoma progression. <i>Neoplasia</i> , 2021, 23, 439-455.	5.3	5
45	Microarray gene expression analysis of neutrophils from elderly septic patients. <i>Genomics Data</i> , 2015, 6, 51-53.	1.3	4
46	Annotation and functional characterization of long noncoding RNAs deregulated in pancreatic adenocarcinoma. <i>Cellular Oncology (Dordrecht)</i> , 2022, 45, 479-504.	4.4	4
47	Concepts on Microarray Design for Genome and Transcriptome Analyses. , 2007, , 265-307.		3
48	Prognostic value of integrin β 4 expression and localization pattern in invasive breast carcinomas. <i>Neoplasia</i> , 2022, 30, 100803.	5.3	3
49	Genome-wide promoter methylation profiling in a cellular model of melanoma progression reveals markers of malignancy and metastasis that predict melanoma survival. <i>Clinical Epigenetics</i> , 2022, 14, .	4.1	3
50	Transcriptome analysis of nicotine-exposed cells from the brainstem of neonate spontaneously hypertensive and Wistar Kyoto rats. <i>Pharmacogenomics Journal</i> , 2010, 10, 134-160.	2.0	2
51	Noncoding Gene Families of the Human Genome. , 2021, , 139-180.		1
52	Where do we aspire to publish? A position paper on scientific communication in biochemistry and molecular biology. <i>Brazilian Journal of Medical and Biological Research</i> , 2019, 52, e8935.	1.5	1
53	Genes regulated by DNA methylation are involved in distinct phenotypes during melanoma progression and are prognostic factors for patients. <i>Molecular Oncology</i> , 2022, 16, 1913-1930.	4.6	1