Ricardo Z Vâncio

List of Publications by Year
in descending order

55	2,794	331670	182427
papers	citations	21	51
		h-index	g-index

56	56	56	4870
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Prostate cancer reprogramming and dedifferentiation into induced pluripotent stem cells. , 2021, , 163-189.		3
2	Halobacterium salinarum and Haloferax volcanii Comparative Transcriptomics Reveals Conserved Transcriptional Processing Sites. Genes, 2021, 12, 1018.	2.4	5
3	Environmental Influences Measured by Epigenetic Clock and Vulnerability Components at Birth Impact Clinical ASD Heterogeneity. Genes, 2021, 12, 1433.	2.4	3
4	<i>Plasmodium vivax</i> spleen-dependent genes encode antigens associated with cytoadhesion and clinical protection. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 13056-13065.	7.1	29
5	Lineage relationship between prostate adenocarcinoma and small cell carcinoma. BMC Cancer, 2019, 19, 518.	2.6	5
6	The Primary Antisense Transcriptome of Halobacterium salinarum NRC-1. Genes, 2019, 10, 280.	2.4	11
7	Internal RNAs overlapping coding sequences can drive the production of alternative proteins in archaea. RNA Biology, 2018, 15, 1-14.	3.1	14
8	Conversion of Prostate Adenocarcinoma to Small Cell Carcinomaâ€Like by Reprogramming. Journal of Cellular Physiology, 2016, 231, 2040-2047.	4.1	14
9	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	8.8	308
10	Processing of voided urine for prostate cancer RNA biomarker analysis. Prostate, 2015, 75, 1886-1895.	2.3	8
11	SIFTER-T: A scalable and optimized framework for the SIFTER phylogenomic method of probabilistic protein domain annotation. BioTechniques, 2015, 58, 140-142.	1.8	1
12	Convergence Analysis of a New Self Organizing Map Based Optimization (SOMO) Algorithm. Cognitive Computation, 2015, 7, 477-486.	5.2	3
13	Reprogramming of Prostate Cancer Cells - Technical Challenges. Current Urology Reports, 2015, 16, 468.	2.2	5
14	A Methodology for the Development of RESTful Semantic Web Services for Gene Expression Analysis. PLoS ONE, 2015, 10, e0134011.	2.5	7
15	Transcription Start Site Associated RNAs (TSSaRNAs) Are Ubiquitous in All Domains of Life. PLoS ONE, 2014, 9, e107680.	2.5	14
16	Semantic integration of gene expression analysis tools and data sources using software connectors. BMC Genomics, 2013, 14, S2.	2.8	4
17	Gene Expression Profiling Reveals Regulation of ERK Phosphorylation by Androgen-Induced Tumor Suppressor U19/EAF2 in the Mouse Prostate. Cancer Microenvironment, 2013, 6, 247-261.	3.1	14
18	A UML profile for the OBO relation ontology. BMC Genomics, 2012, 13, S3.	2.8	9

#	ARTICLE	IF	CITATIONS
19	Reprogramming of prostate cancerâ€associated stromal cells to embryonic stemâ€like. Prostate, 2012, 72, 1453-1463.	2.3	21
20	Bladder expression of CD cell surface antigens and cell-type-specific transcriptomes. Cell and Tissue Research, 2012, 348, 589-600.	2.9	27
21	Combining P values to improve classification of differential gene expression in the HTself software. Genetics and Molecular Research, 2011, 10, 3586-3595.	0.2	4
22	Insights on PRAME and osteosarcoma by means of gene expression profiling. Journal of Orthopaedic Science, 2011, 16, 458-466.	1.1	12
23	Differential Inductive Signaling of CD90+ Prostate Cancer-Associated Fibroblasts Compared to Normal Tissue Stromal Mesenchyme Cells. Cancer Microenvironment, 2011, 4, 51-59.	3.1	19
24	Lineage relationship of prostate cancer cell types based on gene expression. BMC Medical Genomics, 2011, 4, 46.	1.5	22
25	Stromal-epithelial interactions in early neoplasia. Cancer Biomarkers, 2011, 9, 141-155.	1.7	9
26	ProbFAST: Probabilistic Functional Analysis System Tool. BMC Bioinformatics, 2010, 11, 161.	2.6	2
27	Global Gene Expression Analysis during Germination in the Chytridiomycete <i>Blastocladiella emersonii</i>. Eukaryotic Cell, 2009, 8, 170-180.	3.4	10
28	Plasmodium vivax and the importance of the subtelomeric multigene vir superfamily. Trends in Parasitology, 2009, 25, 44-51.	3.3	52
29	Sugarcane genes associated with sucrose content. BMC Genomics, 2009, 10, 120.	2.8	133
30	Gene expression down-regulation in CD90+prostate tumor-associated stromal cells involves potential organ-specific genes. BMC Cancer, 2009, 9, 317.	2.6	39
31	Temporal expression profiling of the effects of secreted factors from prostate stromal cells on embryonal carcinoma stem cells. Prostate, 2009, 69, 1353-1365.	2.3	15
32	Systems biology approach predicts immunogenicity of the yellow fever vaccine in humans. Nature Immunology, 2009, 10, 116-125.	14.5	1,019
33	Gene expression relationship between prostate cancer cells of Gleason 3, 4 and normal epithelial cells as revealed by cell type-specific transcriptomes. BMC Cancer, 2009, 9, 452.	2.6	50
34	Age-Dependent Signature of Metallothionein Expression in Primary CD4 T Cell Responses Is Due to Sustained Zinc Signaling. Rejuvenation Research, 2008, 11, 1001-1011.	1.8	39
35	The Iron Stimulon of <i>Xylella fastidiosa</i> Includes Genes for Type IV Pilus and Colicin V-Like Bacteriocins. Journal of Bacteriology, 2008, 190, 2368-2378.	2.2	44
36	Comparative Transcriptome Analysis of <i>Listeria monocytogenes</i> Strains of the Two Major Lineages Reveals Differences in Virulence, Cell Wall, and Stress Response. Applied and Environmental Microbiology, 2007, 73, 6078-6088.	3.1	66

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37	Multisite fMRI reproducibility of a motor task using identical MR systems. Journal of Magnetic Resonance Imaging, 2007, 26, 1122-1126.	3.4	58
38	Common molecular pathways involved in human CD133+/CD34+ progenitor cell expansion and cancer. Cancer Cell International, 2007, 7, 11.	4.1	15
39	Simcluster: clustering enumeration gene expression data on the simplex space. BMC Bioinformatics, 2007, 8, 246.	2.6	12
40	ProbCD: enrichment analysis accounting for categorization uncertainty. BMC Bioinformatics, 2007, 8, 383.	2.6	18
41	Signal transduction-related responses to phytohormones and environmental challenges in sugarcane. BMC Genomics, 2007, 8, 71.	2.8	127
42	Statistical Methods in Serial Analysis of Gene Expression (Sage). , 2006, , 209-233.		2
43	Differential transcription profiles in Trypanosoma cruzi associated with clinical forms of Chagas disease: Maxicircle NADH dehydrogenase subunit 7 gene truncation in asymptomatic patient isolates. Molecular and Biochemical Parasitology, 2006, 150, 236-248.	1.1	31
44	BayGO: Bayesian analysis of ontology term enrichment in microarray data. BMC Bioinformatics, 2006, 7, 86.	2.6	56
45	Evaluation of reference-based two-color methods for measurement of gene expression ratios using spotted cDNA microarrays. BMC Genomics, 2006, 7, 35.	2.8	17
46	Global Gene Expression Analysis of the Heat Shock Response in the Phytopathogen Xylella fastidiosa. Journal of Bacteriology, 2006, 188, 5821-5830.	2.2	37
47	SpotWhatR: a user-friendly microarray data analysis system. Genetics and Molecular Research, 2006, 5, 93-107.	0.2	10
48	Transcription Profiling of Signal Transduction-Related Genes in Sugarcane Tissues. DNA Research, 2005, 12, 27-38.	3.4	77
49	HTself: Self-Self Based Statistical Test for Low Replication Microarray Studies. DNA Research, 2005, 12, 211-214.	3.4	45
50	Gene Discovery and Expression Profile Analysis through Sequencing of Expressed Sequence Tags from Different Developmental Stages of the Chytridiomycete Blastocladiella emersonii. Eukaryotic Cell, 2005, 4, 455-464.	3.4	21
51	Whole-Genome Expression Profiling ofXylella fastidiosain Response to Growth on Glucose. OMICS A Journal of Integrative Biology, 2005, 9, 77-90.	2.0	20
52	DNA Microarray-Based Genome Comparison of a Pathogenic and a Nonpathogenic Strain of Xylella fastidiosa Delineates Genes Important for Bacterial Virulence. Journal of Bacteriology, 2004, 186, 5442-5449.	2.2	74
53	DNA microarrays for comparative genomics and analysis of gene expression in Trypanosoma cruzi. Molecular and Biochemical Parasitology, 2004, 138, 183-194.	1.1	21
54	Bayesian model accounting for within-class biological variability in Serial Analysis of Gene Expression (SAGE). BMC Bioinformatics, 2004, 5, 119.	2.6	54

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55	Using credibility intervals instead of hypothesis tests in SAGE analysis. Bioinformatics, 2003, 19, 2461-2464.	4.1	28