

Ricardo Z VÃncio

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

2,794
citations

331670

21
h-index

182427

51
g-index

56
all docs

56
docs citations

56
times ranked

4870
citing authors

#	ARTICLE	IF	CITATIONS
1	Systems biology approach predicts immunogenicity of the yellow fever vaccine in humans. <i>Nature Immunology</i> , 2009, 10, 116-125.	14.5	1,019
2	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184.	8.8	308
3	Sugarcane genes associated with sucrose content. <i>BMC Genomics</i> , 2009, 10, 120.	2.8	133
4	Signal transduction-related responses to phytohormones and environmental challenges in sugarcane. <i>BMC Genomics</i> , 2007, 8, 71.	2.8	127
5	Transcription Profiling of Signal Transduction-Related Genes in Sugarcane Tissues. <i>DNA Research</i> , 2005, 12, 27-38.	3.4	77
6	DNA Microarray-Based Genome Comparison of a Pathogenic and a Nonpathogenic Strain of <i>Xylella fastidiosa</i> Delineates Genes Important for Bacterial Virulence. <i>Journal of Bacteriology</i> , 2004, 186, 5442-5449.	2.2	74
7	Comparative Transcriptome Analysis of <i>Listeria monocytogenes</i> Strains of the Two Major Lineages Reveals Differences in Virulence, Cell Wall, and Stress Response. <i>Applied and Environmental Microbiology</i> , 2007, 73, 6078-6088.	3.1	66
8	Multisite fMRI reproducibility of a motor task using identical MR systems. <i>Journal of Magnetic Resonance Imaging</i> , 2007, 26, 1122-1126.	3.4	58
9	BayGO: Bayesian analysis of ontology term enrichment in microarray data. <i>BMC Bioinformatics</i> , 2006, 7, 86.	2.6	56
10	Bayesian model accounting for within-class biological variability in Serial Analysis of Gene Expression (SAGE). <i>BMC Bioinformatics</i> , 2004, 5, 119.	2.6	54
11	<i>Plasmodium vivax</i> and the importance of the subtelomeric multigene <i>vir</i> superfamily. <i>Trends in Parasitology</i> , 2009, 25, 44-51.	3.3	52
12	Gene expression relationship between prostate cancer cells of Gleason 3, 4 and normal epithelial cells as revealed by cell type-specific transcriptomes. <i>BMC Cancer</i> , 2009, 9, 452.	2.6	50
13	HTself: Self-Self Based Statistical Test for Low Replication Microarray Studies. <i>DNA Research</i> , 2005, 12, 211-214.	3.4	45
14	The Iron Stimulon of <i>Xylella fastidiosa</i> Includes Genes for Type IV Pilus and Colicin V-Like Bacteriocins. <i>Journal of Bacteriology</i> , 2008, 190, 2368-2378.	2.2	44
15	Age-Dependent Signature of Metallothionein Expression in Primary CD4 T Cell Responses Is Due to Sustained Zinc Signaling. <i>Rejuvenation Research</i> , 2008, 11, 1001-1011.	1.8	39
16	Gene expression down-regulation in CD90+prostate tumor-associated stromal cells involves potential organ-specific genes. <i>BMC Cancer</i> , 2009, 9, 317.	2.6	39
17	Global Gene Expression Analysis of the Heat Shock Response in the Phytopathogen <i>Xylella fastidiosa</i> . <i>Journal of Bacteriology</i> , 2006, 188, 5821-5830.	2.2	37
18	Differential transcription profiles in <i>Trypanosoma cruzi</i> associated with clinical forms of Chagas disease: Maxicircle NADH dehydrogenase subunit 7 gene truncation in asymptomatic patient isolates. <i>Molecular and Biochemical Parasitology</i> , 2006, 150, 236-248.	1.1	31

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19	<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
20	Using credibility intervals instead of hypothesis tests in SAGE analysis. Bioinformatics, 2003, 19, 2461-2464.	4.1	28
21	Bladder expression of CD cell surface antigens and cell-type-specific transcriptomes. Cell and Tissue Research, 2012, 348, 589-600.	2.9	27
22	Lineage relationship of prostate cancer cell types based on gene expression. BMC Medical Genomics, 2011, 4, 46.	1.5	22
23	DNA microarrays for comparative genomics and analysis of gene expression in <i>Trypanosoma cruzi</i> . Molecular and Biochemical Parasitology, 2004, 138, 183-194.	1.1	21
24	Gene Discovery and Expression Profile Analysis through Sequencing of Expressed Sequence Tags from Different Developmental Stages of the Chytridiomycete <i>Blastocladiella emersonii</i> . Eukaryotic Cell, 2005, 4, 455-464.	3.4	21
25	Reprogramming of prostate cancer-associated stromal cells to embryonic stem-like. Prostate, 2012, 72, 1453-1463.	2.3	21
26	Whole-Genome Expression Profiling of <i>Xylella fastidiosa</i> Response to Growth on Glucose. OMICS A Journal of Integrative Biology, 2005, 9, 77-90.	2.0	20
27	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
28	ProbCD: enrichment analysis accounting for categorization uncertainty. BMC Bioinformatics, 2007, 8, 383.	2.6	18
29	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
30	Common molecular pathways involved in human CD133+/CD34+ progenitor cell expansion and cancer. Cancer Cell International, 2007, 7, 11.	4.1	15
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	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
33	Transcription Start Site Associated RNAs (TSSaRNAs) Are Ubiquitous in All Domains of Life. PLoS ONE, 2014, 9, e107680.	2.5	14
34	Conversion of Prostate Adenocarcinoma to Small Cell Carcinoma-like by Reprogramming. Journal of Cellular Physiology, 2016, 231, 2040-2047.	4.1	14
35	Internal RNAs overlapping coding sequences can drive the production of alternative proteins in archaea. RNA Biology, 2018, 15, 1-14.	3.1	14
36	Simcluster: clustering enumeration gene expression data on the simplex space. BMC Bioinformatics, 2007, 8, 246.	2.6	12

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37	Insights on PRAME and osteosarcoma by means of gene expression profiling. <i>Journal of Orthopaedic Science</i> , 2011, 16, 458-466.	1.1	12
38	The Primary Antisense Transcriptome of <i>Halobacterium salinarum</i> NRC-1. <i>Genes</i> , 2019, 10, 280.	2.4	11
39	Global Gene Expression Analysis during Germination in the Chytridiomycete <i>Blastocladiella emersonii</i> . <i>Eukaryotic Cell</i> , 2009, 8, 170-180.	3.4	10
40	SpotWhatR: a user-friendly microarray data analysis system. <i>Genetics and Molecular Research</i> , 2006, 5, 93-107.	0.2	10
41	Stromal-epithelial interactions in early neoplasia. <i>Cancer Biomarkers</i> , 2011, 9, 141-155.	1.7	9
42	A UML profile for the OBO relation ontology. <i>BMC Genomics</i> , 2012, 13, S3.	2.8	9
43	Processing of voided urine for prostate cancer RNA biomarker analysis. <i>Prostate</i> , 2015, 75, 1886-1895.	2.3	8
44	A Methodology for the Development of RESTful Semantic Web Services for Gene Expression Analysis. <i>PLoS ONE</i> , 2015, 10, e0134011.	2.5	7
45	Reprogramming of Prostate Cancer Cells - Technical Challenges. <i>Current Urology Reports</i> , 2015, 16, 468.	2.2	5
46	Lineage relationship between prostate adenocarcinoma and small cell carcinoma. <i>BMC Cancer</i> , 2019, 19, 518.	2.6	5
47	<i>Halobacterium salinarum</i> and <i>Haloferax volcanii</i> Comparative Transcriptomics Reveals Conserved Transcriptional Processing Sites. <i>Genes</i> , 2021, 12, 1018.	2.4	5
48	Combining P values to improve classification of differential gene expression in the HTself software. <i>Genetics and Molecular Research</i> , 2011, 10, 3586-3595.	0.2	4
49	Semantic integration of gene expression analysis tools and data sources using software connectors. <i>BMC Genomics</i> , 2013, 14, S2.	2.8	4
50	Convergence Analysis of a New Self Organizing Map Based Optimization (SOMO) Algorithm. <i>Cognitive Computation</i> , 2015, 7, 477-486.	5.2	3
51	Prostate cancer reprogramming and dedifferentiation into induced pluripotent stem cells. , 2021, , 163-189.		3
52	Environmental Influences Measured by Epigenetic Clock and Vulnerability Components at Birth Impact Clinical ASD Heterogeneity. <i>Genes</i> , 2021, 12, 1433.	2.4	3
53	Statistical Methods in Serial Analysis of Gene Expression (Sage). , 2006, , 209-233.		2
54	ProbFAST: Probabilistic Functional Analysis System Tool. <i>BMC Bioinformatics</i> , 2010, 11, 161.	2.6	2

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55	SIFTER-T: A scalable and optimized framework for the SIFTER phylogenomic method of probabilistic protein domain annotation. <i>BioTechniques</i> , 2015, 58, 140-142.	1.8	1