

Francisco Azuaje

List of Publications by Year in descending order

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Version: 2024-02-01

71
papers

2,974
citations

186265
28
h-index

189892
50
g-index

78
all docs

78
docs citations

78
times ranked

5269
citing authors

#	ARTICLE	IF	CITATIONS
1	Oncolytic H-1 parvovirus binds to sialic acid on laminins for cell attachment and entry. <i>Nature Communications</i> , 2021, 12, 3834.	12.8	15
2	Patient-derived organoids and orthotopic xenografts of primary and recurrent gliomas represent relevant patient avatars for precision oncology. <i>Acta Neuropathologica</i> , 2020, 140, 919-949.	7.7	72
3	Temozolomide-Induced RNA Interactome Uncovers Novel LncRNA Regulatory Loops in Glioblastoma. <i>Cancers</i> , 2020, 12, 2583.	3.7	6
4	Machine learning-assisted neurotoxicity prediction in human midbrain organoids. <i>Parkinsonism and Related Disorders</i> , 2020, 75, 105-109.	2.2	41
5	Extracellular ATP and CD39 Activate cAMP-Mediated Mitochondrial Stress Response to Promote Cytarabine Resistance in Acute Myeloid Leukemia. <i>Cancer Discovery</i> , 2020, 10, 1544-1565.	9.4	39
6	Fisetin protects against cardiac cell death through reduction of ROS production and caspases activity. <i>Scientific Reports</i> , 2020, 10, 2896.	3.3	37
7	Deconvolution of transcriptomes and miRNomes by independent component analysis provides insights into biological processes and clinical outcomes of melanoma patients. <i>BMC Medical Genomics</i> , 2019, 12, 132.	1.5	22
8	Connecting Histopathology Imaging and Proteomics in Kidney Cancer through Machine Learning. <i>Journal of Clinical Medicine</i> , 2019, 8, 1535.	2.4	27
9	Stem cell-associated heterogeneity in Glioblastoma results from intrinsic tumor plasticity shaped by the microenvironment. <i>Nature Communications</i> , 2019, 10, 1787.	12.8	379
10	Long-term treatment with valganciclovir improves lentiviral suicide gene therapy of glioblastoma. <i>Neuro-Oncology</i> , 2019, 21, 890-900.	1.2	23
11	Artificial intelligence for precision oncology: beyond patient stratification. <i>Npj Precision Oncology</i> , 2019, 3, 6.	5.4	90
12	A deep neural network approach to predicting clinical outcomes of neuroblastoma patients. <i>BMC Medical Genomics</i> , 2019, 12, 178.	1.5	15
13	Analysis of correlation-based biomolecular networks from different omics data by fitting stochastic block models. <i>F1000Research</i> , 2019, 8, 465.	1.6	1
14	Analysis of correlation-based biomolecular networks from different omics data by fitting stochastic block models. <i>F1000Research</i> , 2019, 8, 465.	1.6	2
15	CD47 is a direct target of SNAI1 and ZEB1 and its blockade activates the phagocytosis of breast cancer cells undergoing EMT. <i>Oncolmmunology</i> , 2018, 7, e1345415.	4.6	63
16	Predicting clinical outcome of neuroblastoma patients using an integrative network-based approach. <i>Biology Direct</i> , 2018, 13, 12.	4.6	13
17	Hub genes in a pan-cancer co-expression network show potential for predicting drug responses. <i>F1000Research</i> , 2018, 7, 1906.	1.6	4
18	Hub genes in a pan-cancer co-expression network show potential for predicting drug responses. <i>F1000Research</i> , 2018, 7, 1906.	1.6	3

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19	Computational models for predicting drug responses in cancer research. Briefings in Bioinformatics, 2017, 18, bbw065.	6.5	124
20	The angiogenic switch leads to a metabolic shift in human glioblastoma. Neuro-Oncology, 2017, 19, now175.	1.2	50
21	Molecular crosstalk between tumour and brain parenchyma instructs histopathological features in glioblastoma. Oncotarget, 2016, 7, 31955-31971.	1.8	69
22	<scp>LIMT</scp> is a novel metastasis inhibiting lnc<scp>RNA</scp> suppressed by <scp>EGF</scp> and downregulated in aggressive breast cancer. EMBO Molecular Medicine, 2016, 8, 1052-1064.	6.9	77
23	Analysis of the dynamic co-expression network of heart regeneration in the zebrafish. Scientific Reports, 2016, 6, 26822.	3.3	32
24	Permanent Culture of Macrophages at Physiological Oxygen Attenuates the Antioxidant and Immunomodulatory Properties of Dimethyl Fumarate. Journal of Cellular Physiology, 2015, 230, 1128-1138.	4.1	19
25	Therapeutic control and resistance of the EGFR-driven signaling network in glioblastoma. Cell Communication and Signaling, 2015, 13, 23.	6.5	39
26	Transcriptional response to cardiac injury in the zebrafish: systematic identification of genes with highly concordant activity across in vivo models. BMC Genomics, 2014, 15, 852.	2.8	10
27	Databases for lncRNAs: a comparative evaluation of emerging tools. Rna, 2014, 20, 1655-1665.	3.5	81
28	Linking Biochemical Pathways and Networks to Adverse Drug Reactions. IEEE Transactions on Nanobioscience, 2014, 13, 131-137.	3.3	12
29	A gene mapping bottleneck in the translational route from zebrafish to human. Frontiers in Genetics, 2014, 5, 470.	2.3	2
30	Analysis of a gene co-expression network establishes robust association between Col5a2 and ischemic heart disease. BMC Medical Genomics, 2013, 6, 13.	1.5	34
31	Drug interaction networks: an introduction to translational and clinical applications. Cardiovascular Research, 2013, 97, 631-641.	3.8	36
32	Gene set analysis in the cloud. Bioinformatics, 2012, 28, 294-295.	4.1	38
33	Use of Circulating MicroRNAs to Diagnose Acute Myocardial Infarction. Clinical Chemistry, 2012, 58, 559-567.	3.2	239
34	Low Levels of Vascular Endothelial Growth Factor B Predict Left Ventricular Remodeling After Acute Myocardial Infarction. Journal of Cardiac Failure, 2012, 18, 330-337.	1.7	25
35	Systems-Based Approaches to Cardiovascular Biomarker Discovery. Circulation: Cardiovascular Genetics, 2012, 5, 360-367.	5.1	32
36	Systems-based biological concordance and predictive reproducibility of gene set discovery methods in cardiovascular disease. Journal of Biomedical Informatics, 2011, 44, 637-647.	4.3	6

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37	Proof-of-principle investigation of an algorithmic model of adenosine-mediated angiogenesis. Theoretical Biology and Medical Modelling, 2011, 8, 7.	2.1	3
38	Transforming growth factor β 2 receptor 1 is a new candidate prognostic biomarker after acute myocardial infarction. BMC Medical Genomics, 2011, 4, 83.	1.5	32
39	Computational discrete models of tissue growth and regeneration. Briefings in Bioinformatics, 2011, 12, 64-77.	6.5	27
40	Why is it so difficult to data mine relevant genome-scale biomarkers?. Expert Opinion on Medical Diagnostics, 2011, 5, 1-4.	1.6	2
41	Prognostic transcriptional association networks: a new supervised approach based on regression trees. Bioinformatics, 2011, 27, 252-258.	4.1	12
42	What does systems biology mean for biomarker discovery?. Expert Opinion on Medical Diagnostics, 2010, 4, 1-10.	1.6	13
43	Integrated protein network and microarray analysis to identify potential biomarkers after myocardial infarction. Functional and Integrative Genomics, 2010, 10, 329-337.	3.5	36
44	Coordinated modular functionality and prognostic potential of a heart failure biomarker-driven interaction network. BMC Systems Biology, 2010, 4, 60.	3.0	32
45	Transcriptional networks characterize ventricular dysfunction after myocardial infarction: A proof-of-concept investigation. Journal of Biomedical Informatics, 2010, 43, 812-819.	4.3	13
46	eNelator: A simulation system for large-scale vulnerability analysis of species-, disease- and process-specific protein networks. Journal of Computational Science, 2010, 1, 197-205.	2.9	6
47	Integration of Gene Ontology-based similarities for supporting analysis of protein-protein interaction networks. Pattern Recognition Letters, 2010, 31, 2073-2082.	4.2	12
48	A knowledge-driven probabilistic framework for the prediction of protein-protein interaction networks. Computers in Biology and Medicine, 2010, 40, 306-317.	7.0	16
49	Identification of potential targets in biological signalling systems through network perturbation analysis. BioSystems, 2010, 100, 55-64.	2.0	11
50	Ontology- and graph-based similarity assessment in biological networks. Bioinformatics, 2010, 26, 2643-2644.	4.1	17
51	Integrative Pathway-Centric Modeling of Ventricular Dysfunction after Myocardial Infarction. PLoS ONE, 2010, 5, e9661.	2.5	20
52	Computational biology for cardiovascular biomarker discovery. Briefings in Bioinformatics, 2009, 10, 367-377.	6.5	33
53	Innovative methods in assessing political risk for business internationalization. Research in International Business and Finance, 2009, 23, 144-156.	5.9	24
54	Challenges and Standards in Reporting Diagnostic and Prognostic Biomarker Studies. Clinical and Translational Science, 2009, 2, 156-161.	3.1	11

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55	Identification of dilated cardiomyopathy signature genes through gene expression and network data integration. Genomics, 2008, 92, 404-413.	2.9	43
56	Inferring Adaptive Regulation Thresholds and Association Rules from Gene Expression Data through Combinatorial Optimization Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 624-634.	3.0	24
57	Poisson-Based Self-Organizing Feature Maps and Hierarchical Clustering for Serial Analysis of Gene Expression Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 163-175.	3.0	21
58	Supervised Statistical and Machine Learning Approaches to Inferring Pairwise and Module-Based Protein Interaction Networks. , 2007, , .		7
59	Linking Gene Expression and Functional Network Data in Human Heart Failure. PLoS ONE, 2007, 2, e1347.	2.5	40
60	Predictive Integration of Gene Ontology-Driven Similarity and Functional Interactions. , 2006, 2006, 114-119.		19
61	Semi-Supervised Clustering Models for Clinical Risk Assessment. , 2006, , .		3
62	An assessment of recently published gene expression data analyses: reporting experimental design and statistical factors. BMC Medical Informatics and Decision Making, 2006, 6, 27.	3.0	127
63	A Supervised Learning Approach to Predicting Coronary Heart Disease Complications in Type 2 Diabetes Mellitus Patients. , 2006, , .		15
64	Multiple SVM-RFE for Gene Selection in Cancer Classification With Expression Data. IEEE Transactions on Nanobioscience, 2005, 4, 228-234.	3.3	357
65	Non-linear mapping for exploratory data analysis in functional genomics. BMC Bioinformatics, 2005, 6, 13.	2.6	11
66	Gene expression correlation and gene ontology-based similarity: an assessment of quantitative relationships. , 2004, 2004, 25-31.		98
67	An Integrative and Interactive Framework for Improving Biomedical Pattern Discovery and Visualization. IEEE Transactions on Information Technology in Biomedicine, 2004, 8, 16-27.	3.2	24
68	Genomic data sampling and its effect on classification performance assessment. BMC Bioinformatics, 2003, 4, 5.	2.6	29
69	Clustering-based approaches to discovering and visualising microarray data patterns. Briefings in Bioinformatics, 2003, 4, 31-42.	6.5	28
70	Retrieval strategies for case-based reasoning: a categorised bibliography. Knowledge Engineering Review, 2000, 15, 371-379.	2.6	8
71	Guest Commentary on Chapter 5: Advances in Biomarker Discovery with Gene Expression Data. , 0, , 89-92.		0