

# 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	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
2	Multiple SVM-RFE for Gene Selection in Cancer Classification With Expression Data. <i>IEEE Transactions on Nanobioscience</i> , 2005, 4, 228-234.	3.3	357
3	Use of Circulating MicroRNAs to Diagnose Acute Myocardial Infarction. <i>Clinical Chemistry</i> , 2012, 58, 559-567.	3.2	239
4	An assessment of recently published gene expression data analyses: reporting experimental design and statistical factors. <i>BMC Medical Informatics and Decision Making</i> , 2006, 6, 27.	3.0	127
5	Computational models for predicting drug responses in cancer research. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw065.	6.5	124
6	Gene expression correlation and gene ontology-based similarity: an assessment of quantitative relationships. , 2004, 2004, 25-31.		98
7	Artificial intelligence for precision oncology: beyond patient stratification. <i>Npj Precision Oncology</i> , 2019, 3, 6.	5.4	90
8	Databases for lncRNAs: a comparative evaluation of emerging tools. <i>Rna</i> , 2014, 20, 1655-1665.	3.5	81
9	<scp>LIMT</scp> is a novel metastasis inhibiting lnc<scp>RNA</scp> suppressed by <scp>EGF</scp> and downregulated in aggressive breast cancer. <i>EMBO Molecular Medicine</i> , 2016, 8, 1052-1064.	6.9	77
10	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
11	Molecular crosstalk between tumour and brain parenchyma instructs histopathological features in glioblastoma. <i>Oncotarget</i> , 2016, 7, 31955-31971.	1.8	69
12	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
13	The angiogenic switch leads to a metabolic shift in human glioblastoma. <i>Neuro-Oncology</i> , 2017, 19, now175.	1.2	50
14	Identification of dilated cardiomyopathy signature genes through gene expression and network data integration. <i>Genomics</i> , 2008, 92, 404-413.	2.9	43
15	Machine learning-assisted neurotoxicity prediction in human midbrain organoids. <i>Parkinsonism and Related Disorders</i> , 2020, 75, 105-109.	2.2	41
16	Linking Gene Expression and Functional Network Data in Human Heart Failure. <i>PLoS ONE</i> , 2007, 2, e1347.	2.5	40
17	Therapeutic control and resistance of the EGFR-driven signaling network in glioblastoma. <i>Cell Communication and Signaling</i> , 2015, 13, 23.	6.5	39
18	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

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19	Gene set analysis in the cloud. <i>Bioinformatics</i> , 2012, 28, 294-295.	4.1	38
20	Fisetin protects against cardiac cell death through reduction of ROS production and caspases activity. <i>Scientific Reports</i> , 2020, 10, 2896.	3.3	37
21	Integrated protein network and microarray analysis to identify potential biomarkers after myocardial infarction. <i>Functional and Integrative Genomics</i> , 2010, 10, 329-337.	3.5	36
22	Drug interaction networks: an introduction to translational and clinical applications. <i>Cardiovascular Research</i> , 2013, 97, 631-641.	3.8	36
23	Analysis of a gene co-expression network establishes robust association between Col5a2 and ischemic heart disease. <i>BMC Medical Genomics</i> , 2013, 6, 13.	1.5	34
24	Computational biology for cardiovascular biomarker discovery. <i>Briefings in Bioinformatics</i> , 2009, 10, 367-377.	6.5	33
25	Coordinated modular functionality and prognostic potential of a heart failure biomarker-driven interaction network. <i>BMC Systems Biology</i> , 2010, 4, 60.	3.0	32
26	Transforming growth factor $\beta$ 2 receptor 1 is a new candidate prognostic biomarker after acute myocardial infarction. <i>BMC Medical Genomics</i> , 2011, 4, 83.	1.5	32
27	Systems-Based Approaches to Cardiovascular Biomarker Discovery. <i>Circulation: Cardiovascular Genetics</i> , 2012, 5, 360-367.	5.1	32
28	Analysis of the dynamic co-expression network of heart regeneration in the zebrafish. <i>Scientific Reports</i> , 2016, 6, 26822.	3.3	32
29	Genomic data sampling and its effect on classification performance assessment. <i>BMC Bioinformatics</i> , 2003, 4, 5.	2.6	29
30	Clustering-based approaches to discovering and visualising microarray data patterns. <i>Briefings in Bioinformatics</i> , 2003, 4, 31-42.	6.5	28
31	Computational discrete models of tissue growth and regeneration. <i>Briefings in Bioinformatics</i> , 2011, 12, 64-77.	6.5	27
32	Connecting Histopathology Imaging and Proteomics in Kidney Cancer through Machine Learning. <i>Journal of Clinical Medicine</i> , 2019, 8, 1535.	2.4	27
33	Low Levels of Vascular Endothelial Growth Factor B Predict Left Ventricular Remodeling After Acute Myocardial Infarction. <i>Journal of Cardiac Failure</i> , 2012, 18, 330-337.	1.7	25
34	An Integrative and Interactive Framework for Improving Biomedical Pattern Discovery and Visualization. <i>IEEE Transactions on Information Technology in Biomedicine</i> , 2004, 8, 16-27.	3.2	24
35	Inferring Adaptive Regulation Thresholds and Association Rules from Gene Expression Data through Combinatorial Optimization Learning. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2007, 4, 624-634.	3.0	24
36	Innovative methods in assessing political risk for business internationalization. <i>Research in International Business and Finance</i> , 2009, 23, 144-156.	5.9	24

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37	Long-term treatment with valganciclovir improves lentiviral suicide gene therapy of glioblastoma. <i>Neuro-Oncology</i> , 2019, 21, 890-900.	1.2	23
38	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
39	Poisson-Based Self-Organizing Feature Maps and Hierarchical Clustering for Serial Analysis of Gene Expression Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2007, 4, 163-175.	3.0	21
40	Integrative Pathway-Centric Modeling of Ventricular Dysfunction after Myocardial Infarction. <i>PLoS ONE</i> , 2010, 5, e9661.	2.5	20
41	Predictive Integration of Gene Ontology-Driven Similarity and Functional Interactions. , 2006, 2006, 114-119.		19
42	Permanent Culture of Macrophages at Physiological Oxygen Attenuates the Antioxidant and Immunomodulatory Properties of Dimethyl Fumarate. <i>Journal of Cellular Physiology</i> , 2015, 230, 1128-1138.	4.1	19
43	Ontology- and graph-based similarity assessment in biological networks. <i>Bioinformatics</i> , 2010, 26, 2643-2644.	4.1	17
44	A knowledge-driven probabilistic framework for the prediction of protein-protein interaction networks. <i>Computers in Biology and Medicine</i> , 2010, 40, 306-317.	7.0	16
45	A Supervised Learning Approach to Predicting Coronary Heart Disease Complications in Type 2 Diabetes Mellitus Patients. , 2006, , .		15
46	A deep neural network approach to predicting clinical outcomes of neuroblastoma patients. <i>BMC Medical Genomics</i> , 2019, 12, 178.	1.5	15
47	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
48	What does systems biology mean for biomarker discovery?. <i>Expert Opinion on Medical Diagnostics</i> , 2010, 4, 1-10.	1.6	13
49	Transcriptional networks characterize ventricular dysfunction after myocardial infarction: A proof-of-concept investigation. <i>Journal of Biomedical Informatics</i> , 2010, 43, 812-819.	4.3	13
50	Predicting clinical outcome of neuroblastoma patients using an integrative network-based approach. <i>Biology Direct</i> , 2018, 13, 12.	4.6	13
51	Integration of Gene Ontology-based similarities for supporting analysis of protein-protein interaction networks. <i>Pattern Recognition Letters</i> , 2010, 31, 2073-2082.	4.2	12
52	Prognostic transcriptional association networks: a new supervised approach based on regression trees. <i>Bioinformatics</i> , 2011, 27, 252-258.	4.1	12
53	Linking Biochemical Pathways and Networks to Adverse Drug Reactions. <i>IEEE Transactions on Nanobioscience</i> , 2014, 13, 131-137.	3.3	12
54	Non-linear mapping for exploratory data analysis in functional genomics. <i>BMC Bioinformatics</i> , 2005, 6, 13.	2.6	11

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55	Challenges and Standards in Reporting Diagnostic and Prognostic Biomarker Studies. <i>Clinical and Translational Science</i> , 2009, 2, 156-161.	3.1	11
56	Identification of potential targets in biological signalling systems through network perturbation analysis. <i>BioSystems</i> , 2010, 100, 55-64.	2.0	11
57	Transcriptional response to cardiac injury in the zebrafish: systematic identification of genes with highly concordant activity across in vivo models. <i>BMC Genomics</i> , 2014, 15, 852.	2.8	10
58	Retrieval strategies for case-based reasoning: a categorised bibliography. <i>Knowledge Engineering Review</i> , 2000, 15, 371-379.	2.6	8
59	Supervised Statistical and Machine Learning Approaches to Inferring Pairwise and Module-Based Protein Interaction Networks. , 2007, , .		7
60	eNelator: A simulation system for large-scale vulnerability analysis of species-, disease- and process-specific protein networks. <i>Journal of Computational Science</i> , 2010, 1, 197-205.	2.9	6
61	Systems-based biological concordance and predictive reproducibility of gene set discovery methods in cardiovascular disease. <i>Journal of Biomedical Informatics</i> , 2011, 44, 637-647.	4.3	6
62	Temozolomide-Induced RNA Interactome Uncovers Novel LncRNA Regulatory Loops in Glioblastoma. <i>Cancers</i> , 2020, 12, 2583.	3.7	6
63	Hub genes in a pan-cancer co-expression network show potential for predicting drug responses. <i>F1000Research</i> , 2018, 7, 1906.	1.6	4
64	Semi-Supervised Clustering Models for Clinical Risk Assessment. , 2006, , .		3
65	Proof-of-principle investigation of an algorithmic model of adenosine-mediated angiogenesis. <i>Theoretical Biology and Medical Modelling</i> , 2011, 8, 7.	2.1	3
66	Hub genes in a pan-cancer co-expression network show potential for predicting drug responses. <i>F1000Research</i> , 2018, 7, 1906.	1.6	3
67	Why is it so difficult to data mine relevant genome-scale biomarkers?. <i>Expert Opinion on Medical Diagnostics</i> , 2011, 5, 1-4.	1.6	2
68	A gene mapping bottleneck in the translational route from zebrafish to human. <i>Frontiers in Genetics</i> , 2014, 5, 470.	2.3	2
69	Analysis of correlation-based biomolecular networks from different omics data by fitting stochastic block models. <i>F1000Research</i> , 2019, 8, 465.	1.6	2
70	Analysis of correlation-based biomolecular networks from different omics data by fitting stochastic block models. <i>F1000Research</i> , 2019, 8, 465.	1.6	1
71	Guest Commentary on Chapter 5: Advances in Biomarker Discovery with Gene Expression Data. , 0, , 89-92.		0