

Fatima Sanchez-Cabo

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

66

papers

11,127

citations

26

h-index

71

g-index

71

ext. papers

13,362

ext. citations

9.6

avg, IF

5.74

L-index

#	Paper	IF	Citations
66	Type, density, and location of immune cells within human colorectal tumors predict clinical outcome. <i>Science</i> , 2006 , 313, 1960-4	33.3	4329
65	Effector memory T cells, early metastasis, and survival in colorectal cancer. <i>New England Journal of Medicine</i> , 2005 , 353, 2654-66	59.2	1560
64	Unidirectional transfer of microRNA-loaded exosomes from T cells to antigen-presenting cells. <i>Nature Communications</i> , 2011 , 2, 282	17.4	1246
63	Sumoylated hnRNPA2B1 controls the sorting of miRNAs into exosomes through binding to specific motifs. <i>Nature Communications</i> , 2013 , 4, 2980	17.4	1109
62	GOplot: an R package for visually combining expression data with functional analysis. <i>Bioinformatics</i> , 2015 , 31, 2912-4	7.2	659
61	Gene expression profiling of human mesenchymal stem cells derived from bone marrow during expansion and osteoblast differentiation. <i>BMC Genomics</i> , 2007 , 8, 70	4.5	276
60	Mitochondrial and nuclear DNA matching shapes metabolism and healthy ageing. <i>Nature</i> , 2016 , 535, 561-5	50.4	248
59	CARMAweb: comprehensive R- and bioconductor-based web service for microarray data analysis. <i>Nucleic Acids Research</i> , 2006 , 34, W498-503	20.1	187
58	The neural crest is a source of mesenchymal stem cells with specialized hematopoietic stem cell niche function. <i>ELife</i> , 2014 , 3, e03696	8.9	184
57	ATTRACT-a database of RNA-binding proteins and associated motifs. <i>Database: the Journal of Biological Databases and Curation</i> , 2016 , 2016,	5	115
56	PathwayExplorer: web service for visualizing high-throughput expression data on biological pathways. <i>Nucleic Acids Research</i> , 2005 , 33, W633-7	20.1	105
55	Analysis of the DNA-binding profile and function of TALE homeoproteins reveals their specialization and specific interactions with Hox genes/proteins. <i>Cell Reports</i> , 2013 , 3, 1321-33	10.6	90
54	Global gene expression profiling reveals widespread yet distinctive translational responses to different eukaryotic translation initiation factor 2B-targeting stress pathways. <i>Molecular and Cellular Biology</i> , 2005 , 25, 9340-9	4.8	84
53	Assessment of a six gene panel for the molecular detection of circulating tumor cells in the blood of female cancer patients. <i>BMC Cancer</i> , 2010 , 10, 666	4.8	78
52	Comparative transcriptomics of human multipotent stem cells during adipogenesis and osteoblastogenesis. <i>BMC Genomics</i> , 2008 , 9, 340	4.5	72
51	Spatial and temporal gene expression differences in core and periinfarct areas in experimental stroke: a microarray analysis. <i>PLoS ONE</i> , 2012 , 7, e52121	3.7	52
50	Caveolar domain organization and trafficking is regulated by Abl kinases and mDia1. <i>Journal of Cell Science</i> , 2012 , 125, 3097-113	5.3	48

49	Embryological-origin-dependent differences in homeobox expression in adult aorta: role in regional phenotypic variability and regulation of NF- κ B activity. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2013 , 33, 1248-56	9.4	47
48	DNA Methylation of miR-7 is a Mechanism Involved in Platinum Response through Overexpression in Cancer Cells. <i>Theranostics</i> , 2017 , 7, 4118-4134	12.1	36
47	ArrayNorm: comprehensive normalization and analysis of microarray data. <i>Bioinformatics</i> , 2004 , 20, 1971-3	17.3	34
46	CTCF counter-regulates cardiomyocyte development and maturation programs in the embryonic heart. <i>PLoS Genetics</i> , 2017 , 13, e1006985	6	33
45	Deciphering the Dynamic Transcriptional and Post-transcriptional Networks of Macrophages in the Healthy Heart and after Myocardial Injury. <i>Cell Reports</i> , 2018 , 23, 622-636	10.6	33
44	Reconstruction of gene association network reveals a transmembrane protein required for adipogenesis and targeted by PPAR α . <i>Cellular and Molecular Life Sciences</i> , 2010 , 67, 4049-64	10.3	32
43	Aryl hydrocarbon receptor contributes to the MEK/ERK-dependent maintenance of the immature state of human dendritic cells. <i>Blood</i> , 2013 , 121, e108-17	2.2	29
42	Procyanidins modulate microRNA expression in pancreatic islets. <i>Journal of Agricultural and Food Chemistry</i> , 2013 , 61, 355-63	5.7	27
41	FineSplice, enhanced splice junction detection and quantification: a novel pipeline based on the assessment of diverse RNA-Seq alignment solutions. <i>Nucleic Acids Research</i> , 2014 , 42, e71	20.1	26
40	A quantization method based on threshold optimization for microarray short time series. <i>BMC Bioinformatics</i> , 2005 , 6 Suppl 4, S11	3.6	24
39	Metoprolol exerts a non-class effect against ischaemia-reperfusion injury by abrogating exacerbated inflammation. <i>European Heart Journal</i> , 2020 , 41, 4425-4440	9.5	24
38	JNK-mediated disruption of bile acid homeostasis promotes intrahepatic cholangiocarcinoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 16492-16499	11.5	22
37	Cooperativity of stress-responsive transcription factors in core hypoxia-inducible factor binding regions. <i>PLoS ONE</i> , 2012 , 7, e45708	3.7	22
36	PGC-1 β regulates translocated in liposarcoma activity: role in oxidative stress gene expression. <i>Antioxidants and Redox Signaling</i> , 2011 , 15, 325-37	8.4	22
35	Aging-Associated miR-217 Aggravates Atherosclerosis and Promotes Cardiovascular Dysfunction. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2020 , 40, 2408-2424	9.4	22
34	Loss of SRSF3 in Cardiomyocytes Leads to Decapping of Contraction-Related mRNAs and Severe Systolic Dysfunction. <i>Circulation Research</i> , 2019 , 125, 170-183	15.7	18
33	Alternative Splicing of NOX4 in the Failing Human Heart. <i>Frontiers in Physiology</i> , 2017 , 8, 935	4.6	18
32	Statistical analysis principles for Omics data. <i>Methods in Molecular Biology</i> , 2011 , 719, 113-31	1.4	17

31	Glycated Hemoglobin and Subclinical Atherosclerosis in People Without Diabetes. <i>Journal of the American College of Cardiology</i> , 2021 , 77, 2777-2791	15.1	17
30	The novel RUNX3/p33 isoform is induced upon monocyte-derived dendritic cell maturation and downregulates IL-8 expression. <i>Immunobiology</i> , 2010 , 215, 812-20	3.4	16
29	Data integration and exploration for the identification of molecular mechanisms in tumor-immune cells interaction. <i>BMC Genomics</i> , 2010 , 11 Suppl 1, S7	4.5	15
28	Oxidized Low-Density Lipoprotein Receptor in Lymphocytes Prevents Atherosclerosis and Predicts Subclinical Disease. <i>Circulation</i> , 2019 , 139, 243-255	16.7	15
27	Machine Learning Improves Cardiovascular Risk Definition for Young, Asymptomatic Individuals. <i>Journal of the American College of Cardiology</i> , 2020 , 76, 1674-1685	15.1	14
26	Proximo-distal positional information encoded by an Fgf-regulated gradient of homeodomain transcription factors in the vertebrate limb. <i>Science Advances</i> , 2020 , 6, eaaz0742	14.3	13
25	A genome-wide shRNA screen for new OxPhos related genes. <i>Mitochondrion</i> , 2011 , 11, 467-75	4.9	10
24	Disease-modifying factors in hereditary angioedema: an RNA expression-based screening. <i>Orphanet Journal of Rare Diseases</i> , 2013 , 8, 77	4.2	9
23	The curse of normalization. <i>Comparative and Functional Genomics</i> , 2002 , 3, 375-9		9
22	Digitaldsorter: Deep-Learning on scRNA-Seq to Deconvolute Gene Expression Data. <i>Frontiers in Genetics</i> , 2019 , 10, 978	4.5	8
21	Adaptive trimmed t-statistics for identifying predominantly high expression in a microarray experiment. <i>Statistics in Medicine</i> , 2011 , 30, 52-61	2.3	8
20	Sox17 Controls Emergence and Remodeling of Nestin-Expressing Coronary Vessels. <i>Circulation Research</i> , 2020 , 127, e252-e270	15.7	8
19	Colchicine in Recently Hospitalized Patients with COVID-19: A Randomized Controlled Trial (COL-COVID). <i>International Journal of General Medicine</i> , 2021 , 14, 5517-5526	2.3	8
18	Harmine and Piperlongumine Revert TRIB2-Mediated Drug Resistance. <i>Cancers</i> , 2020 , 12,	6.6	7
17	A fully Bayesian model to cluster gene-expression profiles. <i>Bioinformatics</i> , 2005 , 21 Suppl 2, ii130-6	7.2	7
16	Clonal haematopoiesis and atherosclerosis: a chicken or egg question?. <i>Nature Reviews Cardiology</i> , 2021 , 18, 463-464	14.8	6
15	regulates expression at the exit from pluripotency during gastrulation. <i>Biology Open</i> , 2019 , 8,	2.2	6
14	Deregulation of the imprinted DLK1-DIO3 locus ncRNAs is associated with replicative senescence of human adipose-derived stem cells. <i>PLoS ONE</i> , 2018 , 13, e0206534	3.7	4

13	Axial skeleton anterior-posterior patterning is regulated through feedback regulation between Meis transcription factors and retinoic acid. <i>Development (Cambridge)</i> , 2021 , 148,	6.6	2
12	5-gene differential expression predicts stability of human intestinal allografts. <i>Experimental and Molecular Pathology</i> , 2017 , 103, 163-171	4.4	2
11	Insights into global mechanisms and disease by gene expression profiling. <i>Methods in Molecular Biology</i> , 2011 , 719, 269-98	1.4	2
10	Identification of a peripheral blood gene signature predicting aortic valve calcification. <i>Physiological Genomics</i> , 2020 , 52, 563-574	3.6	2
9	Transcriptome and proteome mapping in the sheep atria reveal molecular features of atrial fibrillation progression. <i>Cardiovascular Research</i> , 2021 , 117, 1760-1775	9.9	2
8	Hypothesis Driven versus Hypothesis-free: Filling the Gaps in CoQ Biosynthesis. <i>Cell Metabolism</i> , 2016 , 24, 525-526	24.6	2
7	Immune synapse instructs epigenomic and transcriptomic functional reprogramming in dendritic cells. <i>Science Advances</i> , 2021 , 7,	14.3	2
6	Differential leucocyte RNA expression in the coronary arteries compared to systemic circulation discriminates between patients with and those without coronary artery disease. <i>Clinica E Investigaci3n En Arteriosclerosis</i> , 2017 , 29, 60-66	1.4	1
5	dSreg: a Bayesian model to integrate changes in splicing and RNA-binding protein activity. <i>Bioinformatics</i> , 2020 , 36, 2134-2141	7.2	1
4	Combined statistical modeling enables accurate mining of circadian transcription. <i>NAR Genomics and Bioinformatics</i> , 2021 , 3, lqab031	3.7	1
3	MiRNA post-transcriptional modification dynamics in T cell activation. <i>iScience</i> , 2021 , 24, 102530	6.1	1
2	The SRSF4-GAS5-Glucocorticoid Receptor Axis Regulates Ventricular Hypertrophy. <i>Circulation Research</i> , 2021 , 129, 669-683	15.7	1
1	Interplay between UNG and AID governs intratumoral heterogeneity in mature B cell lymphoma. <i>PLoS Genetics</i> , 2020 , 16, e1008960	6	0