

# Fatima Sanchez-Cabo

## List of Publications by Year in descending order

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Version: 2024-02-01

67  
papers

14,711  
citations

136740

32  
h-index

98622

67  
g-index

71  
all docs

71  
docs citations

71  
times ranked

25772  
citing authors

#	ARTICLE	IF	CITATIONS
1	Type, Density, and Location of Immune Cells Within Human Colorectal Tumors Predict Clinical Outcome. <i>Science</i> , 2006, 313, 1960-1964.	6.0	5,356
2	Effector Memory T Cells, Early Metastasis, and Survival in Colorectal Cancer. <i>New England Journal of Medicine</i> , 2005, 353, 2654-2666.	13.9	1,860
3	Unidirectional transfer of microRNA-loaded exosomes from T cells to antigen-presenting cells. <i>Nature Communications</i> , 2011, 2, 282.	5.8	1,525
4	Sumoylated hnRNPA2B1 controls the sorting of miRNAs into exosomes through binding to specific motifs. <i>Nature Communications</i> , 2013, 4, 2980.	5.8	1,522
5	GOplot: an R package for visually combining expression data with functional analysis. <i>Bioinformatics</i> , 2015, 31, 2912-2914.	1.8	1,273
6	Mitochondrial and nuclear DNA matching shapes metabolism and healthy ageing. <i>Nature</i> , 2016, 535, 561-565.	13.7	333
7	Gene expression profiling of human mesenchymal stem cells derived from bone marrow during expansion and osteoblast differentiation. <i>BMC Genomics</i> , 2007, 8, 70.	1.2	320
8	The neural crest is a source of mesenchymal stem cells with specialized hematopoietic stem cell niche function. <i>ELife</i> , 2014, 3, e03696.	2.8	240
9	ATTRACT—a database of RNA-binding proteins and associated motifs. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw035.	1.4	215
10	CARMAweb: comprehensive R- and bioconductor-based web service for microarray data analysis. <i>Nucleic Acids Research</i> , 2006, 34, W498-W503.	6.5	209
11	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, 1321-1333.	2.9	125
12	PathwayExplorer: web service for visualizing high-throughput expression data on biological pathways. <i>Nucleic Acids Research</i> , 2005, 33, W633-W637.	6.5	116
13	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.	1.1	96
14	Comparative transcriptomics of human multipotent stem cells during adipogenesis and osteoblastogenesis. <i>BMC Genomics</i> , 2008, 9, 340.	1.2	91
15	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, 9340-9349.	1.1	85
16	Aging-Associated miR-217 Aggravates Atherosclerosis and Promotes Cardiovascular Dysfunction. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2020, 40, 2408-2424.	1.1	73
17	Spatial and Temporal Gene Expression Differences in Core and Periinfarct Areas in Experimental Stroke: A Microarray Analysis. <i>PLoS ONE</i> , 2012, 7, e52121.	1.1	59
18	Metoprolol exerts a non-class effect against ischaemia-induced reperfusion injury by abrogating exacerbated inflammation. <i>European Heart Journal</i> , 2020, 41, 4425-4440.	1.0	59

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19	Caveolar domain organization and trafficking is regulated by Abl kinases and mDia1. <i>Journal of Cell Science</i> , 2012, 125, 3097-113.	1.2	57
20	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.	2.9	56
21	CTCF counter-regulates cardiomyocyte development and maturation programs in the embryonic heart. <i>PLoS Genetics</i> , 2017, 13, e1006985.	1.5	54
22	Embryological-Origin-Dependent Differences in Homeobox Expression in Adult Aorta. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2013, 33, 1248-1256.	1.1	53
23	DNA Methylation of miR-7 is a Mechanism Involved in Platinum Response through MAFG Overexpression in Cancer Cells. <i>Theranostics</i> , 2017, 7, 4118-4134.	4.6	52
24	Glycated Hemoglobin and Subclinical Atherosclerosis in People Without Diabetes. <i>Journal of the American College of Cardiology</i> , 2021, 77, 2777-2791.	1.2	49
25	Cooperativity of Stress-Responsive Transcription Factors in Core Hypoxia-Inducible Factor Binding Regions. <i>PLoS ONE</i> , 2012, 7, e45708.	1.1	46
26	Machine Learning Improves Cardiovascular Risk Definition for Young, Asymptomatic Individuals. <i>Journal of the American College of Cardiology</i> , 2020, 76, 1674-1685.	1.2	44
27	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.	3.3	43
28	Loss of SRSF3 in Cardiomyocytes Leads to Decapping of Contraction-Related mRNAs and Severe Systolic Dysfunction. <i>Circulation Research</i> , 2019, 125, 170-183.	2.0	41
29	Reconstruction of gene association network reveals a transmembrane protein required for adipogenesis and targeted by PPAR $\gamma$ . <i>Cellular and Molecular Life Sciences</i> , 2010, 67, 4049-4064.	2.4	38
30	Aryl hydrocarbon receptor contributes to the MEK/ERK-dependent maintenance of the immature state of human dendritic cells. <i>Blood</i> , 2013, 121, e108-e117.	0.6	37
31	Oxidized Low-Density Lipoprotein Receptor in Lymphocytes Prevents Atherosclerosis and Predicts Subclinical Disease. <i>Circulation</i> , 2019, 139, 243-255.	1.6	36
32	Procyanidins Modulate MicroRNA Expression in Pancreatic Islets. <i>Journal of Agricultural and Food Chemistry</i> , 2013, 61, 355-363.	2.4	35
33	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.	4.7	35
34	ArrayNorm: comprehensive normalization and analysis of microarray data. <i>Bioinformatics</i> , 2004, 20, 1971-1973.	1.8	34
35	Alternative Splicing of NOX4 in the Failing Human Heart. <i>Frontiers in Physiology</i> , 2017, 8, 935.	1.3	32
36	Statistical Analysis Principles for Omics Data. <i>Methods in Molecular Biology</i> , 2011, 719, 113-131.	0.4	31

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37	A quantization method based on threshold optimization for microarray short time series. <i>BMC Bioinformatics</i> , 2005, 6, S11.	1.2	30
38	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-e71.	6.5	30
39	Colchicine in Recently Hospitalized Patients with COVID-19: A Randomized Controlled Trial (COL-COVID). <i>International Journal of General Medicine</i> , 2021, Volume 14, 5517-5526.	0.8	25
40	PGC-1 $\beta$ Regulates Translocated in Liposarcoma Activity: Role in Oxidative Stress Gene Expression. <i>Antioxidants and Redox Signaling</i> , 2011, 15, 325-337.	2.5	24
41	Digitaldsorter: Deep-Learning on scRNA-Seq to Deconvolute Gene Expression Data. <i>Frontiers in Genetics</i> , 2019, 10, 978.	1.1	22
42	The novel RUNX3/p33 isoform is induced upon monocyte-derived dendritic cell maturation and downregulates IL-8 expression. <i>Immunobiology</i> , 2010, 215, 812-820.	0.8	19
43	Sox17 Controls Emergence and Remodeling of Nestin-Expressing Coronary Vessels. <i>Circulation Research</i> , 2020, 127, e252-e270.	2.0	19
44	Data integration and exploration for the identification of molecular mechanisms in tumor-immune cells interaction. <i>BMC Genomics</i> , 2010, 11, S7.	1.2	16
45	Clonal haematopoiesis and atherosclerosis: a chicken or egg question?. <i>Nature Reviews Cardiology</i> , 2021, 18, 463-464.	6.1	15
46	A genome-wide shRNA screen for new OxPhos related genes. <i>Mitochondrion</i> , 2011, 11, 467-475.	1.6	14
47	Transcriptome and proteome mapping in the sheep atria reveal molecular features of atrial fibrillation progression. <i>Cardiovascular Research</i> , 2021, 117, 1760-1775.	1.8	14
48	Harmine and Piperlongumine Revert TRIB2-Mediated Drug Resistance. <i>Cancers</i> , 2020, 12, 3689.	1.7	14
49	Disease-modifying factors in hereditary angioedema: an RNA expression-based screening. <i>Orphanet Journal of Rare Diseases</i> , 2013, 8, 77.	1.2	12
50	Nanog regulates Pou3f1 expression at the exit from pluripotency during gastrulation. <i>Biology Open</i> , 2019, 8, .	0.6	11
51	Identification of a peripheral blood gene signature predicting aortic valve calcification. <i>Physiological Genomics</i> , 2020, 52, 563-574.	1.0	11
52	The SRSF4-GAS5-Glucocorticoid Receptor Axis Regulates Ventricular Hypertrophy. <i>Circulation Research</i> , 2021, 129, 669-683.	2.0	11
53	The Curse of Normalization. <i>Comparative and Functional Genomics</i> , 2002, 3, 375-379.	2.0	10
54	Immune synapse instructs epigenomic and transcriptomic functional reprogramming in dendritic cells. <i>Science Advances</i> , 2021, 7, .	4.7	10

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55	MiRNA post-transcriptional modification dynamics in T cell activation. <i>IScience</i> , 2021, 24, 102530.	1.9	10
56	A fully Bayesian model to cluster gene-expression profiles. <i>Bioinformatics</i> , 2005, 21, ii130-ii136.	1.8	9
57	Adaptive trimmed $t$ -statistics for identifying predominantly high expression in a microarray experiment. <i>Statistics in Medicine</i> , 2011, 30, 52-61.	0.8	9
58	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.	1.1	9
59	Axial skeleton anterior-posterior patterning is regulated through feedback regulation between Meis transcription factors and retinoic acid. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	8
60	Combined statistical modeling enables accurate mining of circadian transcription. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab031.	1.5	6
61	5-gene differential expression predicts stability of human intestinal allografts. <i>Experimental and Molecular Pathology</i> , 2017, 103, 163-171.	0.9	3
62	Interplay between UNG and AID governs intratumoral heterogeneity in mature B cell lymphoma. <i>PLoS Genetics</i> , 2020, 16, e1008960.	1.5	3
63	Variant pathogenic prediction by locus variability: the importance of the current picture of evolution. <i>European Journal of Human Genetics</i> , 2022, 30, 555-559.	1.4	3
64	Insights into Global Mechanisms and Disease by Gene Expression Profiling. <i>Methods in Molecular Biology</i> , 2011, 719, 269-298.	0.4	2
65	Hypothesis Driven versus Hypothesis-free: Filling the Gaps in CoQ Biosynthesis. <i>Cell Metabolism</i> , 2016, 24, 525-526.	7.2	2
66	Differential leucocyte RNA expression in the coronary arteries compared to systemic circulation discriminates between patients with and those without coronary artery disease. <i>Clínica E Investigaci3n En Arteriosclerosis</i> , 2017, 29, 60-66.	0.4	2
67	dSreg: a Bayesian model to integrate changes in splicing and RNA-binding protein activity. <i>Bioinformatics</i> , 2020, 36, 2134-2141.	1.8	1