

# Pedro Carmona-Saez

## List of Publications by Year in Descending Order

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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.

61  
papers

1,967  
citations

20  
h-index

43  
g-index

71  
ext. papers

2,434  
ext. citations

7.6  
avg, IF

4.72  
L-index

#	Paper	IF	Citations
61	sRNAbench and sRNAtoolbox 2022 update: accurate miRNA and sncRNA profiling for model and non-model organisms.. <i>Nucleic Acids Research</i> , <b>2022</b> ,	20.1	2
60	Transcription Factor Activity Inference in Systemic Lupus Erythematosus. <i>Life</i> , <b>2021</b> , 11,	3	1
59	A comprehensive database for integrated analysis of omics data in autoimmune diseases. <i>BMC Bioinformatics</i> , <b>2021</b> , 22, 343	3.6	3
58	A survey of gene expression meta-analysis: methods and applications. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22, 1694-1705	13.4	16
57	DatAC: A visual analytics platform to explore climate and air quality indicators associated with the COVID-19 pandemic in Spain. <i>Science of the Total Environment</i> , <b>2021</b> , 750, 141424	10.2	25
56	Integrative Analysis Reveals a Molecular Stratification of Systemic Autoimmune Diseases. <i>Arthritis and Rheumatology</i> , <b>2021</b> , 73, 1073-1085	9.5	27
55	DREIMT: a drug repositioning database and prioritization tool for immunomodulation. <i>Bioinformatics</i> , <b>2021</b> , 37, 578-579	7.2	2
54	Detecting Differentially Methylated Promoters in Genes Related to Disease Phenotypes Using R. <i>Bio-protocol</i> , <b>2021</b> , 11, e4033	0.9	
53	The SWI/SNF complex regulates the expression of miR-222, a tumor suppressor microRNA in lung adenocarcinoma. <i>Human Molecular Genetics</i> , <b>2021</b> , 30, 2263-2271	5.6	1
52	Placental DNA methylation signatures of maternal smoking during pregnancy and potential impacts on fetal growth. <i>Nature Communications</i> , <b>2021</b> , 12, 5095	17.4	5
51	Identification of Exosomal MicroRNA Signature by Liquid Biopsy in Hereditary Hemorrhagic Telangiectasia Patients. <i>International Journal of Molecular Sciences</i> , <b>2021</b> , 22,	6.3	2
50	GARP is a key molecule for mesenchymal stromal cell responses to TGF- $\beta$ and fundamental to control mitochondrial ROS levels. <i>Stem Cells Translational Medicine</i> , <b>2020</b> , 9, 636-650	6.9	9
49	Direct Detection of miR-122 in Hepatotoxicity Using Dynamic Chemical Labeling Overcomes Stability and isomiR Challenges. <i>Analytical Chemistry</i> , <b>2020</b> , 92, 3388-3395	7.8	12
48	Extracellular Protease ADAMTS1 Is Required at Early Stages of Human Uveal Melanoma Development by Inducing Stemness and Endothelial-Like Features on Tumor Cells. <i>Cancers</i> , <b>2020</b> , 12,	6.6	9
47	The value of lncRNAFENDRRandFOXF1 as a prognostic factor for survival of lung adenocarcinoma. <i>Oncotarget</i> , <b>2020</b> , 11, 1172-1185	3.3	8
46	The molecular clock protein Bmal1 regulates cell differentiation in mouse embryonic stem cells. <i>Life Science Alliance</i> , <b>2020</b> , 3,	5.8	6
45	iPS-Derived Early Oligodendrocyte Progenitor Cells from SPMS Patients Reveal Deficient In Vitro Cell Migration Stimulation. <i>Cells</i> , <b>2020</b> , 9,	7.9	5

44	Analysis of Menstrual Blood Stromal Cells Reveals SOX15 Triggers Oocyte-Based Human Cell Reprogramming. <i>IScience</i> , <b>2020</b> , 23, 101376	6.1	3
43	Computational Methods and Software Tools for Functional Analysis of miRNA Data. <i>Biomolecules</i> , <b>2020</b> , 10,	5.9	2
42	Polycomb regulation is coupled to cell cycle transition in pluripotent stem cells. <i>Science Advances</i> , <b>2020</b> , 6, eaay4768	14.3	10
41	NOMePlot: analysis of DNA methylation and nucleosome occupancy at the single molecule. <i>Scientific Reports</i> , <b>2019</b> , 9, 8140	4.9	2
40	Drug Repurposing From Transcriptome Data: Methods and Applications <b>2019</b> , 303-327		2
39	mCSEA: detecting subtle differentially methylated regions. <i>Bioinformatics</i> , <b>2019</b> , 35, 3257-3262	7.2	19
38	Exosomal miRNA profile as complementary tool in the diagnostic and prediction of treatment response in localized breast cancer under neoadjuvant chemotherapy. <i>Breast Cancer Research</i> , <b>2019</b> , 21, 21	8.3	76
37	ImaGEO: integrative gene expression meta-analysis from GEO database. <i>Bioinformatics</i> , <b>2019</b> , 35, 880-882	7.2	43
36	Gut Microbiota Composition Is Associated With the Global DNA Methylation Pattern in Obesity. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 613	4.5	24
35	Differential Treatments Based on Drug-induced Gene Expression Signatures and Longitudinal Systemic Lupus Erythematosus Stratification. <i>Scientific Reports</i> , <b>2019</b> , 9, 15502	4.9	12
34	Stratification of Systemic Lupus Erythematosus Patients Into Three Groups of Disease Activity Progression According to Longitudinal Gene Expression. <i>Arthritis and Rheumatology</i> , <b>2018</b> , 70, 2025-2035	8.5	53
33	Methodology for Y Chromosome Capture: A complete genome sequence of Y chromosome using flow cytometry, laser microdissection and magnetic streptavidin-beads. <i>Scientific Reports</i> , <b>2018</b> , 8, 9436	4.9	9
32	Support for phosphoinositol 3 kinase and mTOR inhibitors as treatment for lupus using in-silico drug-repurposing analysis. <i>Arthritis Research and Therapy</i> , <b>2017</b> , 19, 54	5.7	10
31	MetaGenyo: a web tool for meta-analysis of genetic association studies. <i>BMC Bioinformatics</i> , <b>2017</b> , 18, 563	3.6	55
30	Metagene projection characterizes GEN2.2 and CAL-1 as relevant human plasmacytoid dendritic cell models. <i>Bioinformatics</i> , <b>2017</b> , 33, 3691-3695	7.2	9
29	Prognostic factor analysis of circulating tumor cells in peripheral blood of patients with peritoneal carcinomatosis of colon cancer origin treated with cytoreductive surgery plus an intraoperative hyperthermic intraperitoneal chemotherapy procedure (CRS + HIPEC). <i>Surgery</i> , <b>2016</b> , 159, 728-35	3.6	15
28	Genetic polymorphisms influence on the response to clopidogrel in peripheral artery disease patients following percutaneous transluminal angioplasty. <i>Pharmacogenomics</i> , <b>2016</b> , 17, 1327-38	2.6	8
27	Prognostic role of genetic biomarkers in clinical progression of prostate cancer. <i>Experimental and Molecular Medicine</i> , <b>2015</b> , 47, e176	12.8	14

26	Influence of the HER2 Ile655Val polymorphism on trastuzumab-induced cardiotoxicity in HER2-positive breast cancer patients: a meta-analysis. <i>Pharmacogenetics and Genomics</i> , <b>2015</b> , 25, 388-93 <sup>1.9</sup>	24
25	Shared signatures between rheumatoid arthritis, systemic lupus erythematosus and Sjögren's syndrome uncovered through gene expression meta-analysis. <i>Arthritis Research and Therapy</i> , <b>2014</b> , 16, 489	5.7 51
24	Finding closed frequent item sets by intersecting transactions <b>2011</b> ,	13
23	MARQ: an online tool to mine GEO for experiments with similar or opposite gene expression signatures. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, W228-32	20.1 22
22	GeneCodis: interpreting gene lists through enrichment analysis and integration of diverse biological information. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, W317-22	20.1 354
21	SENT: semantic features in text. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, W153-9	20.1 4
20	A free radical-generating system induces the cholesterol biosynthesis pathway: a role in Alzheimer's disease. <i>Aging Cell</i> , <b>2009</b> , 8, 128-39	9.9 30
19	Ribavirin acts via multiple pathways in inhibition of leukemic cell proliferation. <i>Anticancer Research</i> , <b>2009</b> , 29, 1971-80	2.3 13
18	SPACE: an algorithm to predict and quantify alternatively spliced isoforms using microarrays. <i>Genome Biology</i> , <b>2008</b> , 9, R46	18.3 23
17	ChIPCodis: mining complex regulatory systems in yeast by concurrent enrichment analysis of chip-on-chip data. <i>Bioinformatics</i> , <b>2008</b> , 24, 1208-9	7.2 7
16	bioNMF: a web-based tool for nonnegative matrix factorization in biology. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, W523-8	20.1 25
15	GENECODIS: a web-based tool for finding significant concurrent annotations in gene lists. <i>Genome Biology</i> , <b>2007</b> , 8, R3	18.3 490
14	A literature-based similarity metric for biological processes. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 363	3.6 8
13	bioNMF: a versatile tool for non-negative matrix factorization in biology. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 366	3.6 62
12	Discovering semantic features in the literature: a foundation for building functional associations. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 41	3.6 55
11	Integrated analysis of gene expression by Association Rules Discovery. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 54	3.6 73
10	Biclustering of gene expression data by Non-smooth Non-negative Matrix Factorization. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 78	3.6 120
9	Transcriptional profiling of MCF7 breast cancer cells in response to 5-Fluorouracil: relationship with cell cycle changes and apoptosis, and identification of novel targets of p53. <i>International Journal of Cancer</i> , <b>2006</b> , 119, 1164-75	7.5 61

8	Knowledge Discovery in the Identification of Differentially Expressed Genes in Tumoricidal Macrophage. <i>Lecture Notes in Computer Science</i> , <b>2005</b> , 74-85	0.9
7	Two-way clustering of gene expression profiles by sparse matrix factorization	5
6	Deep Learning in Omics Data Analysis and Precision Medicine37-53	16
5	mCSEA: Detecting subtle differentially methylated regions	1
4	Integrative Analysis Reveals a Molecular Stratification of Systemic Autoimmune Diseases	1
3	DREIMT: a drug repositioning database and prioritization tool for immunomodulation	1
2	Placental DNA methylation signatures of maternal smoking during pregnancy and potential impacts on fetal growth	3
1	GeneCodis 4: Expanding the modular enrichment analysis to regulatory elements	3