

Pedro Carmona-Saez

List of Publications by Citations

Source: <https://exaly.com/author-pdf/5350448/pedro-carmona-saez-publications-by-citations.pdf>

Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	GENECODIS: a web-based tool for finding significant concurrent annotations in gene lists. <i>Genome Biology</i> , 2007 , 8, R3	18.3	490
60	GeneCodis: interpreting gene lists through enrichment analysis and integration of diverse biological information. <i>Nucleic Acids Research</i> , 2009 , 37, W317-22	20.1	354
59	Biclustering of gene expression data by Non-smooth Non-negative Matrix Factorization. <i>BMC Bioinformatics</i> , 2006 , 7, 78	3.6	120
58	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> , 2019 , 21, 21	8.3	76
57	Integrated analysis of gene expression by Association Rules Discovery. <i>BMC Bioinformatics</i> , 2006 , 7, 54	3.6	73
56	bioNMF: a versatile tool for non-negative matrix factorization in biology. <i>BMC Bioinformatics</i> , 2006 , 7, 366	3.6	62
55	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> , 2006 , 119, 1164-75	7.5	61
54	MetaGenyo: a web tool for meta-analysis of genetic association studies. <i>BMC Bioinformatics</i> , 2017 , 18, 563	3.6	55
53	Discovering semantic features in the literature: a foundation for building functional associations. <i>BMC Bioinformatics</i> , 2006 , 7, 41	3.6	55
52	Stratification of Systemic Lupus Erythematosus Patients Into Three Groups of Disease Activity Progression According to Longitudinal Gene Expression. <i>Arthritis and Rheumatology</i> , 2018 , 70, 2025-2038	9.5	53
51	Shared signatures between rheumatoid arthritis, systemic lupus erythematosus and Sjögren's syndrome uncovered through gene expression meta-analysis. <i>Arthritis Research and Therapy</i> , 2014 , 16, 489	5.7	51
50	ImaGEO: integrative gene expression meta-analysis from GEO database. <i>Bioinformatics</i> , 2019 , 35, 880-882	9.2	43
49	A free radical-generating system induces the cholesterol biosynthesis pathway: a role in Alzheimer's disease. <i>Aging Cell</i> , 2009 , 8, 128-39	9.9	30
48	Integrative Analysis Reveals a Molecular Stratification of Systemic Autoimmune Diseases. <i>Arthritis and Rheumatology</i> , 2021 , 73, 1073-1085	9.5	27
47	bioNMF: a web-based tool for nonnegative matrix factorization in biology. <i>Nucleic Acids Research</i> , 2008 , 36, W523-8	20.1	25
46	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> , 2021 , 750, 141424	10.2	25
45	Gut Microbiota Composition Is Associated With the Global DNA Methylation Pattern in Obesity. <i>Frontiers in Genetics</i> , 2019 , 10, 613	4.5	24

44	Influence of the HER2 Ile655Val polymorphism on trastuzumab-induced cardiotoxicity in HER2-positive breast cancer patients: a meta-analysis. <i>Pharmacogenetics and Genomics</i> , 2015 , 25, 388-93 ^{1.9}	24
43	SPACE: an algorithm to predict and quantify alternatively spliced isoforms using microarrays. <i>Genome Biology</i> , 2008 , 9, R46	18.3 23
42	MARQ: an online tool to mine GEO for experiments with similar or opposite gene expression signatures. <i>Nucleic Acids Research</i> , 2010 , 38, W228-32	20.1 22
41	mCSEA: detecting subtle differentially methylated regions. <i>Bioinformatics</i> , 2019 , 35, 3257-3262	7.2 19
40	Deep Learning in Omics Data Analysis and Precision Medicine ³⁷⁻⁵³	16
39	A survey of gene expression meta-analysis: methods and applications. <i>Briefings in Bioinformatics</i> , 2021 , 22, 1694-1705	13.4 16
38	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> , 2016 , 159, 728-35	3.6 15
37	Prognostic role of genetic biomarkers in clinical progression of prostate cancer. <i>Experimental and Molecular Medicine</i> , 2015 , 47, e176	12.8 14
36	Finding closed frequent item sets by intersecting transactions 2011 ,	13
35	Ribavirin acts via multiple pathways in inhibition of leukemic cell proliferation. <i>Anticancer Research</i> , 2009 , 29, 1971-80	2.3 13
34	Direct Detection of miR-122 in Hepatotoxicity Using Dynamic Chemical Labeling Overcomes Stability and isomiR Challenges. <i>Analytical Chemistry</i> , 2020 , 92, 3388-3395	7.8 12
33	Differential Treatments Based on Drug-induced Gene Expression Signatures and Longitudinal Systemic Lupus Erythematosus Stratification. <i>Scientific Reports</i> , 2019 , 9, 15502	4.9 12
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> , 2017 , 19, 54	5.7 10
31	Polycomb regulation is coupled to cell cycle transition in pluripotent stem cells. <i>Science Advances</i> , 2020 , 6, eaay4768	14.3 10
30	GARP is a key molecule for mesenchymal stromal cell responses to TGF- β and fundamental to control mitochondrial ROS levels. <i>Stem Cells Translational Medicine</i> , 2020 , 9, 636-650	6.9 9
29	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> , 2020 , 12,	6.6 9
28	Metagene projection characterizes GEN2.2 and CAL-1 as relevant human plasmacytoid dendritic cell models. <i>Bioinformatics</i> , 2017 , 33, 3691-3695	7.2 9
27	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> , 2018 , 8, 9436 ^{4.9}	9

26	A literature-based similarity metric for biological processes. <i>BMC Bioinformatics</i> , 2006 , 7, 363	3.6	8
25	The value of lncRNA FENDRR and FOXF1 as a prognostic factor for survival of lung adenocarcinoma. <i>Oncotarget</i> , 2020 , 11, 1172-1185	3.3	8
24	Genetic polymorphisms influence on the response to clopidogrel in peripheral artery disease patients following percutaneous transluminal angioplasty. <i>Pharmacogenomics</i> , 2016 , 17, 1327-38	2.6	8
23	ChIPCodis: mining complex regulatory systems in yeast by concurrent enrichment analysis of chip-on-chip data. <i>Bioinformatics</i> , 2008 , 24, 1208-9	7.2	7
22	The molecular clock protein Bmal1 regulates cell differentiation in mouse embryonic stem cells. <i>Life Science Alliance</i> , 2020 , 3,	5.8	6
21	Two-way clustering of gene expression profiles by sparse matrix factorization		5
20	iPS-Derived Early Oligodendrocyte Progenitor Cells from SPMS Patients Reveal Deficient In Vitro Cell Migration Stimulation. <i>Cells</i> , 2020 , 9,	7.9	5
19	Placental DNA methylation signatures of maternal smoking during pregnancy and potential impacts on fetal growth. <i>Nature Communications</i> , 2021 , 12, 5095	17.4	5
18	SENT: semantic features in text. <i>Nucleic Acids Research</i> , 2009 , 37, W153-9	20.1	4
17	Placental DNA methylation signatures of maternal smoking during pregnancy and potential impacts on fetal growth		3
16	Analysis of Menstrual Blood Stromal Cells Reveals SOX15 Triggers Oocyte-Based Human Cell Reprogramming. <i>iScience</i> , 2020 , 23, 101376	6.1	3
15	GeneCodis 4: Expanding the modular enrichment analysis to regulatory elements		3
14	A comprehensive database for integrated analysis of omics data in autoimmune diseases. <i>BMC Bioinformatics</i> , 2021 , 22, 343	3.6	3
13	NOMePlot: analysis of DNA methylation and nucleosome occupancy at the single molecule. <i>Scientific Reports</i> , 2019 , 9, 8140	4.9	2
12	Drug Repurposing From Transcriptome Data: Methods and Applications 2019 , 303-327		2
11	Computational Methods and Software Tools for Functional Analysis of miRNA Data. <i>Biomolecules</i> , 2020 , 10,	5.9	2
10	DREIMT: a drug repositioning database and prioritization tool for immunomodulation. <i>Bioinformatics</i> , 2021 , 37, 578-579	7.2	2
9	Identification of Exosomal MicroRNA Signature by Liquid Biopsy in Hereditary Hemorrhagic Telangiectasia Patients. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	2

8	sRNAbench and sRNAtoolbox 2022 update: accurate miRNA and sncRNA profiling for model and non-model organisms.. <i>Nucleic Acids Research</i> , 2022 ,	20.1	2
7	mCSEA: Detecting subtle differentially methylated regions		1
6	Integrative Analysis Reveals a Molecular Stratification of Systemic Autoimmune Diseases		1
5	DREIMT: a drug repositioning database and prioritization tool for immunomodulation		1
4	Transcription Factor Activity Inference in Systemic Lupus Erythematosus. <i>Life</i> , 2021 , 11,	3	1
3	The SWI/SNF complex regulates the expression of miR-222, a tumor suppressor microRNA in lung adenocarcinoma. <i>Human Molecular Genetics</i> , 2021 , 30, 2263-2271	5.6	1
2	Knowledge Discovery in the Identification of Differentially Expressed Genes in Tumoricidal Macrophage. <i>Lecture Notes in Computer Science</i> , 2005 , 74-85	0.9	
1	Detecting Differentially Methylated Promoters in Genes Related to Disease Phenotypes Using R. <i>Bio-protocol</i> , 2021 , 11, e4033	0.9	