

# Pedro Madrigal

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8119281/publications.pdf>

Version: 2024-02-01

28  
papers

4,279  
citations

471509

17  
h-index

526287

27  
g-index

36  
all docs

36  
docs citations

36  
times ranked

8791  
citing authors

#	ARTICLE	IF	CITATIONS
1	Space omics research in Europe: Contributions, geographical distribution and ESA member state funding schemes. <i>IScience</i> , 2022, 25, 103920.	4.1	6
2	Modeling HNF1B-associated monogenic diabetes using human iPSCs reveals an early stage impairment of the pancreatic developmental program. <i>Stem Cell Reports</i> , 2021, 16, 2289-2304.	4.8	7
3	Mutational synergy during leukemia induction remodels chromatin accessibility, histone modifications and three-dimensional DNA topology to alter gene expression. <i>Nature Genetics</i> , 2021, 53, 1443-1455.	21.4	19
4	Mannose Metabolism Is a Metabolic Vulnerability Unveiled By Standard and Novel Therapies in Acute Myeloid Leukemia. <i>Blood</i> , 2021, 138, 508-508.	1.4	1
5	Functional Divergence of the Arabidopsis Florigen-Interacting bZIP Transcription Factors FD and FDP. <i>Cell Reports</i> , 2020, 31, 107717.	6.4	49
6	Single-cell RNA-sequencing of differentiating iPSCs reveals dynamic genetic effects on gene expression. <i>Nature Communications</i> , 2020, 11, 810.	12.8	235
7	GATA6 Cooperates with EOMES/SMAD2/3 to Deploy the Gene Regulatory Network Governing Human Definitive Endoderm and Pancreas Formation. <i>Stem Cell Reports</i> , 2019, 12, 57-70.	4.8	33
8	A SINGLE CELL STUDY OF LYMPHOMA EVOLUTION. <i>Experimental Hematology</i> , 2019, 76, S56.	0.4	0
9	Functional data analysis for computational biology. <i>Bioinformatics</i> , 2019, 35, 3211-3213.	4.1	14
10	The SMAD2/3 interactome reveals that TGF $\beta$ 2 controls m6A mRNA methylation in pluripotency. <i>Nature</i> , 2018, 555, 256-259.	27.8	283
11	AP-1 Takes Centre Stage in Enhancer Chromatin Dynamics. <i>Trends in Cell Biology</i> , 2018, 28, 509-511.	7.9	50
12	hiPSC hepatocyte model demonstrates the role of unfolded protein response and inflammatory networks in $\alpha$ 1-antitrypsin deficiency. <i>Journal of Hepatology</i> , 2018, 69, 851-860.	3.7	48
13	fCCAC: functional canonical correlation analysis to evaluate covariance between nucleic acid sequencing datasets. <i>Bioinformatics</i> , 2017, 33, 746-748.	4.1	3
14	Postdocs, What Would You Tell Your Younger Self?. <i>Cell</i> , 2017, 168, 745-748.	28.9	0
15	Divergence of regulatory networks governed by the orthologous transcription factors FLC and PEP1 in Brassicaceae species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E11037-E11046.	7.1	50
16	Reconstruction of the mouse extrahepatic biliary tree using primary human extrahepatic cholangiocyte organoids. <i>Nature Medicine</i> , 2017, 23, 954-963.	30.7	210
17	Initiation of stem cell differentiation involves cell cycle-dependent regulation of developmental genes by Cyclin D. <i>Genes and Development</i> , 2016, 30, 421-433.	5.9	115
18	A survey of best practices for RNA-seq data analysis. <i>Genome Biology</i> , 2016, 17, 13.	8.8	1,898

#	ARTICLE	IF	CITATIONS
19	On Accounting for Sequence-Specific Bias in Genome-Wide Chromatin Accessibility Experiments: Recent Advances and Contradictions. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 144.	4.1	23
20	Uncovering correlated variability in epigenomic datasets using the Karhunen-Loeve transform. <i>BioData Mining</i> , 2015, 8, 20.	4.0	15
21	Cholangiocytes derived from human induced pluripotent stem cells for disease modeling and drug validation. <i>Nature Biotechnology</i> , 2015, 33, 845-852.	17.5	318
22	Combinatorial activities of SHORT VEGETATIVE PHASE and FLOWERING LOCUS C define distinct modes of flowering regulation in Arabidopsis. <i>Genome Biology</i> , 2015, 16, 31.	8.8	150
23	Activin/Nodal signaling and NANOG orchestrate human embryonic stem cell fate decisions by controlling the H3K4me3 chromatin mark. <i>Genes and Development</i> , 2015, 29, 702-717.	5.9	115
24	CexoR: an R/Bioconductor package to uncover high-resolution protein-DNA interactions in ChIP-exo replicates. <i>EMBnet Journal</i> , 2015, 21, .	0.6	7
25	Dynamics of chromatin accessibility and gene regulation by MADS-domain transcription factors in flower development. <i>Genome Biology</i> , 2014, 15, R41.	9.6	210
26	Practical Guidelines for the Comprehensive Analysis of ChIP-seq Data. <i>PLoS Computational Biology</i> , 2013, 9, e1003326.	3.2	221
27	Current bioinformatic approaches to identify DNase I hypersensitive sites and genomic footprints from DNase-seq data. <i>Frontiers in Genetics</i> , 2012, 3, 230.	2.3	29
28	Flowering and Plant Development at the 38th Spanish Society of Genetics Congress, Murcia, 2011. <i>Journal of Plant Growth Regulation</i> , 2012, 31, 136-138.	5.1	0