

# Pedro G Ferreira

## List of Publications by Year in descending order

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Version: 2024-02-01

45  
papers

35,684  
citations

185998

28  
h-index

243296

44  
g-index

50  
all docs

50  
docs citations

50  
times ranked

59638  
citing authors

#	ARTICLE	IF	CITATIONS
1	Deep learning for drug response prediction in cancer. Briefings in Bioinformatics, 2021, 22, 360-379.	3.2	116
2	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell, 2021, 184, 2633-2648.e19.	13.5	94
3	Predicting Gastric Cancer Molecular Subtypes from Gene Expression Data. Proceedings (mdpi), 2020, 54, 59.	0.2	1
4	A Quantitative Proteome Map of the Human Body. Cell, 2020, 183, 269-283.e19.	13.5	243
5	Gender Differential Transcriptome in Gastric and Thyroid Cancers. Frontiers in Genetics, 2020, 11, 808.	1.1	11
6	A vast resource of allelic expression data spanning human tissues. Genome Biology, 2020, 21, 234.	3.8	68
7	The effects of death and post-mortem cold ischemia on human tissue transcriptomes. Nature Communications, 2018, 9, 490.	5.8	198
8	Improving genetic diagnosis in Mendelian disease with transcriptome sequencing. Science Translational Medicine, 2017, 9, .	5.8	516
9	Time-dependent genetic effects on gene expression implicate aging processes. Genome Research, 2017, 27, 545-552.	2.4	31
10	Dynamic landscape and regulation of RNA editing in mammals. Nature, 2017, 550, 249-254.	13.7	495
11	Landscape of X chromosome inactivation across human tissues. Nature, 2017, 550, 244-248.	13.7	764
12	The impact of rare variation on gene expression across tissues. Nature, 2017, 550, 239-243.	13.7	229
13	Genetic effects on gene expression across human tissues. Nature, 2017, 550, 204-213.	13.7	3,500
14	Learning influential genes on cancer gene expression data with stacked denoising autoencoders. , 2017, , .		11
15	Sequence variation between 462 human individuals fine-tunes functional sites of RNA processing. Scientific Reports, 2016, 6, 32406.	1.6	28
16	Spatiotemporal Control of Forkhead Binding to DNA Regulates the Meiotic Gene Expression Program. Cell Reports, 2016, 14, 885-895.	2.9	12
17	Biased Allelic Expression in Human Primary Fibroblast Single Cells. American Journal of Human Genetics, 2015, 96, 70-80.	2.6	117
18	Short Term Exposure of Beta Cells to Low Concentrations of Interleukin-1 $\beta$ Improves Insulin Secretion through Focal Adhesion and Actin Remodeling and Regulation of Gene Expression. Journal of Biological Chemistry, 2015, 290, 6653-6669.	1.6	28

#	ARTICLE	IF	CITATIONS
19	The human transcriptome across tissues and individuals. <i>Science</i> , 2015, 348, 660-665.	6.0	1,127
20	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. <i>Science</i> , 2015, 348, 648-660.	6.0	4,659
21	Effect of predicted protein-truncating genetic variants on the human transcriptome. <i>Science</i> , 2015, 348, 666-669.	6.0	252
22	Molecular signatures of plastic phenotypes in two eusocial insect species with simple societies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13970-13975.	3.3	192
23	Tandem RNA Chimeras Contribute to Transcriptome Diversity in Human Population and Are Associated with Intronic Genetic Variants. <i>PLoS ONE</i> , 2014, 9, e104567.	1.1	31
24	Identification of genetic variants associated with alternative splicing using sQTLseeker. <i>Nature Communications</i> , 2014, 5, 4698.	5.8	121
25	Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. <i>Genome Research</i> , 2014, 24, 212-226.	2.4	175
26	Putative cis-regulatory drivers in colorectal cancer. <i>Nature</i> , 2014, 512, 87-90.	13.7	136
27	Transcriptome analyses of primitively eusocial wasps reveal novel insights into the evolution of sociality and the origin of alternative phenotypes. <i>Genome Biology</i> , 2013, 14, R20.	13.9	139
28	Transcriptome and genome sequencing uncovers functional variation in humans. <i>Nature</i> , 2013, 501, 506-511.	13.7	1,857
29	CPEB1 coordinates alternative 3' UTR formation with translational regulation. <i>Nature</i> , 2013, 495, 121-125.	13.7	156
30	Sporadic and reversible chromothripsis in chronic lymphocytic leukemia revealed by longitudinal genomic analysis. <i>Leukemia</i> , 2013, 27, 2376-2379.	3.3	29
31	Immune response is a personal matter. <i>ELife</i> , 2013, 2, e00899.	2.8	1
32	RNA secondary structure mediates alternative 3' UTR selection in <i>Saccharomyces cerevisiae</i> . <i>Rna</i> , 2012, 18, 1103-1115.	1.6	38
33	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	13.7	15,516
34	Landscape of transcription in human cells. <i>Nature</i> , 2012, 489, 101-108.	13.7	4,484
35	Evolutionary patterns at the RNase based gametophytic self - incompatibility system in two divergent Rosaceae groups (Maloideae and Prunus). <i>BMC Evolutionary Biology</i> , 2010, 10, 200.	3.2	29
36	Mitotic cell-cycle progression is regulated by CPEB1 and CPEB4-dependent translational control. <i>Nature Cell Biology</i> , 2010, 12, 447-456.	4.6	138

#	ARTICLE	IF	CITATIONS
37	Deterministic Pattern Mining On Genetic Sequences. , 2010, , 277-301.		0
38	Using Data Mining Techniques to Probe the Role of Hydrophobic Residues in Protein Folding and Unfolding Simulations. , 2010, , 258-276.		0
39	Spatial Clustering of Molecular Dynamics Trajectories in Protein Unfolding Simulations. Lecture Notes in Computer Science, 2009, , 156-166.	1.0	2
40	A Closer Look on Protein Unfolding Simulations through Hierarchical Clustering. , 2007, , .		3
41	Evaluating deterministic motif significance measures in protein databases. Algorithms for Molecular Biology, 2007, 2, 16.	0.3	16
42	Evaluating Protein Motif Significance Measures: A Case Study on Prosite Patterns. , 2007, , .		4
43	Establishing Fraud Detection Patterns Based on Signatures. Lecture Notes in Computer Science, 2006, , 526-538.	1.0	26
44	Mining Approximate Motifs in Time Series. Lecture Notes in Computer Science, 2006, , 89-101.	1.0	33
45	Protein Sequence Classification Through Relevant Sequence Mining and Bayes Classifiers. Lecture Notes in Computer Science, 2005, , 236-247.	1.0	19