Pedro G Ferreira

List of Publications by Year
in descending order

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	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	13.7	15,516
2	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. Science, 2015, 348, 648-660.	6.0	4,659
3	Landscape of transcription in human cells. Nature, 2012, 489, 101-108.	13.7	4,484
4	Genetic effects on gene expression across human tissues. Nature, 2017, 550, 204-213.	13.7	3,500
5	Transcriptome and genome sequencing uncovers functional variation in humans. Nature, 2013, 501, 506-511.	13.7	1,857
6	The human transcriptome across tissues and individuals. Science, 2015, 348, 660-665.	6.0	1,127
7	Landscape of X chromosome inactivation across human tissues. Nature, 2017, 550, 244-248.	13.7	764
8	Improving genetic diagnosis in Mendelian disease with transcriptome sequencing. Science Translational Medicine, 2017, 9, .	5.8	516
9	Dynamic landscape and regulation of RNA editing in mammals. Nature, 2017, 550, 249-254.	13.7	495
10	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	6.0	252
11	A Quantitative Proteome Map of the Human Body. Cell, 2020, 183, 269-283.e19.	13.5	243
12	The impact of rare variation on gene expression across tissues. Nature, 2017, 550, 239-243.	13.7	229
13	The effects of death and post-mortem cold ischemia on human tissue transcriptomes. Nature Communications, 2018, 9, 490.	5.8	198
14	Molecular signatures of plastic phenotypes in two eusocial insect species with simple societies. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13970-13975.	3.3	192
15	Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. Genome Research, 2014, 24, 212-226.	2.4	175
16	CPEB1 coordinates alternative 3â€²-UTR formation with translational regulation. Nature, 2013, 495, 121-125.	13.7	156
17	Transcriptome analyses of primitively eusocial wasps reveal novel insights into the evolution of sociality and the origin of alternative phenotypes. Genome Biology, 2013, 14, R20.	13.9	139
18	Mitotic cell-cycle progression is regulated by CPEB1 and CPEB4-dependent translational control. Nature Cell Biology, 2010, 12, 447-456.	4.6	138

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19	Putative cis-regulatory drivers in colorectal cancer. Nature, 2014, 512, 87-90.	13.7	136
20	Identification of genetic variants associated with alternative splicing using sQTLseekeR. Nature Communications, 2014, 5, 4698.	5.8	121
21	Biased Allelic Expression in Human Primary Fibroblast Single Cells. American Journal of Human Genetics, 2015, 96, 70-80.	2.6	117
22	Deep learning for drug response prediction in cancer. Briefings in Bioinformatics, 2021, 22, 360-379.	3.2	116
23	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell, 2021, 184, 2633-2648.e19.	13.5	94
24	A vast resource of allelic expression data spanning human tissues. Genome Biology, 2020, 21, 234.	3.8	68
25	RNA secondary structure mediates alternative 3â€²ss selection in <i>Saccharomyces cerevisiae</i>. Rna, 2012, 18, 1103-1115.	1.6	38
26	Mining Approximate Motifs in Time Series. Lecture Notes in Computer Science, 2006, , 89-101.	1.0	33
27	Tandem RNA Chimeras Contribute to Transcriptome Diversity in Human Population and Are Associated with Intronic Genetic Variants. PLoS ONE, 2014, 9, e104567.	1.1	31
28	Time-dependent genetic effects on gene expression implicate aging processes. Genome Research, 2017, 27, 545-552.	2.4	31
29	Evolutionary patterns at the RNase based gametophytic self - incompatibility system in two divergent Rosaceae groups (Maloideae and Prunus). BMC Evolutionary Biology, 2010, 10, 200.	3.2	29
30	Sporadic and reversible chromothripsis in chronic lymphocytic leukemia revealed by longitudinal genomic analysis. Leukemia, 2013, 27, 2376-2379.	3.3	29
31	Short Term Exposure of Beta Cells to Low Concentrations of Interleukin-1Î² 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
32	Sequence variation between 462 human individuals fine-tunes functional sites of RNA processing. Scientific Reports, 2016, 6, 32406.	1.6	28
33	Establishing Fraud Detection Patterns Based on Signatures. Lecture Notes in Computer Science, 2006, , 526-538.	1.0	26
34	Protein Sequence Classification Through Relevant Sequence Mining and Bayes Classifiers. Lecture Notes in Computer Science, 2005, , 236-247.	1.0	19
35	Evaluating deterministic motif significance measures in protein databases. Algorithms for Molecular Biology, 2007, 2, 16.	0.3	16
36	Spatiotemporal Control of Forkhead Binding to DNA Regulates the Meiotic Gene Expression Program. Cell Reports, 2016, 14, 885-895.	2.9	12

#	Article	IF	Citations
37	Learning influential genes on cancer gene expression data with stacked denoising autoencoders. , 2017, , .		11
38	Gender Differential Transcriptome in Gastric and Thyroid Cancers. Frontiers in Genetics, 2020, 11, 808.	1.1	11
39	Evaluating Protein Motif Significance Measures: A Case Study on Prosite Patterns. , 2007, , .		4
40	A Closer Look on Protein Unfolding Simulations through Hierarchical Clustering. , 2007, , .		3
41	Spatial Clustering of Molecular Dynamics Trajectories in Protein Unfolding Simulations. Lecture Notes in Computer Science, 2009, , 156-166.	1.0	2
42	Predicting Gastric Cancer Molecular Subtypes from Gene Expression Data. Proceedings (mdpi), 2020, 54, 59.	0.2	1
43	Immune response is a personal matter. ELife, 2013, 2, e00899.	2.8	1
44	Deterministic Pattern Mining On Genetic Sequences. , 2010, , 277-301.		0
45	Using Data Mining Techniques to Probe the Role of Hydrophobic Residues in Protein Folding and Unfolding Simulations. , 2010, , 258-276.		0