

Pedro G Ferreira

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

35,684
citations

186265

28
h-index

243625

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. <i>Briefings in Bioinformatics</i> , 2021, 22, 360-379.	6.5	116
2	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. <i>Cell</i> , 2021, 184, 2633-2648.e19.	28.9	94
3	Predicting Gastric Cancer Molecular Subtypes from Gene Expression Data. <i>Proceedings (mdpi)</i> , 2020, 54, 59.	0.2	1
4	A Quantitative Proteome Map of the Human Body. <i>Cell</i> , 2020, 183, 269-283.e19.	28.9	243
5	Gender Differential Transcriptome in Gastric and Thyroid Cancers. <i>Frontiers in Genetics</i> , 2020, 11, 808.	2.3	11
6	A vast resource of allelic expression data spanning human tissues. <i>Genome Biology</i> , 2020, 21, 234.	8.8	68
7	The effects of death and post-mortem cold ischemia on human tissue transcriptomes. <i>Nature Communications</i> , 2018, 9, 490.	12.8	198
8	Improving genetic diagnosis in Mendelian disease with transcriptome sequencing. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	516
9	Time-dependent genetic effects on gene expression implicate aging processes. <i>Genome Research</i> , 2017, 27, 545-552.	5.5	31
10	Dynamic landscape and regulation of RNA editing in mammals. <i>Nature</i> , 2017, 550, 249-254.	27.8	495
11	Landscape of X chromosome inactivation across human tissues. <i>Nature</i> , 2017, 550, 244-248.	27.8	764
12	The impact of rare variation on gene expression across tissues. <i>Nature</i> , 2017, 550, 239-243.	27.8	229
13	Genetic effects on gene expression across human tissues. <i>Nature</i> , 2017, 550, 204-213.	27.8	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. <i>Scientific Reports</i> , 2016, 6, 32406.	3.3	28
16	Spatiotemporal Control of Forkhead Binding to DNA Regulates the Meiotic Gene Expression Program. <i>Cell Reports</i> , 2016, 14, 885-895.	6.4	12
17	Biased Allelic Expression in Human Primary Fibroblast Single Cells. <i>American Journal of Human Genetics</i> , 2015, 96, 70-80.	6.2	117
18	Short Term Exposure of Beta Cells to Low Concentrations of Interleukin-1 β Improves Insulin Secretion through Focal Adhesion and Actin Remodeling and Regulation of Gene Expression. <i>Journal of Biological Chemistry</i> , 2015, 290, 6653-6669.	3.4	28

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19	The human transcriptome across tissues and individuals. <i>Science</i> , 2015, 348, 660-665.	12.6	1,127
20	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. <i>Science</i> , 2015, 348, 648-660.	12.6	4,659
21	Effect of predicted protein-truncating genetic variants on the human transcriptome. <i>Science</i> , 2015, 348, 666-669.	12.6	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.	7.1	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.	2.5	31
24	Identification of genetic variants associated with alternative splicing using sQTLseeker. <i>Nature Communications</i> , 2014, 5, 4698.	12.8	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.	5.5	175
26	Putative cis-regulatory drivers in colorectal cancer. <i>Nature</i> , 2014, 512, 87-90.	27.8	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.	9.6	139
28	Transcriptome and genome sequencing uncovers functional variation in humans. <i>Nature</i> , 2013, 501, 506-511.	27.8	1,857
29	CPEB1 coordinates alternative 3' UTR formation with translational regulation. <i>Nature</i> , 2013, 495, 121-125.	27.8	156
30	Sporadic and reversible chromothripsis in chronic lymphocytic leukemia revealed by longitudinal genomic analysis. <i>Leukemia</i> , 2013, 27, 2376-2379.	7.2	29
31	Immune response is a personal matter. <i>ELife</i> , 2013, 2, e00899.	6.0	1
32	RNA secondary structure mediates alternative 3' UTR selection in <i>Saccharomyces cerevisiae</i> . <i>Rna</i> , 2012, 18, 1103-1115.	3.5	38
33	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	27.8	15,516
34	Landscape of transcription in human cells. <i>Nature</i> , 2012, 489, 101-108.	27.8	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.	10.3	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.	1.3	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.	1.2	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.	1.3	26
44	Mining Approximate Motifs in Time Series. Lecture Notes in Computer Science, 2006, , 89-101.	1.3	33
45	Protein Sequence Classification Through Relevant Sequence Mining and Bayes Classifiers. Lecture Notes in Computer Science, 2005, , 236-247.	1.3	19