Pejman Mohammadi

List of Publications by Year
in descending order

35 papers	9,162 citations	236925 25 h-index	330143 37 g-index
53 all docs	53 docs citations	53 times ranked	20263 citing authors

#	Article	IF	Citations
1	Genetic effects on gene expression across human tissues. Nature, 2017, 550, 204-213.	27.8	3,500
2	Landscape of X chromosome inactivation across human tissues. Nature, 2017, 550, 244-248.	27.8	764
3	Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics. Nature Communications, 2018, 9, 1825.	12.8	748
4	A primer on deep learning in genomics. Nature Genetics, 2019, 51, 12-18.	21.4	542
5	Dynamic landscape and regulation of RNA editing in mammals. Nature, 2017, 550, 249-254.	27.8	495
6	Tools and best practices for data processing in allelic expression analysis. Genome Biology, 2015, 16, 195.	8.8	335
7	The impact of sex on gene expression across human tissues. Science, 2020, 369, .	12.6	329
8	A Quantitative Proteome Map of the Human Body. Cell, 2020, 183, 269-283.e19.	28.9	243
9	IFI16 is required for DNA sensing in human macrophages by promoting production and function of cGAMP. Nature Communications, 2017, 8, 14391.	12.8	236
10	The impact of rare variation on gene expression across tissues. Nature, 2017, 550, 239-243.	27.8	229
11	Modified penetrance of coding variants by cis-regulatory variation contributes to disease risk. Nature Genetics, 2018, 50, 1327-1334.	21.4	167
12	Genetic regulatory effects modified by immune activation contribute to autoimmune disease associations. Nature Communications, 2017, 8, 266.	12.8	157
13	24 Hours in the Life of HIV-1 in a T Cell Line. PLoS Pathogens, 2013, 9, e1003161.	4.7	134
14	Quantifying the regulatory effect size of *cis*-acting genetic variation using allelic fold change. Genome Research, 2017, 27, 1872-1884.	5.5	114
15	Rare variant phasing and haplotypic expression from RNA sequencing with phASER. Nature Communications, 2016, 7, 12817.	12.8	105
16	Genetic regulatory variation in populations informs transcriptome analysis in rare disease. Science, 2019, 366, 351-356.	12.6	99
17	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell, 2021, 184, 2633-2648.e19.	28.9	94
18	Transcriptomic signatures across human tissues identify functional rare genetic variation. Science, 2020, 369, .	12.6	89

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19	Dynamics of HIV Latency and Reactivation in a Primary CD4+ T Cell Model. PLoS Pathogens, 2014, 10, e1004156.	4.7	70
20	A vast resource of allelic expression data spanning human tissues. Genome Biology, 2020, 21, 234.	8.8	68
21	Promoter-interacting expression quantitative trait loci are enriched for functional genetic variants. Nature Genetics, 2021, 53, 110-119.	21.4	62
22	TiMEx: a waiting time model for mutually exclusive cancer alterations. Bioinformatics, 2016, 32, 968-975.	4.1	57
23	Integrative genomic analyses identify susceptibility genes underlying COVID-19 hospitalization. Nature Communications, 2021, 12, 4569.	12.8	47
24	Automated Design of Synthetic Cell Classifier Circuits Using a Two-Step Optimization Strategy. Cell Systems, 2017, 4, 207-218.e14.	6.2	36
25	The Characteristics of Heterozygous Protein Truncating Variants in the Human Genome. PLoS Computational Biology, 2015, 11, e1004647.	3.2	34
26	Analysis of Stop-Gain and Frameshift Variants in Human Innate Immunity Genes. PLoS Computational Biology, 2014, 10, e1003757.	3.2	32
27	Differential expression of lncRNAs during the HIV replication cycle: an underestimated layer in the HIV-host interplay. Scientific Reports, 2016, 6, 36111.	3.3	28
28	Proteo-Transcriptomic Dynamics of Cellular Response to HIV-1 Infection. Scientific Reports, 2019, 9, 213.	3.3	24
29	HIV-1 RNAs are Not Part of the Argonaute 2 Associated RNA Interference Pathway in Macrophages. PLoS ONE, 2015, 10, e0132127.	2.5	15
30	Transcription factor regulation of eQTL activity across individuals and tissues. PLoS Genetics, 2022, 18, e1009719.	3.5	14
31	Bioinformatics and HIV Latency. Current HIV/AIDS Reports, 2015, 12, 97-106.	3.1	12
32	BMix: probabilistic modeling of occurring substitutions in PAR-CLIP data. Bioinformatics, 2016, 32, 976-983.	4.1	12
33	Allele-specific expression: applications in cancer and technical considerations. Current Opinion in Genetics and Development, 2021, 66, 10-19.	3.3	11
34	Dynamic models of viral replication and latency. Current Opinion in HIV and AIDS, 2015, 10, 90-95.	3.8	8
35	Genetic variation near CXCL12 is associated with susceptibility to HIV-related non-Hodgkin lymphoma. Haematologica, 2021, 106, 2233-2241.	3.5	4