

Pejman Mohammadi

List of Publications by Year in descending order

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Version: 2024-02-01

35
papers

9,162
citations

236612

25
h-index

329751

37
g-index

53
all docs

53
docs citations

53
times ranked

20263
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcription factor regulation of eQTL activity across individuals and tissues. <i>PLoS Genetics</i> , 2022, 18, e1009719.	1.5	14
2	Genetic variation near CXCL12 is associated with susceptibility to HIV-related non-Hodgkin lymphoma. <i>Haematologica</i> , 2021, 106, 2233-2241.	1.7	4
3	Promoter-interacting expression quantitative trait loci are enriched for functional genetic variants. <i>Nature Genetics</i> , 2021, 53, 110-119.	9.4	62
4	Allele-specific expression: applications in cancer and technical considerations. <i>Current Opinion in Genetics and Development</i> , 2021, 66, 10-19.	1.5	11
5	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. <i>Cell</i> , 2021, 184, 2633-2648.e19.	13.5	94
6	Integrative genomic analyses identify susceptibility genes underlying COVID-19 hospitalization. <i>Nature Communications</i> , 2021, 12, 4569.	5.8	47
7	A Quantitative Proteome Map of the Human Body. <i>Cell</i> , 2020, 183, 269-283.e19.	13.5	243
8	Transcriptomic signatures across human tissues identify functional rare genetic variation. <i>Science</i> , 2020, 369, .	6.0	89
9	The impact of sex on gene expression across human tissues. <i>Science</i> , 2020, 369, .	6.0	329
10	A vast resource of allelic expression data spanning human tissues. <i>Genome Biology</i> , 2020, 21, 234.	3.8	68
11	Genetic regulatory variation in populations informs transcriptome analysis in rare disease. <i>Science</i> , 2019, 366, 351-356.	6.0	99
12	Proteo-Transcriptomic Dynamics of Cellular Response to HIV-1 Infection. <i>Scientific Reports</i> , 2019, 9, 213.	1.6	24
13	A primer on deep learning in genomics. <i>Nature Genetics</i> , 2019, 51, 12-18.	9.4	542
14	Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics. <i>Nature Communications</i> , 2018, 9, 1825.	5.8	748
15	Modified penetrance of coding variants by cis-regulatory variation contributes to disease risk. <i>Nature Genetics</i> , 2018, 50, 1327-1334.	9.4	167
16	IFI16 is required for DNA sensing in human macrophages by promoting production and function of cGAMP. <i>Nature Communications</i> , 2017, 8, 14391.	5.8	236
17	Automated Design of Synthetic Cell Classifier Circuits Using a Two-Step Optimization Strategy. <i>Cell Systems</i> , 2017, 4, 207-218.e14.	2.9	36
18	Dynamic landscape and regulation of RNA editing in mammals. <i>Nature</i> , 2017, 550, 249-254.	13.7	495

#	ARTICLE	IF	CITATIONS
19	Landscape of X chromosome inactivation across human tissues. <i>Nature</i> , 2017, 550, 244-248.	13.7	764
20	The impact of rare variation on gene expression across tissues. <i>Nature</i> , 2017, 550, 239-243.	13.7	229
21	Genetic effects on gene expression across human tissues. <i>Nature</i> , 2017, 550, 204-213.	13.7	3,500
22	Quantifying the regulatory effect size of <i>cis</i> -acting genetic variation using allelic fold change. <i>Genome Research</i> , 2017, 27, 1872-1884.	2.4	114
23	Genetic regulatory effects modified by immune activation contribute to autoimmune disease associations. <i>Nature Communications</i> , 2017, 8, 266.	5.8	157
24	Differential expression of lncRNAs during the HIV replication cycle: an underestimated layer in the HIV-host interplay. <i>Scientific Reports</i> , 2016, 6, 36111.	1.6	28
25	Rare variant phasing and haplotypic expression from RNA sequencing with phASER. <i>Nature Communications</i> , 2016, 7, 12817.	5.8	105
26	BMix: probabilistic modeling of occurring substitutions in PAR-CLIP data. <i>Bioinformatics</i> , 2016, 32, 976-983.	1.8	12
27	TiME: a waiting time model for mutually exclusive cancer alterations. <i>Bioinformatics</i> , 2016, 32, 968-975.	1.8	57
28	Tools and best practices for data processing in allelic expression analysis. <i>Genome Biology</i> , 2015, 16, 195.	3.8	335
29	The Characteristics of Heterozygous Protein Truncating Variants in the Human Genome. <i>PLoS Computational Biology</i> , 2015, 11, e1004647.	1.5	34
30	Bioinformatics and HIV Latency. <i>Current HIV/AIDS Reports</i> , 2015, 12, 97-106.	1.1	12
31	Dynamic models of viral replication and latency. <i>Current Opinion in HIV and AIDS</i> , 2015, 10, 90-95.	1.5	8
32	HIV-1 RNAs are Not Part of the Argonaute 2 Associated RNA Interference Pathway in Macrophages. <i>PLoS ONE</i> , 2015, 10, e0132127.	1.1	15
33	Dynamics of HIV Latency and Reactivation in a Primary CD4+ T Cell Model. <i>PLoS Pathogens</i> , 2014, 10, e1004156.	2.1	70
34	Analysis of Stop-Gain and Frameshift Variants in Human Innate Immunity Genes. <i>PLoS Computational Biology</i> , 2014, 10, e1003757.	1.5	32
35	24 Hours in the Life of HIV-1 in a T Cell Line. <i>PLoS Pathogens</i> , 2013, 9, e1003161.	2.1	134