

Pejman Mohammadi

List of Publications by Year in descending order

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Version: 2024-02-01

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	Transcription factor regulation of eQTL activity across individuals and tissues. PLoS Genetics, 2022, 18, e1009719.	3.5	14
2	Genetic variation near CXCL12 is associated with susceptibility to HIV-related non-Hodgkin lymphoma. Haematologica, 2021, 106, 2233-2241.	3.5	4
3	Promoter-interacting expression quantitative trait loci are enriched for functional genetic variants. Nature Genetics, 2021, 53, 110-119.	21.4	62
4	Allele-specific expression: applications in cancer and technical considerations. Current Opinion in Genetics and Development, 2021, 66, 10-19.	3.3	11
5	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell, 2021, 184, 2633-2648.e19.	28.9	94
6	Integrative genomic analyses identify susceptibility genes underlying COVID-19 hospitalization. Nature Communications, 2021, 12, 4569.	12.8	47
7	A Quantitative Proteome Map of the Human Body. Cell, 2020, 183, 269-283.e19.	28.9	243
8	Transcriptomic signatures across human tissues identify functional rare genetic variation. Science, 2020, 369, .	12.6	89
9	The impact of sex on gene expression across human tissues. Science, 2020, 369, .	12.6	329
10	A vast resource of allelic expression data spanning human tissues. Genome Biology, 2020, 21, 234.	8.8	68
11	Genetic regulatory variation in populations informs transcriptome analysis in rare disease. Science, 2019, 366, 351-356.	12.6	99
12	Proteo-Transcriptomic Dynamics of Cellular Response to HIV-1 Infection. Scientific Reports, 2019, 9, 213.	3.3	24
13	A primer on deep learning in genomics. Nature Genetics, 2019, 51, 12-18.	21.4	542
14	Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics. Nature Communications, 2018, 9, 1825.	12.8	748
15	Modified penetrance of coding variants by cis-regulatory variation contributes to disease risk. Nature Genetics, 2018, 50, 1327-1334.	21.4	167
16	IFI16 is required for DNA sensing in human macrophages by promoting production and function of cGAMP. Nature Communications, 2017, 8, 14391.	12.8	236
17	Automated Design of Synthetic Cell Classifier Circuits Using a Two-Step Optimization Strategy. Cell Systems, 2017, 4, 207-218.e14.	6.2	36
18	Dynamic landscape and regulation of RNA editing in mammals. Nature, 2017, 550, 249-254.	27.8	495

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19	Landscape of X chromosome inactivation across human tissues. <i>Nature</i> , 2017, 550, 244-248.	27.8	764
20	The impact of rare variation on gene expression across tissues. <i>Nature</i> , 2017, 550, 239-243.	27.8	229
21	Genetic effects on gene expression across human tissues. <i>Nature</i> , 2017, 550, 204-213.	27.8	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.	5.5	114
23	Genetic regulatory effects modified by immune activation contribute to autoimmune disease associations. <i>Nature Communications</i> , 2017, 8, 266.	12.8	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.	3.3	28
25	Rare variant phasing and haplotypic expression from RNA sequencing with phASER. <i>Nature Communications</i> , 2016, 7, 12817.	12.8	105
26	BMix: probabilistic modeling of occurring substitutions in PAR-CLIP data. <i>Bioinformatics</i> , 2016, 32, 976-983.	4.1	12
27	TiMEx: a waiting time model for mutually exclusive cancer alterations. <i>Bioinformatics</i> , 2016, 32, 968-975.	4.1	57
28	Tools and best practices for data processing in allelic expression analysis. <i>Genome Biology</i> , 2015, 16, 195.	8.8	335
29	The Characteristics of Heterozygous Protein Truncating Variants in the Human Genome. <i>PLoS Computational Biology</i> , 2015, 11, e1004647.	3.2	34
30	Bioinformatics and HIV Latency. <i>Current HIV/AIDS Reports</i> , 2015, 12, 97-106.	3.1	12
31	Dynamic models of viral replication and latency. <i>Current Opinion in HIV and AIDS</i> , 2015, 10, 90-95.	3.8	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.	2.5	15
33	Dynamics of HIV Latency and Reactivation in a Primary CD4+ T Cell Model. <i>PLoS Pathogens</i> , 2014, 10, e1004156.	4.7	70
34	Analysis of Stop-Gain and Frameshift Variants in Human Innate Immunity Genes. <i>PLoS Computational Biology</i> , 2014, 10, e1003757.	3.2	32
35	24 Hours in the Life of HIV-1 in a T Cell Line. <i>PLoS Pathogens</i> , 2013, 9, e1003161.	4.7	134