

Alvaro N Barbeira

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

3,605
citations

567281

15
h-index

752698

20
g-index

35
all docs

35
docs citations

35
times ranked

7823
citing authors

#	ARTICLE	IF	CITATIONS
1	Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics. <i>Nature Communications</i> , 2018, 9, 1825.	12.8	748
2	Opportunities and challenges for transcriptome-wide association studies. <i>Nature Genetics</i> , 2019, 51, 592-599.	21.4	592
3	Annotation-free quantification of RNA splicing using LeafCutter. <i>Nature Genetics</i> , 2018, 50, 151-158.	21.4	520
4	The impact of sex on gene expression across human tissues. <i>Science</i> , 2020, 369, .	12.6	329
5	Integrating predicted transcriptome from multiple tissues improves association detection. <i>PLoS Genetics</i> , 2019, 15, e1007889.	3.5	239
6	Cell type-specific genetic regulation of gene expression across human tissues. <i>Science</i> , 2020, 369, .	12.6	210
7	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. <i>Genome Biology</i> , 2021, 22, 49.	8.8	150
8	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. <i>Cell</i> , 2021, 184, 2633-2648.e19.	28.9	94
9	Transcriptomic signatures across human tissues identify functional rare genetic variation. <i>Science</i> , 2020, 369, .	12.6	89
10	PhenomeXcan: Mapping the genome to the phenome through the transcriptome. <i>Science Advances</i> , 2020, 6, .	10.3	83
11	A vast resource of allelic expression data spanning human tissues. <i>Genome Biology</i> , 2020, 21, 234.	8.8	68
12	Impact of admixture and ancestry on eQTL analysis and GWAS colocalization in GTEx. <i>Genome Biology</i> , 2020, 21, 233.	8.8	64
13	PTWAS: investigating tissue-relevant causal molecular mechanisms of complex traits using probabilistic TWAS analysis. <i>Genome Biology</i> , 2020, 21, 232.	8.8	46
14	Fine-mapping and QTL tissue-sharing information improves the reliability of causal gene identification. <i>Genetic Epidemiology</i> , 2020, 44, 854-867.	1.3	28
15	Cancer expression quantitative trait loci (eQTLs) can be determined from heterogeneous tumor gene expression data by modeling variation in tumor purity. <i>Genome Biology</i> , 2018, 19, 130.	8.8	27
16	A scalable unified framework of total and allele-specific counts for cis-QTL, fine-mapping, and prediction. <i>Nature Communications</i> , 2021, 12, 1424.	12.8	23
17	Imputed gene associations identify replicable <i>trans</i> -acting genes enriched in transcription pathways and complex traits. <i>Genetic Epidemiology</i> , 2019, 43, 596-608.	1.3	19
18	sn-spMF: matrix factorization informs tissue-specific genetic regulation of gene expression. <i>Genome Biology</i> , 2020, 21, 235.	8.8	18

#	ARTICLE	IF	CITATIONS
19	Functionally oriented analysis of cardiometabolic traits in a trans-ethnic sample. Human Molecular Genetics, 2019, 28, 1212-1224.	2.9	12
20	Pleiotropy-guided transcriptome imputation from normal and tumor tissues identifies candidate susceptibility genes for breast and ovarian cancer. Human Genetics and Genomics Advances, 2021, 2, 100042.	1.7	6
21	Generating A Database of Phenotypic Consequences of Gene Regulation Across 40 Human Tissues. European Neuropsychopharmacology, 2017, 27, S418.	0.7	0